

-1-

5

Date: <i>June 24, 2003</i>
EXPRESS MAIL LABEL NO. <u>EL 442001379 US</u>

10

Title Of The Invention

**NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
CANDIDA ALBICANS FOR DIAGNOSTICS AND THERAPEUTICS**

15

Cross-Reference to Related Applications

This application is converted from U.S. provisional application Serial Number
60/074,725, filed February 13, 1998 and U.S. provisional application Serial Number
20 60/096,409 filed August 13, 1998.

Field Of The Invention

The invention relates to isolated nucleic acids and polypeptides derived from
Candida albicans that are useful as molecular targets for diagnostics, prophylaxis and
25 treatment of pathological conditions, as well as materials and methods for the
diagnosis, prevention, and amelioration of pathological conditions resulting from
fungal infection.

Background Of The Invention

30 *Candida albicans* is a dimorphic fungus which has both a yeast-like growth
habit and a filamentous form consisting of both hyphae and pseudohyphae. The fungus
is a member of the normal surface flora of most individuals. Although no sexual state
has been described for *C. albicans*, the genome is diploid in most strains (Whelan,
WL et al. (1980) *Mol. Gen. Genet.* 180: 107-113; Whelan, WL and Magee, PT (1981)

J. Bacteriol. 145: 896-903; Poulter, R. (1982) *J. Bacteriol.* 152: 969-975) and rearranges relatively frequently (Rustchenko-Bulgac EP, et al (1990) *J Bacteriol.* 172: 1276-1283; Barton, RC and Scherer, S (1994) *J. Bacteriol.* 176: 756-763). In addition, one non-universal decoding is known in which a leucine codon (CUG) is translated as a serine (Leuker et al. (1994), *Mol. Gen. Genet.* 245: 212-217; Santos et al., (1993) *EMBO Journal* 12:607-616). This creates difficulties in the application of the powerful genetic and molecular methods used in *Saccharomyces* and *Schizosaccharomyces*.

C. albicans exists as part of the normal microbial flora in humans, but can produce opportunistic infections ranging from topical infections such as oral thrush to life-threatening disseminated mycoses (Ampel, NM (1996) *Emerg. Infect. Dis.* 2: 109-116). *Candida* is a major cause of nosocomial infections and was found to account for more than 75% of all fungal nosocomial infections reported by NNIS (National Nosocomial Infections Surveillance) hospitals from 1980-1990 in which fungi alone accounted for 7.9 % of all nosocomial infections (Beck-Sagu, CM and Jarvis, WR (1993) *J. Infect. Dis.* 167: 1247-1251). Although the source of *Candida* in infections is frequently traced to endogenous sources on the patient, it has also been traced to exogenous sources in the hospital environment including contaminated solutions and equipment (Shetertz, RJ et al. (1992) *J. Pediatr.* 120: 455-461; Weems, JJ et al. (1987) *J. Clin. Microbiol.* 1925: 1029-1032), and health care workers (Hunter, PR et al (1990) *J. Med Vet Mycol.* 28: 317-325; Burnie, JP (1986) *J. Hosp. Infect.* 8: 1-4; Doebbeling, BN et al. (1991) *J. Clin. Microbiol.* 29: 1268-1270). Numerous investigations into the molecular basis of pathogenicity have been made implicating the hyphal form (Lo, HJ et al. (1997) *Cell* 90:939-949), surface molecules including adhesins (Fukazawa Y and Kagaya K (1997) *J Med Vet Mycol* 35:87-99), and ATP-binding cassette-containing multi-drug resistance proteins (Prasad, R et al.(1995) *Curr. Genet.* 27: 320-329).

The antimicrobials currently in use against *Candida* are generally of three types: azoles, such as fluconazole, itraconazole, and clotrimazole; polyenes, such as amphotericin B and nystatin; and 5-fluorocytosine. However, invasive infections are treated primarily with fluconazole, amphotericin B, and 5-fluorocytosine, although the latter two compounds have significant toxic side effects. The development of resistance to fluconazole by *C. albicans* has been noted by a number of researchers

(Redding, S (1994) *Clin Infect. Dis.* 18: 339-346; Sargeorzan, JA (1994) *Am. J. Med.* 97: 339-346; Revankar, SG et al. (1996) *J. Infect. Dis.* 174: 821-827; Marr, KA et al. (1997) *Clin. Infect. Dis.* 25: 908-910). Relatively short treatments seem to result in few if any resistant isolates, but extended treatments including prophylactic
5 treatments such as are required among immunocompromised and AIDS patients, result in the appearance of fluconazole-resistant strains (Johnson, EM (1995) *J. Antimicrob. Chemother.* 35: 103-114). Development of fluconazole-resistance has been observed to be associated with the development of amphotericin-resistance (Vazquez, JA (1996) *Antimicrob. Agents Chemother.* 40: 2511-2516; Nolte, FS et al.
10 (1997) *Antimicrob. Agents Chemother.* 41: 196-199; White, TC (1997) *ASM News* 63: 427-433) consistent with the action of both drugs on ergosterol in the membrane.

The difficulty in diagnosing *C. albicans* infections, the limited spectrum of current therapeutic drugs and the development of drug resistant strains of *C. albicans* provide the rationale for the identification of targets for more rapid and effective
15 methods of identification, prevention, and treatment of candidiasis. The elucidation of the genome of *C. albicans* would enhance the understanding of how *C. albicans*, as well as other fungi, causes invasive disease and how best to combat fungal infection.

Summary Of The Invention

20 The present invention fulfills the need for diagnostic tools and therapeutics by providing fungal-specific compositions and methods for detecting, treating, and preventing fungal infection, in particular *C. albicans* infection. They also have use as biocontrol agents for plants.

The present invention encompasses isolated nucleic acids and polypeptides
25 derived from *C. albicans* that are useful as reagents for diagnosis of fungal disease, components of effective antifungal vaccines, and/or as targets for antifungal drugs including anti-*C. albicans* drugs. They can also be used to detect the presence of *C. albicans* and other *Candida* species in a sample; and in screening compounds for the ability to interfere with the *C. albicans* life cycle or to inhibit *C. albicans* infection.

30 More specifically, this invention features compositions of nucleic acids corresponding to entire coding sequences of *C. albicans* proteins, including surface or

secreted proteins or parts thereof, nucleic acids capable of binding mRNA from *C. albicans* proteins to block protein translation, and methods for producing *C. albicans* proteins or parts thereof using peptide synthesis and recombinant DNA techniques. This invention also features antibodies and nucleic acids useful as probes to detect *C. albicans* infection. In addition, vaccine compositions and methods for the protection or treatment of infection by *C. albicans* are within the scope of this invention.

The nucleotide sequences provided in SEQ ID NO: 1 - SEQ ID NO: 14103, a fragment thereof, or a nucleotide sequence at least about 99.5% identical to a sequence contained within SEQ ID NO: 1 - SEQ ID NO: 14103 may be "provided" in a variety of medias to facilitate use thereof. As used herein, "provided" refers to a manufacture, other than an isolated nucleic acid molecule, which contains a nucleotide sequence of the present invention, i.e., the nucleotide sequence provided in SEQ ID NO: 1 - SEQ ID NO: 14103, a fragment thereof, or a nucleotide sequence at least about 99.5% identical to a sequence contained within SEQ ID NO: 1 - SEQ ID NO: 14103. Uses for and methods for providing nucleotide sequences in a variety of media is well known in the art (see e.g., EPO Publication No. EP 0 756 006).

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any media which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage media, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A person skilled in the art can readily appreciate how any of the presently known computer readable media can be used to create a manufacture comprising computer readable media having recorded thereon a nucleotide sequence of the present invention.

As used herein, "recorded" refers to a process for storing information on computer readable media. A person skilled in the art can readily adopt any of the presently known methods for recording information on computer readable media to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a person skilled in the art for creating a computer readable media having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition,
5 a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable media. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as
10 DB2, Sybase, Oracle, or the like. A person skilled in the art can readily adapt any number of data processor structuring formats (e.g. text file or database) in order to obtain computer readable media having recorded thereon the nucleotide sequence information of the present invention.

By providing the nucleotide sequence of SEQ ID NO: 1 - SEQ ID NO: 14103,
15 a fragment thereof, or a nucleotide sequence at least about 99.5% identical to SEQ ID NO: 1 - SEQ ID NO: 14103 in computer readable form, a person skilled in the art can routinely access the coding sequence information for a variety of purposes. Computer software is publicly available which allows a person skilled in the art to access sequence information provided in a computer readable media. Examples of such
20 computer software include programs of the "Staden Package", "DNA Star", "MacVector", GCG "Wisconsin Package" (Genetics Computer Group, Madison, WI) and "NCBI Toolbox" (National Center For Biotechnology Information). Suitable programs are described, for example, in Martin J. Bishop, ed., *Guide to Human Genome Computing*, 2d Edition, Academic Press, San Diego, CA. (1998); and
25 Leonard F. Peruski, Jr., and Anne Harwood Peruski, *The Internet and the New Biology: Tools for Genomic and Molecular Research*, American Society for Microbiology, Washington, D.C. (1997).

Computer algorithms enable the identification of *C. albicans* open reading frames (ORFs) within SEQ ID NO: 1 - SEQ ID NO: 14103 which contain homology
30 to ORFs or proteins from other organisms. Examples of such similarity-search algorithms include the BLAST [Altschul et al., J. Mol. Biol. 215:403-410 (1990)] and Smith-Waterman [Smith and Waterman (1981) *Advances in Applied Mathematics*, 2:482-489] search algorithms. Suitable search algorithms are described, for example,

in Martin J. Bishop, ed., *Guide to Human Genome Computing*, 2d Edition, Academic Press, San Diego, CA. (1998); and Leonard F. Peruski, Jr., and Anne Harwood Peruski, *The Internet and the New Biology: Tools for Genomic and Molecular Research*, American Society for Microbiology, Washington, D.C. (1997). Such

5 algorithms are utilized on computer systems as exemplified below. The ORFs so identified represent protein encoding fragments within the *C. albicans* genome and are useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

The present invention further provides systems, particularly computer-based

10 systems, which contain the sequence information described herein. Such systems are designed to identify commercially important fragments of the *C. albicans* genome. As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based

15 systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A person skilled in the art can readily appreciate that any one of the currently available computer-based systems is suitable for use in the present invention. The computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the

20 present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

25 As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of the *C. albicans* genomewhich are similar to, or "match", a particular target sequence or target motif.

30 A variety of known algorithms are known in the art and have been disclosed publicly, and a variety of commercially available software for conducting homology-based

similarity searches are available and can be used in the computer-based systems of the present invention. Examples of such software include, but are not limited to, FASTA (GCG Wisconsin Package), Bic_SW (Compugen Bioccelerator), BLASTN2, BLASTP2, BLASTX2 (NCBI) and Motifs (GCG). Suitable software programs are

5 described, for example, in Martin J. Bishop, ed., *Guide to Human Genome Computing*, 2d Edition, Academic Press, San Diego, CA. (1998); and Leonard F. Peruski, Jr., and Anne Harwood Peruski, *The Internet and the New Biology: Tools for Genomic and Molecular Research*, American Society for Microbiology, Washington, D.C. (1997). A person skilled in the art will readily recognize that any

10 one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems.

As used herein, a "target sequence" can be any DNA or amino acid sequence of six or more nucleotides or two or more amino acids. A person skilled in the art can readily recognize that the longer a target sequence is, the less likely a target sequence

15 will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 100 amino acids or from about 30 to 300 nucleotide residues. However, it is well recognized that many genes are longer than 500 amino acids, or 1.5 kb in length, and that commercially important fragments of the *C. albicans* genome, such as sequence fragments involved in gene expression

20 and protein processing, will often be shorter than 30 nucleotides.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a specific functional domain or three-dimensional configuration which is formed upon the folding of the target polypeptide. There is a variety of target

25 motifs known in the art. Protein target motifs include, but are not limited to, enzymatic active sites, membrane-spanning regions, and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

A variety of structural formats for the input and output means can be used to

30 input and output the information in the computer-based systems of the present invention. A preferred format for an output means ranks fragments of the *C. albicans*

genome possessing varying degrees of homology to the target sequence or target motif. Such presentation provides a person skilled in the art with a ranking of sequences which contain various amounts of the target sequence or target motif and identifies the degree of homology contained in the identified fragment.

5 A variety of comparing means can be used to compare a target sequence or target motif with the data storage means to identify sequence fragments of the *C. albicans* genome. In the present examples, implementing software which implement the BLASTP2 and bic_SW algorithms (Altschul et al., J Mol. Biol. 215:403-410 (1990); Compugen Biocellator) was used to identify open reading frames within the
10 *C. albicans* genome. A person skilled in the art can readily recognize that any one of the publicly available homology search programs can be used as the search means for the computer- based systems of the present invention. Suitable programs are described, for example, in Martin J. Bishop, ed., *Guide to Human Genome Computing*, 2d Edition, Academic Press, San Diego, CA. (1998); and Leonard F.
15 Peruski, Jr., and Anne Harwood Peruski, *The Internet and the New Biology: Tools for Genomic and Molecular Research*, American Society for Microbiology, Washington, D.C. (1997).

 The invention features *C. albicans* polypeptides, preferably a substantially pure preparation of an *C. albicans* polypeptide, or a recombinant *C. albicans*
20 polypeptide. In preferred embodiments: the polypeptide has biological activity; the polypeptide has an amino acid sequence at least about 60%, 70%, 80%, 90%, 95%, 98%, or 99% identical to an amino acid sequence of the invention contained in the Sequence Listing, preferably it has about 65% sequence identity with an amino acid sequence of the invention contained in the Sequence Listing, and most preferably it
25 has about 92% to about 99% sequence identity with an amino acid sequence of the invention contained in the Sequence Listing; the polypeptide has an amino acid sequence essentially the same as an amino acid sequence of the invention contained in the Sequence Listing; the polypeptide is at least about 5, 10, 20, 50, 100, or 150
30 amino acid residues in length; the polypeptide includes at least about 5, preferably at least about 10, more preferably at least about 20, more preferably at least about 50, 100, or 150 contiguous amino acid residues of the invention contained in the

Sequence Listing. In yet another preferred embodiment, the amino acid sequence which differs in sequence identity by about 7% to about 8% from the *C. albicans* amino acid sequences of the invention contained in the Sequence Listing is also encompassed by the invention.

5 In preferred embodiments: the *C. albicans* polypeptide is encoded by a nucleic acid of the invention contained in the Sequence Listing, or by a nucleic acid having at least about 60%, 70%, 80%, 90%, 95%, 98%, or 99% homology with a nucleic acid of the invention contained in the Sequence Listing.

10 In a preferred embodiment, the subject *C. albicans* polypeptide differs in amino acid sequence at about 1, 2, 3, 5, 10 or more residues from a sequence of the invention contained in the Sequence Listing. The differences, however, are such that the *C. albicans* polypeptide exhibits an *C. albicans* biological activity, e.g., the *C. albicans* polypeptide retains a biological activity of a naturally occurring *C. albicans* enzyme.

15 In preferred embodiments, the polypeptide includes all or a fragment of an amino acid sequence of the invention contained in the Sequence Listing; fused, in reading frame, to additional amino acid residues, preferably to residues encoded by genomic DNA 5' or 3' to the genomic DNA which encodes a sequence of the invention contained in the Sequence Listing.

20 In yet other preferred embodiments, the *C. albicans* polypeptide is a recombinant fusion protein having a first *C. albicans* polypeptide portion and a second polypeptide portion, e.g., a second polypeptide portion having an amino acid sequence unrelated to *C. albicans*. The second polypeptide portion can be, e.g., any of glutathione-S-transferase, a DNA binding domain, or a polymerase activating
25 domain. In preferred embodiment the fusion protein can be used in a two-hybrid assay.

Polypeptides of the invention include those which arise as a result of alternative transcription events, alternative RNA splicing events, and alternative translational and postranslational events.

30 In a preferred embodiment, the encoded *C. albicans* polypeptide differs (e.g., by amino acid substitution, addition or deletion of at least one amino acid residue) in

amino acid sequence at about 1, 2, 3, 5, 10 or more residues, from a sequence of the invention contained in the Sequence Listing. The differences, however, are such that: the *C. albicans* encoded polypeptide exhibits a *C. albicans* biological activity, e.g., the encoded *C. albicans* enzyme retains a biological activity of a naturally occurring

5 *C. albicans*.

In preferred embodiments, the encoded polypeptide includes all or a fragment of an amino acid sequence of the invention contained in the Sequence Listing; fused, in reading frame, to additional amino acid residues, preferably to residues encoded by genomic DNA 5' or 3' to the genomic DNA which encodes a sequence of the

10 invention contained in the Sequence Listing.

The *C. albicans* strain from which the nucleotide sequences have been sequenced is strain SC5314, a clinical isolate which was originally obtained from a patient with disseminated candidiasis.

Included in the invention are: allelic variations; natural mutants; induced
15 mutants; proteins encoded by DNA that hybridize under high or low stringency conditions to a nucleic acid which encodes a polypeptide of the invention contained in the Sequence Listing (for definitions of high and low stringency see Current Protocols in Molecular Biology, John Wiley & Sons, New York, 1989, 6.3.1 - 6.3.6, hereby incorporated by reference); and, polypeptides specifically bound by antisera to *C.*
20 *albicans* polypeptides, especially by antisera to an active site or binding domain of *C. albicans* polypeptide. The invention also includes fragments, preferably biologically active fragments. These and other polypeptides are also referred to herein as *C. albicans* polypeptide analogs or variants.

The invention further provides nucleic acids, e.g., RNA or DNA, encoding a
25 polypeptide of the invention. This includes double stranded nucleic acids as well as coding and antisense single strands.

In preferred embodiments, the subject *C. albicans* nucleic acid will include a transcriptional regulatory sequence, e.g. at least one of a transcriptional promoter or transcriptional enhancer sequence, operably linked to the *C. albicans* gene sequence,
30 e.g., to render the *C. albicans* gene sequence suitable for expression in a recombinant host cell.

In yet a further preferred embodiment, the nucleic acid which encodes an *C. albicans* polypeptide of the invention, hybridizes under stringent conditions to a nucleic acid probe corresponding to at least about 8 consecutive nucleotides of the invention contained in the Sequence Listing; more preferably to at least about 12
5 consecutive nucleotides of the invention contained in the Sequence Listing; more preferably to at least about 20 consecutive nucleotides of the invention contained in the Sequence Listing; more preferably to at least about 40 consecutive nucleotides of the invention contained in the Sequence Listing.

In another aspect, the invention provides a substantially pure nucleic acid
10 having a nucleotide sequence which encodes an *C. albicans* polypeptide. In preferred embodiments: the encoded polypeptide has biological activity; the encoded polypeptide has an amino acid sequence at least about 60%, 70%, 80%, 90%, 95%, 98%, or 99% homologous to an amino acid sequence of the invention contained in the Sequence Listing; the encoded polypeptide has an amino acid sequence essentially the
15 same as an amino acid sequence of the invention contained in the Sequence Listing; the encoded polypeptide is at least about 5, 10, 20, 50, 100, or 150 amino acids in length; the encoded polypeptide comprises at least about 5, preferably at least about 10, more preferably at least about 20, more preferably at least about 50, 100, or 150 contiguous amino acids of the invention contained in the Sequence Listing.

20 In another aspect, the invention encompasses: a vector including a nucleic acid which encodes an *C. albicans* polypeptide or an *C. albicans* polypeptide variant as described herein; a host cell transfected with the vector; and a method of producing a recombinant *C. albicans* polypeptide or *C. albicans* polypeptide variant; including culturing the cell, e.g., in a cell culture medium, and isolating an *C. albicans* or *C.*
25 *albicans* polypeptide variant, e.g., from the cell or from the cell culture medium.

One embodiment of the invention is directed to substantially isolated nucleic acids. Nucleic acids of the invention include sequences comprising at least about 8 nucleotides in length, more preferably at least about 12 nucleotides in length, even more preferably at least about 15-20 nucleotides in length, that correspond to a
30 subsequence of any one of SEQ ID NO: 1 - SEQ ID NO: 14103 or complements thereof. Alternatively, the nucleic acids comprise sequences contained within any ORF (open reading frame), including a complete protein-coding sequence, of which any of SEQ ID NO: 1 - SEQ ID NO: 14103 forms a part. The invention encompasses

sequence-conservative variants and function-conservative variants of these sequences.

The nucleic acids may be DNA, RNA, DNA/RNA duplexes, protein-nucleic acid (PNA), or derivatives thereof.

In another aspect, the invention features, a purified recombinant nucleic acid
5 having at least about 50%, 60%, 70%, 80%, 90%, 95%, 98%, or 99% homology with
a sequence of the invention contained in the Sequence Listing

The invention also encompasses recombinant DNA (including DNA cloning
and expression vectors) comprising these *C. albicans*-derived sequences; host cells
comprising such DNA, including fungal, bacterial, yeast, plant, insect, and
10 mammalian host cells; and methods for producing expression products comprising
RNA and polypeptides encoded by the *C. albicans* sequences. These methods are
carried out by incubating a host cell comprising a *C. albicans*-derived nucleic acid
sequence under conditions in which the sequence is expressed. The host cell may be
native or recombinant. The polypeptides can be obtained by (a) harvesting the
15 incubated cells to produce a cell fraction and a medium fraction; and (b) recovering
the *C. albicans* polypeptide from the cell fraction, the medium fraction, or both. The
polypeptides can also be made by *in vitro* translation.

In another aspect, the invention features nucleic acids capable of binding
mRNA of *C. albicans*. Such nucleic acid is capable of acting as antisense nucleic
20 acid to control the translation of mRNA of *C. albicans*. A further aspect features a
nucleic acid which is capable of binding specifically to a *C. albicans* nucleic acid.
These nucleic acids are also referred to herein as complements and have utility as
probes and as capture reagents.

In another aspect, the invention features an expression system comprising an
25 open reading frame corresponding to *C. albicans* nucleic acid. The nucleic acid
further comprises a control sequence compatible with an intended host. The
expression system is useful for making polypeptides corresponding to *C. albicans*
nucleic acid.

In another aspect, the invention encompasses: a vector including a nucleic acid
30 which encodes a *C. albicans* polypeptide or a *C. albicans* polypeptide variant as
described herein; a host cell transfected with the vector; and a method of producing a

recombinant *C. albicans* polypeptide or *C. albicans* polypeptide variant; including culturing the cell, e.g., in a cell culture medium, and isolating the *C. albicans* or *C. albicans* polypeptide variant, e.g., from the cell or from the cell culture medium.

5 In yet another embodiment of the invention encompasses reagents for detecting fungal infection, including *C. albicans* infection, which comprise at least one *C. albicans*-derived nucleic acid defined by any one of SEQ ID NO: 1 - SEQ ID NO: 14103, or sequence-conservative or function-conservative variants thereof. Alternatively, the diagnostic reagents comprise polypeptide sequences that are contained within any open reading frames (ORFs), including complete protein-coding
10 sequences, contained within any of SEQ ID NO: 1 - SEQ ID NO: 14103, or polypeptide sequences contained within any of SEQ ID NO: 14104 - SEQ ID NO: 28206, or polypeptides of which any of the above sequences forms a part, or antibodies directed against any of the above peptide sequences or function-conservative variants and/or fragments thereof.

15 The invention further provides antibodies, preferably monoclonal antibodies, which specifically bind to the polypeptides of the invention. Methods are also provided for producing antibodies in a host animal. The methods of the invention comprise immunizing an animal with at least one *C. albicans*-derived immunogenic component, wherein the immunogenic component comprises one or more of the
20 polypeptides encoded by any one of SEQ ID NO: 1 - SEQ ID NO: 14103 or sequence-conservative or function-conservative variants thereof; or polypeptides that are contained within any ORFs, including complete protein-coding sequences, of which any of SEQ ID NO: 1 - SEQ ID NO: 14103 forms a part; or polypeptide sequences contained within any of SEQ ID NO: 14104 - SEQ ID NO: 28206; or
25 polypeptides of which any of SEQ ID NO: 14104 - SEQ ID NO: 28206 forms a part. Host animals include any warm blooded animal, including without limitation mammals and birds. Such antibodies have utility as reagents for immunoassays to evaluate the abundance and distribution of *C. albicans*-specific antigens.

In yet another aspect, the invention provides diagnostic methods for detecting
30 *C. albicans* antigenic components or anti-*C. albicans* antibodies in a sample. *C. albicans* antigenic components are detected by a process comprising: (i) contacting a

sample suspected to contain a fungal antigenic component with a fungal-specific antibody, under conditions in which a stable antigen-antibody complex can form between the antibody and fungal antigenic components in the sample; and (ii) detecting any antigen-antibody complex formed in step (i), wherein detection of an antigen-antibody complex indicates the presence of at least one fungal antigenic component in the sample. In different embodiments of this method, the antibodies used are directed against a sequence encoded by any of SEQ ID NO: 1 - SEQ ID NO: 14103 or sequence-conservative or function-conservative variants thereof, or against a polypeptide sequence contained in any of SEQ ID NO: 14104 - SEQ ID NO: 28206 or function-conservative variants thereof.

In yet another aspect, the invention provides a method for detecting antifungal-specific antibodies in a sample, which comprises: (i) contacting a sample suspected to contain antifungal-specific antibodies with a *C. albicans* antigenic component, under conditions in which a stable antigen-antibody complex can form between the *C. albicans* antigenic component and antifungal antibodies in the sample; and (ii) detecting any antigen-antibody complex formed in step (i), wherein detection of an antigen-antibody complex indicates the presence of antifungal antibodies in the sample. In different embodiments of this method, the antigenic component is encoded by a sequence contained in any of SEQ ID NO: 1 - SEQ ID NO: 14103 or sequence-conservative and function-conservative variants thereof, or is a polypeptide sequence contained in any of SEQ ID NO: 14104 - SEQ ID NO: 28206 or function-conservative variants thereof.

In another aspect, the invention features a method of generating vaccines for immunizing an individual against *C. albicans*. The method includes: immunizing a subject with a *C. albicans* polypeptide, e.g., a surface or secreted polypeptide, or a combination of such peptides or active portion(s) thereof, and a pharmaceutically acceptable carrier. Such vaccines have therapeutic and prophylactic utilities.

In another aspect, the invention features a method of evaluating a compound, e.g. a polypeptide, e.g., a fragment of a host cell polypeptide, for the ability to bind a *C. albicans* polypeptide. The method includes: contacting the candidate compound with a *C. albicans* polypeptide and determining if the compound binds or otherwise

interacts with an *C. albicans* polypeptide. Compounds which bind *C. albicans* are candidates as activators or inhibitors of the fungal life cycle. These assays can be performed *in vitro* or *in vivo*.

5 In another aspect, the invention features a method of evaluating a compound, e.g. a polypeptide, e.g., a fragment of a host cell polypeptide, for the ability to bind an *C. albicans* nucleic acid, e.g., DNA or RNA. The method includes: contacting the candidate compound with a *C. albicans* nucleic acid and determining if the compound binds or otherwise interacts with a *C. albicans* polypeptide. Compounds which bind *C. albicans* are candidates as activators or inhibitors of the fungal life cycle. These
10 assays can be performed *in vitro* or *in vivo*.

A particularly preferred embodiment of the invention is directed to a method of screening test compounds for anti-fungal activity, which method comprises: selecting as a target a fungal specific sequence, which sequence is essential to the viability of a fungal species; contacting a test compound with said target sequence;
15 and selecting those test compounds which bind to said target sequence as potential anti-fungal candidates. In one embodiment, the target sequence selected is specific to a single species, or even a single strain, i.e., the *C. albicans* strain SC5314. In a second embodiment, the target sequence is common to at least two species of fungi. In a third embodiment, the target sequence is common to a family of fungi. The target
20 sequence may be a nucleic acid sequence or a polypeptide sequence. Methods employing sequences common to more than one species of microorganism may be used to screen candidates for broad spectrum anti-fungal activity.

The invention also provides methods for preventing or treating disease caused by certain fungi, including *C. albicans*, which are carried out by administering to an
25 animal in need of such treatment, in particular a warm-blooded vertebrate, including but not limited to birds and mammals, a compound that specifically inhibits or interferes with the function of a fungal polypeptide or nucleic acid. In a particularly preferred embodiment, the mammal to be treated is human.

30 DETAILED DESCRIPTION OF THE INVENTION

The sequences of the present invention include the specific nucleic acid and

amino acid sequences set forth in the Sequence Listing that forms a part of the present specification, and which are designated SEQ ID NO: 1 - SEQ ID NO: 28206. Use of the terms "SEQ ID NO: 1 - SEQ ID NO: 14103 ", "SEQ ID NO: 14104 - SEQ ID NO: 28206 " the sequences depicted in Table 2", and like terms, is intended, for

5 convenience, to refer to each individual SEQ ID NO *individually*, and is not intended to refer to the genus of these sequences unless such reference would be indicated. In other words, it is a shorthand for listing all of these sequences individually. The invention encompasses each sequence individually, as well as any combination thereof.

10

Definitions

"Nucleic acid" or "polynucleotide" as used herein refers to purine- and pyrimidine-containing polymers of any length, either polyribonucleotides or polydeoxyribonucleotides or mixed polyribo-polydeoxyribo nucleotides. This
15 includes single- and double-stranded molecules, i.e., DNA-DNA, DNA-RNA and RNA-RNA hybrids, as well as "protein nucleic acids" (PNA) formed by conjugating bases to an amino acid backbone. This also includes nucleic acids containing modified bases.

A nucleic acid or polypeptide sequence that is "derived from" a designated
20 sequence refers to a sequence that corresponds to a region of the designated sequence. For nucleic acid sequences, this encompasses sequences that are homologous or complementary to the sequence, as well as "sequence-conservative variants" and "function-conservative variants." For polypeptide sequences, this encompasses "function-conservative variants." Sequence-conservative variants are those in which
25 a change of one or more nucleotides in a given codon position results in no alteration in the amino acid encoded at that position. Function-conservative variants are those in which a given amino acid residue in a polypeptide has been changed without altering the overall conformation and function of the native polypeptide, including, but not limited to, replacement of an amino acid with one having similar physico-
30 chemical properties (such as, for example, acidic, basic, hydrophobic, and the like). "Function-conservative" variants also include any polypeptides that have the ability to

elicit antibodies specific to a designated polypeptide.

An "*C. albicans*-derived" nucleic acid or polypeptide sequence may or may not be present in other fungal species, and may or may not be present in all *C. albicans* strains. This term is intended to refer to the source from which the sequence was originally isolated. Thus, a *C. albicans*-derived polypeptide, as used herein, may be used, e.g., as a target to screen for a broad spectrum antifungal agent, to search for homologous proteins in other species of fungi or in eukaryotic organisms such as humans, etc.

A purified or isolated polypeptide or a substantially pure preparation of a polypeptide are used interchangeably herein and, as used herein, mean a polypeptide that has been separated from other proteins, lipids, and nucleic acids with which it naturally occurs. Preferably, the polypeptide is also separated from substances, e.g., antibodies or gel matrix, e.g., polyacrylamide, which are used to purify it. Preferably, the polypeptide constitutes at least about 10, 20, 50 70, 80 or 95% dry weight of the purified preparation. Preferably, the preparation contains sufficient polypeptide to allow protein sequencing, which is preferably at least about 1, 10, or 100 mg of the polypeptide.

A purified preparation of cells refers to, in the case of plant or animal cells, an *in vitro* preparation of cells and not an entire intact plant or animal. In the case of cultured cells or microbial cells, it consists of a preparation of at least about 10% and more preferably at least about 50% of the subject cells.

A purified or isolated or a substantially pure nucleic acid, e.g., a substantially pure DNA, (are terms used interchangeably herein) is a nucleic acid which is one or both of the following: not immediately contiguous with both of the coding sequences with which it is immediately contiguous (i.e., one at the 5' end and one at the 3' end) in the naturally-occurring genome of the organism from which the nucleic acid is derived; or which is substantially free of a nucleic acid with which it occurs in the organism from which the nucleic acid is derived. The term includes, for example, a recombinant DNA which is incorporated into a vector, e.g., into an autonomously replicating plasmid or virus, or into the genomic DNA of a prokaryote or eukaryote, or which exists as a separate molecule (e.g., a cDNA or a genomic DNA fragment

produced by PCR or restriction endonuclease treatment) independent of other DNA sequences. Substantially pure DNA also includes a recombinant DNA which is part of a hybrid gene encoding additional *C. albicans* DNA sequence.

5 A "contig" as used herein is a nucleic acid representing a continuous stretch of genomic sequence of an organism.

An "open reading frame", also referred to herein as ORF, is a region of nucleic acid which encodes a polypeptide. This region may represent a portion of a coding sequence or a total sequence and can be determined from a stop to stop codon or from a start to stop codon.

10 As used herein, a "coding sequence" is a nucleic acid which is transcribed into messenger RNA and/or translated into a polypeptide when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a translation start codon at the five prime terminus and a translation stop code at the three prime terminus. A coding sequence can include but is not
15 limited to messenger RNA, synthetic DNA, and recombinant nucleic acid sequences.

A "complement" of a nucleic acid as used herein refers to an anti-parallel or antisense sequence that participates in Watson-Crick base-pairing with the original sequence.

20 A "gene product" is a protein or structural RNA which is specifically encoded by a gene.

As used herein, the term "probe" refers to a nucleic acid, peptide or other chemical entity which specifically binds to a molecule of interest. Probes are often associated with or capable of associating with a label. A label is a chemical moiety capable of detection. Typical labels comprise dyes, radioisotopes, luminescent and
25 chemiluminescent moieties, fluorophores, enzymes, precipitating agents, amplification sequences, and the like. Similarly, a nucleic acid, peptide or other chemical entity which specifically binds to a molecule of interest and immobilizes such molecule is referred herein as a "capture ligand". Capture ligands are typically associated with or capable of associating with a support such as nitro-cellulose, glass,
30 nylon membranes, beads, particles and the like. The specificity of hybridization is dependent on conditions such as the base pair composition of the nucleotides, and the

temperature and salt concentration of the reaction. These conditions are readily discernable to one of ordinary skill in the art using routine experimentation.

“Homologous” refers to the sequence similarity or sequence identity between two polypeptides or between two nucleic acid molecules. When a position in both of the two compared sequences is occupied by the same base or amino acid monomer subunit, e.g., if a position in each of two DNA molecules is occupied by adenine, then the molecules are homologous at that position. The percent of homology between two sequences is a function of the number of matching or homologous positions shared by the two sequences divided by the number of positions compared x 100. For example, if 6 of 10 of the positions in two sequences are matched or homologous then the two sequences are 60% homologous. By way of example, the DNA sequences ATTGCC and TATGGC share 50% homology. Generally, a comparison is made when two sequences are aligned to give maximum homology.

Nucleic acids are hybridizable to each other when at least one strand of a nucleic acid can anneal to the other nucleic acid under defined stringency conditions. Stringency of hybridization is determined by: (a) the temperature at which hybridization and/or washing is performed; and (b) the ionic strength and polarity of the hybridization and washing solutions. Hybridization requires that the two nucleic acids contain complementary sequences; depending on the stringency of hybridization, however, mismatches may be tolerated. Typically, hybridization of two sequences at high stringency (such as, for example, in a solution of 0.5X SSC, at 65° C) requires that the sequences be essentially completely homologous. Conditions of intermediate stringency (such as, for example, 2X SSC at 65 ° C) and low stringency (such as, for example 2X SSC at 55° C), require correspondingly less overall complementarity between the hybridizing sequences. (1X SSC is 0.15 M NaCl, 0.015 M Na citrate).

The terms peptides, proteins, and polypeptides are used interchangeably herein.

As used herein, the term "surface protein" refers to all surface accessible proteins, e.g. inner and outer membrane proteins, proteins adhering to the cell wall, and secreted proteins.

A polypeptide has *C. albicans* biological activity if it has one, two and preferably more of the following properties: (1) if when expressed in the course of a *C. albicans* infection, it can promote, or mediate the attachment of *C. albicans* to a cell; (2) it has an enzymatic activity, structural or regulatory function characteristic of a *C. albicans* protein; (3) or the gene which encodes it can rescue a lethal mutation in a *C. albicans* gene. A polypeptide has biological activity if it is an antagonist, agonist, or super-agonist of a polypeptide having one of the above-listed properties.

A biologically active fragment or analog is one having an *in vivo* or *in vitro* activity which is characteristic of the *C. albicans* polypeptides of the invention contained in the Sequence Listing, or of other naturally occurring *C. albicans* polypeptides, e.g., one or more of the biological activities described herein. Especially preferred are fragments which exist *in vivo*, e.g., fragments which arise from post transcriptional processing or which arise from translation of alternatively spliced RNA's. Fragments include those expressed in native or endogenous cells as well as those made in expression systems, e.g., in CHO (Chinese Hamster Ovary) cells. Because peptides such as *C. albicans* polypeptides often exhibit a range of physiological properties and because such properties may be attributable to different portions of the molecule, a useful *C. albicans* fragment or *C. albicans* analog is one which exhibits a biological activity in any biological assay for *C. albicans* activity. Most preferably the fragment or analog possesses 10%, preferably 40%, more preferably 60%, 70%, 80% or 90% or greater of the activity of *C. albicans*, in any *in vivo* or *in vitro* assay.

Analogous can differ from naturally occurring *C. albicans* polypeptides in amino acid sequence or in ways that do not involve sequence, or both. Non-sequence modifications include changes in acetylation, methylation, phosphorylation, carboxylation, or glycosylation. Preferred analogs include *C. albicans* polypeptides (or biologically active fragments thereof) whose sequences differ from the wild-type sequence by one or more conservative amino acid substitutions or by one or more non-conservative amino acid substitutions, deletions, or insertions which do not substantially diminish the biological activity of the *C. albicans* polypeptide. Conservative substitutions typically include the substitution of one amino acid for

another with similar characteristics, e.g., substitutions within the following groups: valine, glycine; glycine, alanine; valine, isoleucine, leucine; aspartic acid, glutamic acid; asparagine, glutamine; serine, threonine; lysine, arginine; and phenylalanine, tyrosine. Other conservative substitutions can be made in view of the table below.

5 TABLE 1

CONSERVATIVE AMINO ACID REPLACEMENTS

For Amino Acid	Code	Replace with any of
Alanine	A	D-Ala, Gly, beta-Ala, L-Cys, D-Cys
Arginine	R	D-Arg, Lys, D-Lys, homo-Arg, D-homo-Arg, Met, Ile, D-Met, D-Ile, Orn, D-Orn
Asparagine	N	D-Asn, Asp, D-Asp, Glu, D-Glu, Gln, D-Gln
Aspartic Acid	D	D-Asp, D-Asn, Asn, Glu, D-Glu, Gln, D-Gln
Cysteine	C	D-Cys, S-Me-Cys, Met, D-Met, Thr, D-Thr
Glutamine	Q	D-Gln, Asn, D-Asn, Glu, D-Glu, Asp, D-Asp
Glutamic Acid	E	D-Glu, D-Asp, Asp, Asn, D-Asn, Gln, D-Gln
Glycine	G	Ala, D-Ala, Pro, D-Pro, β -Ala, Acp
Isoleucine	I	D-Ile, Val, D-Val, Leu, D-Leu, Met, D-Met
Leucine	L	D-Leu, Val, D-Val, Leu, D-Leu, Met, D-Met
Lysine	K	D-Lys, Arg, D-Arg, homo-Arg, D-homo-Arg, Met, D-Met, Ile, D-Ile, Orn, D-Orn
Methionine	M	D-Met, S-Me-Cys, Ile, D-Ile, Leu, D-Leu, Val, D-Val
Phenylalanine	F	D-Phe, Tyr, D-Thr, L-Dopa, His, D-His, Trp, D-Trp, Trans-3,4, or 5-phenylproline, cis-3,4, or 5-phenylproline
Proline	P	D-Pro, L-I-thiazolidine-4-carboxylic acid, D-or L-I-oxazolidine-4-carboxylic acid
Serine	S	D-Ser, Thr, D-Thr, allo-Thr, Met, D-Met, Met(O), D-Met(O), L-Cys, D-Cys
Threonine	T	D-Thr, Ser, D-Ser, allo-Thr, Met, D-Met, Met(O), D-Met(O), Val, D-Val
Tyrosine	Y	D-Tyr, Phe, D-Phe, L-Dopa, His, D-His
Valine	V	D-Val, Leu, D-Leu, Ile, D-Ile, Met, D-Met

Other analogs within the invention are those with modifications which increase peptide stability; such analogs may contain, for example, one or more non-

peptide bonds (which replace the peptide bonds) in the peptide sequence. Also included are: analogs that include residues other than naturally occurring L-amino acids, e.g., D-amino acids or non-naturally occurring or synthetic amino acids, e.g., β or γ amino acids; and cyclic analogs.

5 As used herein, the term "fragment", as applied to a *C. albicans* analog, will ordinarily be at least about 20 residues, more typically at least about 40 residues, preferably at least about 60 residues in length. Fragments of *C. albicans* polypeptides can be generated by methods known to those skilled in the art. The ability of a candidate fragment to exhibit a biological activity of *C. albicans* polypeptide can be
10 assessed by methods known to those skilled in the art as described herein. Also included are *C. albicans* polypeptides containing residues that are not required for biological activity of the peptide or that result from alternative mRNA splicing or alternative protein processing events.

 An "immunogenic component" as used herein is a moiety, such as a *C.*
15 *albicans* polypeptide, analog or fragment thereof, that is capable of eliciting a humoral and/or cellular immune response in a host animal.

 An "antigenic component" as used herein is a moiety, such as a *C. albicans* polypeptide, analog or fragment thereof, that is capable of binding to a specific antibody with sufficiently high affinity to form a detectable antigen-antibody
20 complex.

 The term "antibody" as used herein is intended to include fragments thereof which are specifically reactive with *C. albicans* polypeptides.

 As used herein, the term "cell-specific promoter" means a DNA sequence that serves as a promoter, i.e., regulates expression of a selected DNA sequence operably
25 linked to the promoter, and which effects expression of the selected DNA sequence in specific cells of a tissue. The term also covers so-called "leaky" promoters, which regulate expression of a selected DNA primarily in one tissue, but cause expression in other tissues as well.

 Misexpression, as used herein, refers to a non-wild type pattern of gene
30 expression. It includes: expression at non-wild type levels, i.e., over or under expression; a pattern of expression that differs from wild type in terms of the time or

stage at which the gene is expressed, e.g., increased or decreased expression (as compared with wild type) at a predetermined developmental period or stage; a pattern of expression that differs from wild type in terms of increased expression (as compared with wild type) in a predetermined cell type or tissue type; a pattern of expression that differs from wild type in terms of the splicing size, amino acid sequence, post-translational modification, or biological activity of the expressed polypeptide; a pattern of expression that differs from wild type in terms of the effect of an environmental stimulus or extracellular stimulus on expression of the gene, e.g., a pattern of increased or decreased expression (as compared with wild type) in the presence of an increase or decrease in the strength of the stimulus.

As used herein, "host cells" and other such terms denoting microorganisms or higher eukaryotic cell lines cultured as unicellular entities refers to cells which can become or have been used as recipients for a recombinant vector or other transfer DNA, and include the progeny of the original cell which has been transfected. It is understood by individuals skilled in the art that the progeny of a single parental cell may not necessarily be completely identical in genomic or total DNA compliment to the original parent, due to accident or deliberate mutation.

As used herein, the term "control sequence" refers to a nucleic acid having a base sequence which is recognized by the host organism to effect the expression of encoded sequences to which they are ligated. The nature of such control sequences differs depending upon the host organism; in prokaryotes, such control sequences generally include a promoter, ribosomal binding site, terminators, and in some cases operators; in eukaryotes, generally such control sequences include promoters, terminators and in some instances, enhancers. The term control sequence is intended to include at a minimum, all components whose presence is necessary for expression, and may also include additional components whose presence is advantageous, for example, leader sequences.

As used herein, the term "operably linked" refers to sequences joined or ligated to function in their intended manner. For example, a control sequence is operably linked to coding sequence by ligation in such a way that expression of the coding sequence is achieved under conditions compatible with the control sequence

and host cell.

The "metabolism" of a substance, as used herein, means any aspect of the expression, function, action, or regulation of the substance. The metabolism of a substance includes modifications, e.g., covalent or non-covalent modifications of the substance. The metabolism of a substance includes modifications, e.g., covalent or non-covalent modification, the substance induces in other substances. The metabolism of a substance also includes changes in the distribution of the substance. The metabolism of a substance includes changes the substance induces in the distribution of other substances.

A "sample" as used herein refers to a biological sample, such as, for example, tissue or fluid isolated from an individual (including without limitation plasma, serum, cerebrospinal fluid, lymph, tears, saliva and tissue sections) or from *in vitro* cell culture constituents, as well as samples from the environment.

Technical and scientific terms used herein have the meanings commonly understood by one of ordinary skill in the art to which the present invention pertains, unless otherwise defined. Reference is made herein to various methodologies known to those of skill in the art. Publications and other materials setting forth such known methodologies to which reference is made are incorporated herein by reference in their entireties as though set forth in full. The practice of the invention will employ, unless otherwise indicated, conventional techniques of chemistry, molecular biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. *See e.g.*, Sambrook, Fritsch, and Maniatis, *Molecular Cloning; Laboratory Manual* 2nd ed. (1989); *DNA Cloning*, Volumes I and II (D.N Glover ed. 1985); *Oligonucleotide Synthesis* (M.J. Gait ed, 1984); *Nucleic Acid Hybridization* (B.D. Hames & S.J. Higgins eds. 1984); the series, *Methods in Enzymology* (Academic Press, Inc.), particularly Vol. 154 and Vol. 155 (Wu and Grossman, eds.); *PCR-A Practical Approach* (McPherson, Quirke, and Taylor, eds., 1991); *Immunology*, 2d Edition, 1989, Roitt *et al.*, C.V. Mosby Company, and New York; *Advanced Immunology*, 2d Edition, 1991, Male *et al.*, Grower Medical Publishing, New York.; *DNA Cloning: A Practical Approach*, Volumes I and II, 1985 (D.N. Glover ed.); *Oligonucleotide Synthesis*, 1984, (M.L.

Gait ed); *Transcription and Translation*, 1984 (Hames and Higgins eds.); *Animal Cell Culture*, 1986 (R.I. Freshney ed.); *Immobilized Cells and Enzymes*, 1986 (IRL Press); Perbal, 1984, *A Practical Guide to Molecular Cloning*; *Gene Transfer Vectors for Mammalian Cells*, 1987 (J. H. Miller and M. P. Calos eds., Cold Spring Harbor Laboratory); Martin J. Bishop, ed., *Guide to Human Genome Computing*, 2d Edition, Academic Press, San Diego, CA. (1998); and Leonard F. Peruski, Jr., and Anne Harwood Peruski, *The Internet and the New Biology: Tools for Genomic and Molecular Research*, American Society for Microbiology, Washington, D.C. (1997).

Any suitable materials and/or methods known to those of skill can be utilized in carrying out the present invention: however preferred materials and/or methods are described. Materials, reagents and the like to which reference is made in the following description and examples are obtainable from commercial sources, unless otherwise noted.

15 C. albicans Genomic Sequence

This invention provides nucleotide sequences of the genome of *C. albicans*, strain SC5314, which thus comprises a DNA sequence library of *C. albicans* genomic DNA. The detailed description that follows provides nucleotide sequences of *C. albicans*, and also describes how the sequences were obtained and how ORFs and protein-coding sequences can be identified. Also described are methods of using the disclosed *C. albicans* sequences in methods including diagnostic and therapeutic applications. Furthermore, the library can be used as a database for identification and comparison of medically important sequences in this and other strains of *C. albicans*.

To determine the genomic sequence of *C. albicans*, DNA from strain SC5314 of *C. albicans* was isolated after Zymolyase digestion, sodium dodecyl sulfate lysis, potassium acetate precipitation, phenol:chloroform extraction and ethanol precipitation (Soll, D.R., T. Srikantha and S.R. Lockhart: Characterizing Developmentally Regulated Genes in *C. albicans*, In *Microbial Genome Methods*, K.W. Adolph, editor. CRC Press. New York. p 17-37.). DNA was sheared hydrodynamically using an HPLC (Oefner, et. al., 1996) to an insert size of 2000-3000 bp. After size fractionation by gel electrophoresis the fragments were blunt-ended, ligated to adapter

oligonucleotides and cloned into the pGTC (Thomann) vector to construct a "shotgun" subclone library.

DNA sequencing was achieved using established ABI sequencing methods on ABI377 automated DNA sequencers. The cloning and sequencing procedures are
5 described in more detail in the Exemplification.

Individual sequence reads were assembled using PHRAP (P. Green, Abstracts of DOE Human Genome Program Contractor-Grantee Workshop V, Jan. 1996, p.157). The average contig length was about 3-4 kb.

All subsequent steps were based on sequencing by ABI377 automated DNA
10 sequencing methods. The cloning and sequencing procedures are described in more detail in the Exemplification.

A variety of approaches is used to order the contigs so as to obtain a continuous sequence representing the entire *C. albicans* genome. Synthetic oligonucleotides are designed that are complementary to sequences at the end of each
15 contig. These oligonucleotides may be hybridized to libraries of *C. albicans* genomic DNA in, for example, lambda phage vectors or plasmid vectors to identify clones that contain sequences corresponding to the junctional regions between individual contigs. Such clones are then used to isolate template DNA and the same oligonucleotides are used as primers in polymerase chain reaction (PCR) to amplify junctional fragments,
20 the nucleotide sequence of which is then determined.

The *C. albicans* sequences were analyzed for the presence of open reading frames (ORFs) comprising at least about 180 nucleotides. As a result of the analysis of ORFs based on stop-to-stop codon reads, it should be understood that these ORFs may not correspond to the ORF of a naturally-occurring *C. albicans* polypeptide.
25 These ORFs may contain start codons which indicate the initiation of protein synthesis of a naturally-occurring *C. albicans* polypeptide. Such start codons within the ORFs provided herein can be identified by those of ordinary skill in the relevant art, and the resulting ORF and the encoded *C. albicans* polypeptide is within the scope of this invention. For example, within the ORFs a codon such as AUG or GUG
30 (encoding methionine or valine) which is part of the initiation signal for protein synthesis can be identified and the portion of an ORF to corresponding to a naturally-

occurring *C. albicans* polypeptide can be recognized. The predicted coding regions were defined by evaluating the coding potential of such sequences with the program GENEMARK[®] (Borodovsky and McIninch, 1993, *Comp. .* 17:123).

Each predicted ORF amino acid sequence was compared with all sequences
5 found in current GENBANK, SWISS-PROT, and PIR databases using the BLAST algorithm. BLAST identifies local alignments occurring by chance between the ORF sequence and the sequence in the databank (Altschul et al., 1990, *L Mol. Biol.* 215:403-410). Homologous ORFs (probabilities less than 10^{-5} by chance) and ORF's that are probably non-homologous (probabilities greater than 10^{-5} by chance) but have
10 good codon usage were identified. Both homologous, sequences and non-homologous sequences with good codon usage, are likely to encode proteins and are encompassed by the invention.

It is to be understood that non-protein-coding sequences contained within SEQ ID NO: 1 - SEQ ID NO: 14103 are also within the scope of the invention. Such
15 sequences include, without limitation, sequences important for replication, recombination, transcription and translation. Non-limiting examples include promoters and regulatory binding sites involved in regulation of gene expression, and 5'- and 3'- untranslated sequences (e.g., ribosome-binding sites) that form part of mRNA molecules.

20 Preferred sequences are those that are useful in diagnostic and/or therapeutic applications. Diagnostic applications include without limitation nucleic-acid-based and antibody-based methods for detecting *C. albicans* infection. Therapeutic applications include without limitation vaccines, passive immunotherapy, and drug treatments directed against gene products that are essential for growth and/or
25 replication. In a particularly preferred aspect of the invention, the nucleic acids encode protein-coding sequences which share homology to other fungal sequences, lack homology to all eukaryotic sequences, and which are essential to the viability of fungi. Such sequences comprise a library of valuable target sequences for drug discovery, in particular, targets which may be used to identify broad spectrum
30 antifungal agents.

C. albicans Nucleic Acids

The present invention provides a library of *C. albicans*-derived nucleic acid sequences. The libraries provide probes, primers, and markers which can be used as markers in epidemiological studies. The present invention also provides a library of *C.*
5 *albicans*-derived nucleic acid sequences which comprise or encode targets for therapeutic drugs.

The nucleic acids of this invention are obtained directly from the DNA of the above referenced *C. albicans* strain by using the polymerase chain reaction (PCR). See "*PCR, A Practical Approach*" (McPherson, Quirke, and Taylor, eds., IRL Press,
10 Oxford, UK, 1991) for details about the PCR. High fidelity PCR can be used to ensure a faithful DNA copy prior to expression. In addition, the authenticity of amplified products can be verified by conventional sequencing methods. Clones carrying the desired sequences described in this invention may also be obtained by screening the libraries by means of the PCR or by hybridization of synthetic
15 oligonucleotide probes to filter lifts of the library colonies or plaques as known in the art (see, e.g., Sambrook et al., *Molecular Cloning, A Laboratory Manual* 2nd edition, 1989, Cold Spring Harbor Press, NY).

It is also possible to obtain nucleic acids encoding *C. albicans* polypeptides from a cDNA library in accordance with protocols herein described. A cDNA
20 encoding a *C. albicans* polypeptide can be obtained by isolating total mRNA from an appropriate strain. Double stranded cDNAs can then be prepared from the total mRNA. Subsequently, the cDNAs can be inserted into a suitable plasmid or viral (e.g., bacteriophage) vector using any one of a number of known techniques. Genes encoding *C. albicans* polypeptides can also be cloned using established polymerase
25 chain reaction techniques in accordance with the nucleotide sequence information provided by the invention. The nucleic acids of the invention can be DNA or RNA. Preferred nucleic acids of the invention are contained in the Sequence Listing.

The nucleic acids of the invention can also be chemically synthesized using standard techniques. Various methods of chemically synthesizing
30 polydeoxynucleotides are known, including solid-phase synthesis which, like peptide synthesis, has been fully automated in commercially available DNA synthesizers (See

e.g., Itakura et al. U.S. Patent No. 4,598,049; Caruthers et al. U.S. Patent No. 4,458,066; and Itakura U.S. Patent Nos. 4,401,796 and 4,373,071, incorporated by reference herein).

5 In another example, DNA can be chemically synthesized using, e.g., the phosphoramidite solid support method of Matteucci *et al.*, 1981, *J. Am. Chem. Soc.* 103:3185, the method of Yoo *et al.*, 1989, *J. Biol. Chem.* 264:17078, or other well known methods. This can be done by sequentially linking a series of oligonucleotide cassettes comprising pairs of synthetic oligonucleotides, as described below.

10 Nucleic acids isolated or synthesized in accordance with features of the present invention are useful, by way of example, without limitation, as probes, primers, capture ligands, antisense genes and for developing expression systems for the synthesis of proteins and peptides corresponding to such sequences. As probes, primers, capture ligands and antisense agents, the nucleic acid normally consists of all or part (approximately twenty or more nucleotides for specificity as well as the ability
15 to form stable hybridization products) of the nucleic acids of the invention contained in the Sequence Listing. These uses are described in further detail below.

Probes

A nucleic acid isolated or synthesized in accordance with the sequence of the invention contained in the Sequence Listing can be used as a probe to specifically
20 detect *C. albicans*. With the sequence information set forth in the present application, sequences of about twenty or more nucleotides are identified which provide the desired inclusivity and exclusivity with respect to *C. albicans* and extraneous nucleic acids likely to be encountered during hybridization conditions. More preferably, the sequence will comprise at least about twenty to thirty nucleotides to convey stability
25 to the hybridization product formed between the probe and the intended target molecules.

Sequences larger than about 1000 nucleotides in length are difficult to synthesize but can be generated by recombinant DNA techniques. Individuals skilled in the art will readily recognize that the nucleic acids, for use as probes, can be
30 provided with a label to facilitate detection of a hybridization product.

Nucleic acid isolated and synthesized in accordance with the sequence of the

invention contained in the Sequence Listing can also be useful as probes to detect homologous regions (especially homologous genes) of other *Candida* species using appropriate stringency hybridization conditions as described herein.

Capture Ligand

5 For use as a capture ligand, the nucleic acid selected in the manner described above with respect to probes, can be readily associated with a support. The manner in which nucleic acid is associated with supports is well known. Nucleic acid having twenty or more nucleotides in a sequence of the invention contained in the Sequence Listing have utility to separate *C. albicans* nucleic acid from one strain from the
10 nucleic acid of other another strain as well as from other organisms. Nucleic acid having twenty or more nucleotides in a sequence of the invention contained in the Sequence Listing can also have utility to separate other *Candida* species from each other and from other organisms. Preferably, the sequence will comprise at least about twenty nucleotides to convey stability to the hybridization product formed between
15 the probe and the intended target molecules. Sequences larger than 1000 nucleotides in length are difficult to synthesize but can be generated by recombinant DNA techniques.

Primers

 Nucleic acid isolated or synthesized in accordance with the sequences
20 described herein have utility as primers for the amplification of *C. albicans* nucleic acid. These nucleic acids may also have utility as primers for the amplification of nucleic acids in other *Candida* species. With respect to polymerase chain reaction (PCR) techniques, nucleic acid sequences of \geq about 10-15 nucleotides of the invention contained in the Sequence Listing have utility in conjunction with suitable
25 enzymes and reagents to create copies of *C. albicans* nucleic acid. More preferably, the sequence will comprise at least about twenty or more nucleotides to convey stability to the hybridization product formed between the primer and the intended target molecules. Binding conditions of primers greater than about 100 nucleotides are often more difficult to control to obtain specificity. High fidelity PCR can be used
30 to ensure a faithful DNA copy prior to expression. In addition, amplified products can be checked by conventional sequencing methods.

The copies can be used in diagnostic assays to detect specific sequences, including genes from *C. albicans* and/or other *Candida* species. The copies can also be incorporated into cloning and expression vectors to generate polypeptides corresponding to the nucleic acid synthesized by PCR, as is described in greater detail
5 herein.

The nucleic acids of the present invention find use as templates for the recombinant production of *C. albicans*-derived peptides or polypeptides.

Antisense

Nucleic acid or nucleic acid-hybridizing derivatives isolated or synthesized in
10 accordance with the sequences described herein have utility as antisense agents to prevent the expression of *C. albicans* genes. These sequences also have utility as antisense agents to prevent expression of genes of other *Candida* species.

In one embodiment, nucleic acid or derivatives corresponding to *C. albicans* nucleic acids is loaded into a suitable carrier such as a liposome or bacteriophage for
15 introduction into fungal cells. For example, a nucleic acid having about twenty or more nucleotides is capable of binding to bacteria nucleic acid or bacteria messenger RNA. Preferably, the antisense nucleic acid is comprised of at least about 20 or more nucleotides to provide necessary stability of a hybridization product of non-naturally occurring nucleic acid and fungal nucleic acid and/or fungal messenger RNA.
20 Nucleic acid having a sequence greater than about 1000 nucleotides in length is difficult to synthesize but can be generated by recombinant DNA techniques. Methods for loading antisense nucleic acid in liposomes are known in the art as exemplified, for example, in U.S. Patent 4,241,046 issued December 23, 1980 to Papahadjopoulos et al.

25 The present invention encompasses isolated polypeptides and nucleic acids derived from *C. albicans* that are useful as reagents for diagnosis of fungal infection, components of effective anti-fungal vaccines, and/or as targets for anti-fungal drugs, including anti-*C. albicans* drugs.

Expression of *C. albicans* Nucleic Acids

Table 2, which is appended herewith and which forms part of the present specification, provides a list of open reading frames (ORFs) in both strands and a putative identification of the particular function of a polypeptide which is encoded by each ORF, based on the homology match (determined by the BLAST algorithm) of the predicted polypeptide with known proteins encoded by ORFs in other organisms. An ORF is a region of nucleic acid which encodes a polypeptide. This region may represent a portion of a coding sequence or a total sequence and was determined from stop to stop codons. The first column contains a designation for the contig from which each ORF was identified (numbered arbitrarily). Each contig represents a continuous stretch of the genomic sequence of the organism. The second column lists the ORF designation. The third and fourth columns list the SEQ ID numbers for the nucleic acid and amino acid sequences corresponding to each ORF, respectively. The fifth and sixth columns list the length of the nucleic acid ORF and the length of the amino acid ORF, respectively. The nucleotide sequence corresponding to each ORF begins at the first nucleotide immediately following a stop codon and ends at the nucleotide immediately preceding the next downstream stop codon in the same reading frame. It will be recognized by one skilled in the art that the natural translation initiation sites will correspond to ATG, GTG, or TTG codons located within the ORFs. The natural initiation sites depend not only on the sequence of a start codon but also on the context of the DNA sequence adjacent to the start codon. Usually, a recognizable ribosome binding site is found within 20 nucleotides upstream from the initiation codon. In some cases where genes are translationally coupled and coordinately expressed together in "operons," ribosome binding sites are not present, but the initiation codon of a downstream gene may occur very close to, or overlap, the stop codon of the an upstream gene in the same operon. The correct start codons can be generally identified without undue experimentation because only a few codons need be tested. It is recognized that the translational machinery in bacteria initiates all polypeptide chains with the amino acid methionine, regardless of the sequence of the start codon. In some cases, polypeptides are post-translationally modified, resulting

in an N-terminal amino acid other than methionine *in vivo*. The seventh column provides, where available, either a public database accession number or our own sequence name. The eighth and ninth columns provide metrics for assessing the likelihood of the homology match (determined by the BLASTP2 algorithm), as is known in the art, to the genes indicated in the eleventh column when the designated ORF was compared against a non-redundant comprehensive protein database. Specifically, the eighth column represents the “Blast Score” for the match (a higher score is a better match), and the ninth column represents the “P-value” for the match (the probability that such a match can have occurred by chance; the lower the value, the more likely the match is valid). If a BLASTP2 score of less than 46 was obtained, no value is reported in the table the “P-value.” Column ten provides the name of the organism that was identified as having the closest homology match. The eleventh column provides, where available, the Swissprot accession number (SP), (SP), the locus name (LN), the Organism (OR), Source of variant (SR), E.C. number (EC), the gene name (GN), the product name (PN), the Function Description (FN), Left End (LE), Right End (RE), Coding Direction (DI), and the description (DE) or notes (NT) for each ORF. Information that is not preceded by a code designation in the eleventh column represents a description of the ORF. This information allows one of ordinary skill in the art to determine a potential use for each identified coding sequence and, as a result, allows to use the polypeptides of the present invention for commercial and industrial purposes.

Using the information provided in SEQ ID NO: 1 - SEQ ID NO: 14103, SEQ ID NO: 14104 - SEQ ID NO: 28206 and in Table 2 together with routine cloning and sequencing methods, one of ordinary skill in the art will be able to clone and sequence all the nucleic acid fragments of interest including open reading frames (ORFs) encoding a large variety proteins of *C. albicans*.

Nucleic acid isolated or synthesized in accordance with the sequences described herein have utility to generate polypeptides. The nucleic acid of the invention exemplified in SEQ ID NO: 1 - SEQ ID NO: 14103 and in Table 2 or fragments of said nucleic acid encoding active portions of *C. albicans* polypeptides

can be cloned into suitable vectors or used to isolate nucleic acid. The isolated nucleic acid is combined with suitable DNA linkers and cloned into a suitable vector.

The function of a specific gene or operon can be ascertained by expression in a fungal strain under conditions where the activity of the gene product(s) specified by the gene or operon in question can be specifically measured. Alternatively, a gene product may be produced in large quantities in an expressing strain for use as an antigen, an industrial reagent, for structural studies, etc. This expression can be accomplished in a mutant strain which lacks the activity of the gene to be tested, or in a strain that does not produce the same gene product(s). This includes, but is not limited to, Eucaryotic species such as the yeast *Saccharomyces cerevisiae* or *Candida putida*, *Methanobacterium* strains or other Archaea, and Eubacteria such as *E. coli*, *B. Subtilis*, *S. Aureus*, *S. Pneumonia* or *Pseudomonas putida*. In some cases the expression host will utilize the natural *C. albicans* promoter whereas in others, it will be necessary to drive the gene with a promoter sequence derived from the expressing organism (e.g., an *E. coli* beta-galactosidase promoter for expression in *E. coli*).

To express a gene product using the natural *C. albicans* promoter, a procedure such as the following can be used. A restriction fragment containing the gene of interest, together with its associated natural promoter element and regulatory sequences (identified using the DNA sequence data) is cloned into an appropriate recombinant plasmid containing an origin of replication that functions in the host organism and an appropriate selectable marker. This can be accomplished by a number of procedures known to those skilled in the art. It is most preferably done by cutting the plasmid and the fragment to be cloned with the same restriction enzyme to produce compatible ends that can be ligated to join the two pieces together. The recombinant plasmid is introduced into the host organism by, for example, electroporation and cells containing the recombinant plasmid are identified by selection for the marker on the plasmid. Expression of the desired gene product is detected using an assay specific for that gene product.

In the case of a gene that requires a different promoter, the body of the gene (coding sequence) is specifically excised and cloned into an appropriate expression plasmid. This subcloning can be done by several methods, but is most easily

accomplished by PCR amplification of a specific fragment and ligation into an expression plasmid after treating the PCR product with a restriction enzyme or exonuclease to create suitable ends for cloning.

5 A suitable host cell for expression of a gene can be any procaryotic or eucaryotic cell. Suitable methods for transforming host cells can be found in Sambrook et al. (Molecular Cloning: A Laboratory Manual, 2nd Edition, Cold Spring Harbor Laboratory press (1989)), and other laboratory textbooks.

For example, a host cell transfected with a nucleic acid vector directing expression of a nucleotide sequence encoding a *C. albicans* polypeptide can be
10 cultured under appropriate conditions to allow expression of the polypeptide to occur. Suitable media for cell culture are well known in the art. Polypeptides of the invention can be isolated from cell culture medium, host cells, or both using techniques known in the art for purifying proteins including ion-exchange chromatography, gel filtration chromatography, ultrafiltration, electrophoresis, and
15 immunoaffinity purification with antibodies specific for such polypeptides. Additionally, in many situations, polypeptides can be produced by chemical cleavage of a native protein (e.g., tryptic digestion) and the cleavage products can then be purified by standard techniques.

In the case of membrane bound proteins, these can be isolated from a host cell
20 by contacting a membrane-associated protein fraction with a detergent forming a solubilized complex, where the membrane-associated protein is no longer entirely embedded in the membrane fraction and is solubilized at least to an extent which allows it to be chromatographically isolated from the membrane fraction. Chromatographic techniques which can be used in the final purification step are
25 known in the art and include hydrophobic interaction, lectin affinity, ion exchange, dye affinity and immunoaffinity.

One strategy to maximize recombinant *C. albicans* peptide expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., Gene Expression
30 Technology: Methods in Enzymology 185, Academic Press, San Diego, California (1990) 119-128). Another strategy would be to alter the nucleic acid encoding a *C.*

albicans peptide to be inserted into an expression vector so that the individual codons for each amino acid would be those preferentially utilized in highly expressed *E. coli* proteins (Wada et al., (1992) *Nuc. Acids Res.* 20:2111-2118). Such alteration of nucleic acids of the invention can be carried out by standard DNA synthesis techniques.

The nucleic acids of the invention can also be chemically synthesized using standard techniques. Various methods of chemically synthesizing polydeoxynucleotides are known, including solid-phase synthesis which, like peptide synthesis, has been fully automated in commercially available DNA synthesizers (See, e.g., Itakura et al. U.S. Patent No. 4,598,049; Caruthers et al. U.S. Patent No. 4,458,066; and Itakura U.S. Patent Nos. 4,401,796 and 4,373,071, incorporated by reference herein). The present invention provides a library of *C. albicans*-derived nucleic acid sequences. The libraries provide probes, primers, and markers which can be used as markers in epidemiological studies. The present invention also provides a library of *C. albicans*-derived nucleic acid sequences which comprise or encode targets for therapeutic drugs.

Nucleic acids comprising any of the sequences disclosed herein or sub-sequences thereof can be prepared by standard methods using the nucleic acid sequence information provided in SEQ ID NO: 1 - SEQ ID NO: 14103. For example, DNA can be chemically synthesized using, e.g., the phosphoramidite solid support method of Matteucci *et al.*, 1981, *J. Am. Chem. Soc.* 103:3185, the method of Yoo *et al.*, 1989, *J. Biol. Chem.* 764:17078, or other well known methods. This can be done by sequentially linking a series of oligonucleotide cassettes comprising pairs of synthetic oligonucleotides, as described below.

Of course, due to the degeneracy of the genetic code, many different nucleotide sequences can encode polypeptides having the amino acid sequences defined by SEQ ID NO: 14104 - SEQ ID NO: 28206 or sub-sequences thereof. The codons can be selected for optimal expression in prokaryotic or eukaryotic systems. Such degenerate variants are also encompassed by this invention.

Insertion of nucleic acids (typically DNAs) encoding the polypeptides of the invention into a vector is easily accomplished when the termini of both the DNAs and

the vector comprise compatible restriction sites. If this cannot be done, it may be necessary to modify the termini of the DNAs and/or vector by digesting back single-stranded DNA overhangs generated by restriction endonuclease cleavage to produce blunt ends, or to achieve the same result by filling in the single-stranded termini with an appropriate DNA polymerase.

Alternatively, any site desired may be produced, e.g., by ligating nucleotide sequences (linkers) onto the termini. Such linkers may comprise specific oligonucleotide sequences that define desired restriction sites. Restriction sites can also be generated by the use of the polymerase chain reaction (PCR). See, e.g., Saiki
10 *et al.*, 1988, *Science* 239:48. The cleaved vector and the DNA fragments may also be modified if required by homopolymeric tailing.

The nucleic acids of the invention may be isolated directly from cells. Alternatively, the polymerase chain reaction (PCR) method can be used to produce the nucleic acids of the invention, using either chemically synthesized strands or
15 genomic material as templates. Primers used for PCR can be synthesized using the sequence information provided herein and can further be designed to introduce appropriate new restriction sites, if desirable, to facilitate incorporation into a given vector for recombinant expression.

The nucleic acids of the present invention may be flanked by natural *C. albicans* regulatory sequences, or may be associated with heterologous sequences,
20 including promoters, enhancers, response elements, signal sequences, polyadenylation sequences, introns, 5'- and 3'- noncoding regions, and the like. The nucleic acids may also be modified by many means known in the art. Non-limiting examples of such modifications include methylation, "caps", substitution of one or more of the naturally
25 occurring nucleotides with an analog, internucleotide modifications such as, for example, those with uncharged linkages (e.g., methyl phosphonates, phosphotriesters, phosphoroamidates, carbamates, etc.) and with charged linkages (e.g., phosphorothioates, phosphorodithioates, etc.). Nucleic acids may contain one or more additional covalently linked moieties, such as, for example, proteins (e.g., nucleases,
30 toxins, antibodies, signal peptides, poly-L-lysine, etc.), intercalators (e.g., acridine, psoralen, etc.), chelators (e.g., metals, radioactive metals, iron, oxidative metals, etc.),

and alkylators. PNAs are also included. The nucleic acid may be derivatized by formation of a methyl or ethyl phosphotriester or an alkyl phosphoramidate linkage. Furthermore, the nucleic acid sequences of the present invention may also be modified with a label capable of providing a detectable signal, either directly or
5 indirectly. Exemplary labels include radioisotopes, fluorescent molecules, biotin, and the like.

The invention also provides nucleic acid vectors comprising the disclosed *C. albicans*-derived sequences or derivatives or fragments thereof. A large number of vectors, including plasmid and fungal vectors, have been described for replication
10 and/or expression in a variety of eukaryotic and prokaryotic hosts, and may be used for cloning or protein expression.

The encoded *C. albicans* polypeptides may be expressed by using many known vectors, such as pUC plasmids, pET plasmids (Novagen, Inc., Madison, WI), or pRSET or pREP (Invitrogen, San Diego, CA), and many appropriate host cells,
15 using methods disclosed or cited herein or otherwise known to those skilled in the relevant art. The particular choice of vector/host is not critical to the practice of the invention.

Recombinant cloning vectors will often include one or more replication systems for cloning or expression, one or more markers for selection in the host, e.g.
20 antibiotic resistance, and one or more expression cassettes. The inserted *C. albicans* coding sequences may be synthesized by standard methods, isolated from natural sources, or prepared as hybrids, etc. Ligation of the *C. albicans* coding sequences to transcriptional regulatory elements and/or to other amino acid coding sequences may be achieved by known methods. Suitable host cells may be
25 transformed/transfected/infected as appropriate by any suitable method including electroporation, CaCl₂ mediated DNA uptake, fungal infection, microinjection, microprojectile, or other established methods.

Appropriate host cells include bacteria, archebacteria, fungi, especially yeast, and plant and animal cells, especially mammalian cells. Of particular interest are *C.*
30 *albicans*, *E. coli*, *B. Subtilis*, *Saccharomyces cerevisiae*, *Saccharomyces carlsbergensis*, *Schizosaccharomyces pombe*, SF9 cells, C129 cells, 293 cells,

Neurospora, and CHO cells, COS cells, HeLa cells, and immortalized mammalian myeloid and lymphoid cell lines. Preferred replication systems include M13, ColE1, SV40, baculovirus, lambda, adenovirus, and the like. A large number of transcription initiation and termination regulatory regions have been isolated and shown to be effective in the transcription and translation of heterologous proteins in the various hosts. Examples of these regions, methods of isolation, manner of manipulation, etc. are known in the art. Under appropriate expression conditions, host cells can be used as a source of recombinantly produced *C. albicans*-derived peptides and polypeptides.

Advantageously, vectors may also include a transcription regulatory element (i.e., a promoter) operably linked to the *C. albicans* portion. The promoter may optionally contain operator portions and/or ribosome binding sites. Non-limiting examples of fungal promoters compatible with *E. coli* include: b-lactamase (penicillinase) promoter; lactose promoter; tryptophan (trp) promoter; araBAD (arabinose) operon promoter; lambda-derived P₁ promoter and N gene ribosome binding site; and the hybrid tac promoter derived from sequences of the trp and lac UV5 promoters. Non-limiting examples of yeast promoters include 3-phosphoglycerate kinase promoter, glyceraldehyde-3-phosphate dehydrogenase (GAPDH) promoter, galactokinase (GAL1) promoter, galactose epimerase promoter, and alcohol dehydrogenase (ADH) promoter. Suitable promoters for mammalian cells include without limitation viral promoters such as that from Simian Virus 40 (SV40), Rous sarcoma virus (RSV), adenovirus (ADV), and bovine papilloma virus (BPV). Mammalian cells may also require terminator sequences, polyA addition sequences and enhancer sequences to increase expression. Sequences which cause amplification of the gene may also be desirable. Furthermore, sequences that facilitate secretion of the recombinant product from cells, including, but not limited to, bacteria, yeast, and animal cells, such as secretory signal sequences and/or prohormone pro region sequences, may also be included. These sequences are well described in the art.

Nucleic acids encoding wild-type or variant *C. albicans*-derived polypeptides may also be introduced into cells by recombination events. For example, such a sequence can be introduced into a cell, and thereby effect homologous recombination at the site of an endogenous gene or a sequence with substantial identity to the gene.

Other recombination-based methods such as nonhomologous recombinations or deletion of endogenous genes by homologous recombination may also be used.

The nucleic acids of the present invention find use as templates for the recombinant production of *C. albicans*-derived peptides or polypeptides.

5

Identification and Use of *C. albicans* Nucleic Acid Sequences

The disclosed *C. albicans* polypeptide and nucleic acid sequences, or other sequences that are contained within ORFs, including complete protein-coding sequences, of which any of the disclosed *C. albicans*-specific sequences forms a part, are useful as target components for diagnosis and/or treatment of *C. albicans*-caused infection

It will be understood that the sequence of an entire protein-coding sequence of which each disclosed nucleic acid sequence forms a part can be isolated and identified based on each disclosed sequence. This can be achieved, for example, by using an isolated nucleic acid encoding the disclosed sequence, or fragments thereof, to prime a sequencing reaction with genomic *C. albicans* DNA as template; this is followed by sequencing the amplified product. The isolated nucleic acid encoding the disclosed sequence, or fragments thereof, can also be hybridized to *C. albicans* genomic libraries to identify clones containing additional complete segments of the protein-coding sequence of which the shorter sequence forms a part. Then, the entire protein-coding sequence, or fragments thereof, or nucleic acids encoding all or part of the sequence, or sequence-conservative or function-conservative variants thereof, may be employed in practicing the present invention.

Preferred sequences are those that are useful in diagnostic and/or therapeutic applications. Diagnostic applications include without limitation nucleic-acid-based and antibody-based methods for detecting fungal infection. Therapeutic applications include without limitation vaccines, passive immunotherapy, and drug treatments directed against gene products that are both unique to fungi and essential for growth and/or replication of fungi.

30

Identification of Nucleic Acids Encoding Vaccine Components and Targets for Agents Effective Against *C. albicans*

The disclosed *C. albicans* genome sequence includes segments that direct the synthesis of ribonucleic acids and polypeptides, as well as origins of replication, promoters, other types of regulatory sequences, and intergenic nucleic acids. The invention encompasses nucleic acids encoding immunogenic components of vaccines and targets for agents effective against *C. albicans*. Identification of said immunogenic components involved in the determination of the function of the disclosed sequences, which can be achieved using a variety of approaches. Non-limiting examples of these approaches are described briefly below.

Homology to known sequences:

Computer-assisted comparison of the disclosed *C. albicans* sequences with previously reported sequences present in publicly available databases is useful for identifying functional *C. albicans* nucleic acid and polypeptide sequences. It will be understood that protein-coding sequences, for example, may be compared as a whole, and that a high degree of sequence homology between two proteins (such as, for example, >80-90%) at the amino acid level indicates that the two proteins also possess some degree of functional homology, such as, for example, among enzymes involved in metabolism, DNA synthesis, or cell wall synthesis, and proteins involved in transport, cell division, etc. In addition, many structural features of particular protein classes have been identified and correlate with specific consensus sequences, such as, for example, binding domains for nucleotides, DNA, metal ions, and other small molecules; sites for covalent modifications such as phosphorylation, acylation, and the like; sites of protein:protein interactions, etc. These consensus sequences may be quite short and thus may represent only a fraction of the entire protein-coding sequence. Identification of such a feature in a *C. albicans* sequence is therefore useful in determining the function of the encoded protein and identifying useful targets of antifungal drugs.

Of particular relevance to the present invention are structural features that are common to secretory, transmembrane, and surface proteins, including secretion signal peptides and hydrophobic transmembrane domains. *C. albicans* proteins identified as

containing putative signal sequences and/or transmembrane domains are useful as immunogenic components of vaccines.

Targets for therapeutic drugs according to the invention include, but are not limited to, polypeptides of the invention, whether unique to *C. albicans* or not, that are essential for growth and/or viability of *C. albicans* under at least one growth condition. Polypeptides essential for growth and/or viability can be determined by examining the effect of deleting and/or disrupting the genes, i.e., by so-called gene "knockout". Alternatively, genetic footprinting can be used (Smith *et al.*, 1995, *Proc. Natl. Acad. Sci. USA* 92:5479-6433; Published International Application WO 94/26933; U.S. Patent No. 5,612,180). Still other methods for assessing essentiality includes the ability to isolate conditional lethal mutations in the specific gene (e.g., temperature sensitive mutations). Other useful targets for therapeutic drugs, which include polypeptides that are not essential for growth or viability *per se* but lead to loss of viability of the cell, can be used to target therapeutic agents to cells.

15

Strain-specific sequences:

Because of the evolutionary relationship between different *C. albicans* strains, it is believed that the presently disclosed *C. albicans* sequences are useful for identifying, and/or discriminating between, previously known and new *C. albicans* strains. It is believed that other *C. albicans* strains will exhibit at least about 70% sequence homology with the presently disclosed sequence. Systematic and routine analyses of DNA sequences derived from samples containing *C. albicans* strains, and comparison with the present sequence allows for the identification of sequences that can be used to discriminate between strains, as well as those that are common to all *C. albicans* strains. In one embodiment, the invention provides nucleic acids, including probes, and peptide and polypeptide sequences that discriminate between different strains of *C. albicans*. Strain-specific components can also be identified functionally by their ability to elicit or react with antibodies that selectively recognize one or more *C. albicans* strains.

25

In another embodiment, the invention provides nucleic acids, including probes, and peptide and polypeptide sequences that are common to all *C. albicans* strains but are *not* found in other fungal species.

5 *C. albicans* Polypeptides

This invention encompasses isolated *C. albicans* polypeptides encoded by the disclosed *C. albicans* genomic sequences, including the polypeptides of the invention contained in the Sequence Listing. Polypeptides of the invention are preferably at least about 5 amino acid residues in length. Using the DNA sequence information
10 provided herein, the amino acid sequences of the polypeptides encompassed by the invention can be deduced using methods well-known in the art. It will be understood that the sequence of an entire nucleic acid encoding a *C. albicans* polypeptide can be isolated and identified based on an ORF that encodes only a fragment of the cognate protein-coding region. This can be achieved, for example, by using the isolated
15 nucleic acid encoding the ORF, or fragments thereof, to prime a polymerase chain reaction with genomic *C. albicans* DNA as template; this is followed by sequencing the amplified product.

The polypeptides of the present invention, including function-conservative variants of the disclosed ORFs, may be isolated from wild-type or mutant *C. albicans*
20 cells, or from heterologous organisms or cells (including, but not limited to, bacteria, fungi, insect, plant, and mammalian cells) including *C. albicans* into which a *C. albicans*-derived protein-coding sequence has been introduced and expressed. Furthermore, the polypeptides may be part of recombinant fusion proteins.

C. albicans polypeptides of the invention can be chemically synthesized using
25 commercially automated procedures such as those referenced herein, including, without limitation, exclusive solid phase synthesis, partial solid phase methods, fragment condensation or classical solution synthesis. The polypeptides are preferably prepared by solid phase peptide synthesis as described by Merrifield, 1963, *J. Am. Chem. Soc.* 85:2149. The synthesis is carried out with amino acids that are
30 protected at the alpha-amino terminus. Trifunctional amino acids with labile side-chains are also protected with suitable groups to prevent undesired chemical reactions from occurring during the assembly of the polypeptides. The alpha-amino protecting group is selectively removed to allow subsequent reaction to take place at the amino-

terminus. The conditions for the removal of the alpha-amino protecting group do not remove the side-chain protecting groups.

Methods for polypeptide purification are well-known in the art, including, without limitation, preparative disc-gel electrophoresis, isoelectric focusing, HPLC, reversed-phase HPLC, gel filtration, ion exchange and partition chromatography, and countercurrent distribution. For some purposes, it is preferable to produce the polypeptide in a recombinant system in which the *C. albicans* protein contains an additional sequence tag that facilitates purification, such as, but not limited to, a polyhistidine sequence. The polypeptide can then be purified from a crude lysate of the host cell by chromatography on an appropriate solid-phase matrix. Alternatively, antibodies produced against a *C. albicans* protein or against peptides derived therefrom can be used as purification reagents. Other purification methods are possible.

The present invention also encompasses derivatives and homologues of *C. albicans*-encoded polypeptides. For some purposes, nucleic acid sequences encoding the peptides may be altered by substitutions, additions, or deletions that provide for functionally equivalent molecules, i.e., function-conservative variants. For example, one or more amino acid residues within the sequence can be substituted by another amino acid of similar properties, such as, for example, positively charged amino acids (arginine, lysine, and histidine); negatively charged amino acids (aspartate and glutamate); polar neutral amino acids; and non-polar amino acids.

The isolated polypeptides may be modified by, for example, phosphorylation, sulfation, acylation, or other protein modifications. They may also be modified with a label capable of providing a detectable signal, either directly or indirectly, including, but not limited to, radioisotopes and fluorescent compounds.

To identify *C. albicans*-derived polypeptides for use in the present invention, essentially the complete genomic sequence of a *C. albicans* isolate was analyzed. While, in very rare instances, a nucleic acid sequencing error may be revealed, resolving a rare sequencing error is well within the art, and such an occurrence will not prevent one skilled in the art from practicing the invention.

Also encompassed are any *C. albicans* polypeptide sequences that are contained within the open reading frames (ORFs), including complete protein-coding sequences, of which any of SEQ ID NO: 1 - SEQ ID NO: 14103 forms a part. Table 2, which is appended herewith and which forms part of the present specification, provides a putative identification of the particular function of a polypeptide which is encoded by each ORF based on the homology match (determined by the BLAST algorithm) of the predicted polypeptide with known proteins encoded by ORFs in other organisms. As a result, one skilled in the art can use the polypeptides of the present invention for commercial and industrial purposes consistent with the type of putative identification of the polypeptide.

The present invention provides a library of *C. albicans*-derived polypeptide sequences, and a corresponding library of nucleic acid sequences encoding the polypeptides, wherein the polypeptides themselves, or polypeptides contained within ORFs of which they form a part, comprise sequences that are contemplated for use as components of vaccines. Non-limiting examples of such sequences are listed by SEQ ID NO in Table 2, which is appended herewith and which forms part of the present specification.

The present invention also provides a library of *C. albicans*-derived polypeptide sequences, and a corresponding library of nucleic acid sequences encoding the polypeptides, wherein the polypeptides themselves, or polypeptides contained within ORFs of which they form a part, comprise sequences lacking homology to any known prokaryotic or eukaryotic sequences. Such libraries provide probes, primers, and markers which can be used to diagnose *C. albicans* infection, including use as markers in epidemiological studies. Non-limiting examples of such sequences are listed by SEQ ID NO in Table 2, which is appended

The present invention also provides a library of *C. albicans*-derived polypeptide sequences, and a corresponding library of nucleic acid sequences encoding the polypeptides, wherein the polypeptides themselves, or polypeptides contained within ORFs of which they form a part, comprise targets for therapeutic drugs.

Specific Example: Determination Of Candidate Protein Antigens For Antibody And Vaccine Development

5 The selection of candidate protein antigens for vaccine development can be derived from the nucleic acids encoding *C. albicans* polypeptides. First, the ORF's can be analyzed for homology to other known exported or membrane proteins and analyzed using the discriminant analysis described by Klein, et al. (Klein, P., Kanehsia, M., and DeLisi, C. (1985) *Biochimica et Biophysica Acta* 815, 468-476) for predicting exported and membrane proteins.

10 Homology searches can be performed using the BLAST algorithm contained in the Wisconsin Sequence Analysis Package (Genetics Computer Group, University Research Park, 575 Science Drive, Madison, WI 53711) to compare each predicted ORF amino acid sequence with all sequences found in the current GenBank, SWISS-PROT and PIR databases. BLAST searches for local alignments between the ORF
15 and the databank sequences and reports a probability score which indicates the probability of finding this sequence by chance in the database. ORF's with significant homology (e.g. probabilities lower than 1×10^{-6} that the homology is only due to random chance) to membrane or exported proteins represent protein antigens for vaccine development. Possible functions can be provided to *C. albicans* genes based
20 on sequence homology to genes cloned in other organisms.

Discriminant analysis (Klein, et al. supra) can be used to examine the ORF amino acid sequences. This algorithm uses the intrinsic information contained in the ORF amino acid sequence and compares it to information derived from the properties of known membrane and exported proteins. This comparison predicts which proteins
25 will be exported, membrane associated or cytoplasmic. ORF amino acid sequences identified as exported or membrane associated by this algorithm are likely protein antigens for vaccine development.

Production of Fragments and Analogs of *C. albicans* Nucleic Acids and Polypeptides

30 Based on the discovery of the *C. albicans* gene products of the invention provided in the Sequence Listing, one skilled in the art can alter the disclosed

structure of *C. albicans* genes, e.g., by producing fragments or analogs, and test the newly produced structures for activity. Examples of techniques known to those skilled in the relevant art which allow the production and testing of fragments and analogs are discussed below. These, or analogous methods can be used to make and
5 screen libraries of polypeptides, e.g., libraries of random peptides or libraries of fragments or analogs of cellular proteins for the ability to bind *C. albicans* polypeptides. Such screens are useful for the identification of inhibitors of *C. albicans*.

10 Generation of Fragments

Fragments of a protein can be produced in several ways, e.g., recombinantly, by proteolytic digestion, or by chemical synthesis. Internal or terminal fragments of a polypeptide can be generated by removing one or more nucleotides from one end (for a terminal fragment) or both ends (for an internal fragment) of a nucleic acid which
15 encodes the polypeptide. Expression of the mutagenized DNA produces polypeptide fragments. Digestion with "end-nibbling" endonucleases can thus generate DNAs which encode an array of fragments. DNAs which encode fragments of a protein can also be generated by random shearing, restriction digestion or a combination of the above-discussed methods.

20 Fragments can also be chemically synthesized using techniques known in the art such as conventional Merrifield solid phase f-Moc or t-Boc chemistry. For example, peptides of the present invention may be arbitrarily divided into fragments of desired length with no overlap of the fragments, or divided into overlapping fragments of a desired length.

25

Alteration of Nucleic Acids and Polypeptides: Random Methods

Amino acid sequence variants of a protein can be prepared by random mutagenesis of DNA which encodes a protein or a particular domain or region of a protein. Useful methods include PCR mutagenesis and saturation mutagenesis. A
30 library of random amino acid sequence variants can also be generated by the synthesis of a set of degenerate oligonucleotide sequences. (Methods for screening proteins in a

library of variants are elsewhere herein).

PCR Mutagenesis

In PCR mutagenesis, reduced Taq polymerase fidelity is used to introduce random mutations into a cloned fragment of DNA (Leung et al., 1989, *Technique* 1:11-15). The DNA region to be mutagenized is amplified using the polymerase chain reaction (PCR) under conditions that reduce the fidelity of DNA synthesis by Taq DNA polymerase, e.g., by using a dGTP/dATP ratio of five and adding Mn^{2+} to the PCR reaction. The pool of amplified DNA fragments are inserted into appropriate cloning vectors to provide random mutant libraries.

10 Saturation Mutagenesis

Saturation mutagenesis allows for the rapid introduction of a large number of single base substitutions into cloned DNA fragments (Mayers et al., 1985, *Science* 229:242). This technique includes generation of mutations, e.g., by chemical treatment or irradiation of single-stranded DNA *in vitro*, and synthesis of a complimentary DNA strand. The mutation frequency can be modulated by modulating the severity of the treatment, and essentially all possible base substitutions can be obtained. Because this procedure does not involve a genetic selection for mutant fragments both neutral substitutions, as well as those that alter function, are obtained. The distribution of point mutations is not biased toward conserved sequence elements.

20 Degenerate Oligonucleotides

A library of homologs can also be generated from a set of degenerate oligonucleotide sequences. Chemical synthesis of a degenerate sequences can be carried out in an automatic DNA synthesizer, and the synthetic genes then ligated into an appropriate expression vector. The synthesis of degenerate oligonucleotides is known in the art (see for example, Narang, SA (1983) *Tetrahedron* 39:3; Itakura et al. (1981) *Recombinant DNA, Proc 3rd Cleveland Sympos. Macromolecules*, ed. AG Walton, Amsterdam: Elsevier pp273-289; Itakura et al. (1984) *Annu. Rev. Biochem.* 53:323; Itakura et al. (1984) *Science* 198:1056; Ike et al. (1983) *Nucleic Acid Res.* 11:477. Such techniques have been employed in the directed evolution of other proteins (see, for example, Scott et al. (1990) *Science* 249:386-390; Roberts et al.

(1992) *PNAS* 89:2429-2433; Devlin et al. (1990) *Science* 249: 404-406; Cwirla et al. (1990) *PNAS* 87: 6378-6382; as well as U.S. Patents Nos. 5,223,409, 5,198,346, and 5,096,815).

5 Alteration of Nucleic Acids and Polypeptides: Methods for Directed Mutagenesis

Non-random or directed, mutagenesis techniques can be used to provide specific sequences or mutations in specific regions. These techniques can be used to create variants which include, e.g., deletions, insertions, or substitutions, of residues of the known amino acid sequence of a protein. The sites for mutation can be
10 modified individually or in series, e.g., by (1) substituting first with conserved amino acids and then with more radical choices depending upon results achieved, (2) deleting the target residue, or (3) inserting residues of the same or a different class adjacent to the located site, or combinations of options 1-3.

Alanine Scanning Mutagenesis

15 Alanine scanning mutagenesis is a useful method for identification of certain residues or regions of the desired protein that are preferred locations or domains for mutagenesis, Cunningham and Wells (*Science* 244:1081-1085, 1989). In alanine scanning, a residue or group of target residues are identified (e.g., charged residues such as Arg, Asp, His, Lys, and Glu) and replaced by a neutral or negatively charged
20 amino acid (most preferably alanine or polyalanine). Replacement of an amino acid can affect the interaction of the amino acids with the surrounding aqueous environment in or outside the cell. Those domains demonstrating functional sensitivity to the substitutions are then refined by introducing further or other variants at or for the sites of substitution. Thus, while the site for introducing an amino acid
25 sequence variation is predetermined, the nature of the mutation per se need not be predetermined. For example, to optimize the performance of a mutation at a given site, alanine scanning or random mutagenesis may be conducted at the target codon or region and the expressed desired protein subunit variants are screened for the optimal combination of desired activity.

30 Oligonucleotide-Mediated Mutagenesis

Oligonucleotide-mediated mutagenesis is a useful method for preparing

substitution, deletion, and insertion variants of DNA, see, e.g., Adelman et al., (*DNA* 2:183, 1983). Briefly, the desired DNA is altered by hybridizing an oligonucleotide encoding a mutation to a DNA template, where the template is the single-stranded form of a plasmid or bacteriophage containing the unaltered or native DNA sequence of the desired protein. After hybridization, a DNA polymerase is used to synthesize an entire second complementary strand of the template that will thus incorporate the oligonucleotide primer, and will code for the selected alteration in the desired protein DNA. Generally, oligonucleotides of at least about 25 nucleotides in length are used. An optimal oligonucleotide will have 12 to 15 nucleotides that are completely complementary to the template on either side of the nucleotide(s) coding for the mutation. This ensures that the oligonucleotide will hybridize properly to the single-stranded DNA template molecule. The oligonucleotides are readily synthesized using techniques known in the art such as that described by Crea et al. (*Proc. Natl. Acad. Sci. USA*, 75: 5765[1978]).

Cassette Mutagenesis

Another method for preparing variants, cassette mutagenesis, is based on the technique described by Wells et al. (*Gene*, 34:315[1985]). The starting material is a plasmid (or other vector) which includes the protein subunit DNA to be mutated. The codon(s) in the protein subunit DNA to be mutated are identified. There must be a unique restriction endonuclease site on each side of the identified mutation site(s). If no such restriction sites exist, they may be generated using the above-described oligonucleotide-mediated mutagenesis method to introduce them at appropriate locations in the desired protein subunit DNA. After the restriction sites have been introduced into the plasmid, the plasmid is cut at these sites to linearize it. A double-stranded oligonucleotide encoding the sequence of the DNA between the restriction sites but containing the desired mutation(s) is synthesized using standard procedures. The two strands are synthesized separately and then hybridized together using standard techniques. This double-stranded oligonucleotide is referred to as the cassette. This cassette is designed to have 3' and 5' ends that are comparable with the ends of the linearized plasmid, such that it can be directly ligated to the plasmid. This plasmid now contains the mutated desired protein subunit DNA sequence.

Combinatorial Mutagenesis

Combinatorial mutagenesis can also be used to generate mutants (Ladner et al., WO 88/06630). In this method, the amino acid sequences for a group of homologs or other related proteins are aligned, preferably to promote the highest
5 homology possible. All of the amino acids which appear at a given position of the aligned sequences can be selected to create a degenerate set of combinatorial sequences. The variegated library of variants is generated by combinatorial mutagenesis at the nucleic acid level, and is encoded by a variegated gene library. For example, a mixture of synthetic oligonucleotides can be enzymatically ligated into
10 gene sequences such that the degenerate set of potential sequences are expressible as individual peptides, or alternatively, as a set of larger fusion proteins containing the set of degenerate sequences.

Other Modifications of *C. albicans* Nucleic Acids and Polypeptides

15 It is possible to modify the structure of a *C. albicans* polypeptide for such purposes as increasing solubility, enhancing stability (e.g., shelf life *ex vivo* and resistance to proteolytic degradation *in vivo*). A modified *C. albicans* protein or peptide can be produced in which the amino acid sequence has been altered, such as by amino acid substitution, deletion, or addition as described herein.

20 An *C. albicans* peptide can also be modified by substitution of cysteine residues preferably with alanine, serine, threonine, leucine or glutamic acid residues to minimize dimerization via disulfide linkages. In addition, amino acid side chains of fragments of the protein of the invention can be chemically modified. Another modification is cyclization of the peptide.

25 In order to enhance stability and/or reactivity, a *C. albicans* polypeptide can be modified to incorporate one or more polymorphisms in the amino acid sequence of the protein resulting from any natural allelic variation. Additionally, D-amino acids, non-natural amino acids, or non-amino acid analogs can be substituted or added to produce a modified protein within the scope of this invention. Furthermore, a *C.*
30 *albicans* polypeptide can be modified using polyethylene glycol (PEG) according to the method of A. Schon and co-workers (Wie et al., *supra*) to produce a protein

conjugated with PEG. In addition, PEG can be added during chemical synthesis of the protein. Other modifications of *C. albicans* proteins include reduction/alkylation (Tarr, *Methods of Protein Microcharacterization*, J. E. Silver ed., Humana Press, Clifton NJ 155-194 (1986)); acylation (Tarr, *supra*); chemical coupling to an appropriate carrier (Mishell and Shiigi, eds, *Selected Methods in Cellular Immunology*, WH Freeman, San Francisco, CA (1980), U.S. Patent 4,939,239; or mild formalin treatment (Marsh, (1971) *Int. Arch. of Allergy and Appl. Immunol.*, 41: 199 - 215).

To facilitate purification and potentially increase solubility of a *C. albicans* protein or peptide, it is possible to add an amino acid fusion moiety to the peptide backbone. For example, hexa-histidine can be added to the protein for purification by immobilized metal ion affinity chromatography (Hochuli, E. et al., (1988) *Bio/Technology*, 6: 1321 - 1325). In addition, to facilitate isolation of peptides free of irrelevant sequences, specific endoprotease cleavage sites can be introduced between the sequences of the fusion moiety and the peptide.

To potentially aid proper antigen processing of epitopes within a *C. albicans* polypeptide, canonical protease sensitive sites can be engineered between regions, each comprising at least one epitope via recombinant or synthetic methods. For example, charged amino acid pairs, such as KK or RR, can be introduced between regions within a protein or fragment during recombinant construction thereof. The resulting peptide can be rendered sensitive to cleavage by cathepsin and/or other trypsin-like enzymes which would generate portions of the protein containing one or more epitopes. In addition, such charged amino acid residues can result in an increase in the solubility of the peptide.

25

Primary Methods for Screening Polypeptides and Analogs

Various techniques are known in the art for screening generated mutant gene products. Techniques for screening large gene libraries often include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the genes under conditions in which detection of a desired activity, e.g., in this case, binding to *C. albicans* polypeptide or

30

an interacting protein, facilitates relatively easy isolation of the vector encoding the gene whose product was detected. Each of the techniques described below is amenable to high through-put analysis for screening large numbers of sequences created, e.g., by random mutagenesis techniques.

5 Two Hybrid Systems

Two hybrid assays such as the system described below (as with the other screening methods described herein), can be used to identify polypeptides, e.g., fragments or analogs of a naturally-occurring *C. albicans* polypeptide, e.g., of cellular proteins, or of randomly generated polypeptides which bind to a *C. albicans* protein.
10 (The *C. albicans* domain is used as the bait protein and the library of variants are expressed as prey fusion proteins.) In an analogous fashion, a two hybrid assay (as with the other screening methods described herein), can be used to find polypeptides which bind a *C. albicans* polypeptide.

Display Libraries

15
15 In one approach to screening assays, the candidate peptides are displayed on the surface of a cell or viral particle, and the ability of particular cells or viral particles to bind an appropriate receptor protein via the displayed product is detected in a "panning assay". For example, the gene library can be cloned into the gene for a surface membrane protein of a fungal cell, and the resulting fusion protein detected by
20 panning (Ladner et al., WO 88/06630; Fuchs et al. (1991) *Bio/Technology* 9:1370-1371; and Goward et al. (1992) *TIBS* 18:136-140). In a similar fashion, a detectably labeled ligand can be used to score for potentially functional peptide homologs. Fluorescently labeled ligands, e.g., receptors, can be used to detect homologs which retain ligand-binding activity. The use of fluorescently labeled ligands, allows cells to
25 be visually inspected and separated under a fluorescence microscope, or, where the morphology of the cell permits, to be separated by a fluorescence-activated cell sorter.

A gene library can be expressed as a fusion protein on the surface of a viral particle. For instance, in the filamentous phage system, foreign peptide sequences can be expressed on the surface of infectious phage, thereby conferring two significant
30 benefits. First, since these phage can be applied to affinity matrices at concentrations

well over 10^{13} phage per milliliter, a large number of phage can be screened at one time. Second, since each infectious phage displays a gene product on its surface, if a particular phage is recovered from an affinity matrix in low yield, the phage can be amplified by another round of infection. The group of almost identical *E. coli* filamentous phages, M13, fd., and f1, are most often used in phage display libraries. Either of the phage gIII or gVIII coat proteins can be used to generate fusion proteins without disrupting the ultimate packaging of the viral particle. Foreign epitopes can be expressed at the NH₂-terminal end of pIII and phage bearing such epitopes recovered from a large excess of phage lacking this epitope (Ladner et al. PCT publication WO 90/02909; Garrard et al., PCT publication WO 92/09690; Marks et al. (1992) *J. Biol. Chem.* 267:16007-16010; Griffiths et al. (1993) *EMBO J* 12:725-734; Clackson et al. (1991) *Nature* 352:624-628; and Barbas et al. (1992) *PNAS* 89:4457-4461).

A common approach uses the maltose receptor of *E. coli* (the outer membrane protein, LamB) as a peptide fusion partner (Charbit et al. (1986) *EMBO* 5, 3029-3037). Oligonucleotides have been inserted into plasmids encoding the LamB gene to produce peptides fused into one of the extracellular loops of the protein. These peptides are available for binding to ligands, e.g., to antibodies, and can elicit an immune response when the cells are administered to animals. Other cell surface proteins, e.g., OmpA (Schorr et al. (1991) *Vaccines* 91, pp. 387-392), PhoE (Agterberg, et al. (1990) *Gene* 88, 37-45), and PAL (Fuchs et al. (1991) *Bio/Tech* 9, 1369-1372), as well as large bacterial surface structures have served as vehicles for peptide display. Peptides can be fused to pilin, a protein which polymerizes to form the pilus-a conduit for interbacterial exchange of genetic information (Thiry et al. (1989) *Appl. Environ. Microbiol.* 55, 984-993). Because of its role in interacting with other cells, the pilus provides a useful support for the presentation of peptides to the extracellular environment. Another large surface structure used for peptide display is the bacterial motive organ, the flagellum. Fusion of peptides to the subunit protein flagellin offers a dense array of many peptide copies on the host cells (Kuwajima et al. (1988) *Bio/Tech.* 6, 1080-1083). Surface proteins of other bacterial species have also served as peptide fusion partners. Examples include the *Staphylococcus* protein

A and the outer membrane IgA protease of *Neisseria* (Hansson et al. (1992) *J. Bacteriol.* 174, 4239-4245 and Klauser et al. (1990) *EMBO J.* 9, 1991-1999).

In the filamentous phage systems and the LamB system described above, the physical link between the peptide and its encoding DNA occurs by the containment of the DNA within a particle (cell or phage) that carries the peptide on its surface. Capturing the peptide captures the particle and the DNA within. An alternative scheme uses the DNA-binding protein LacI to form a link between peptide and DNA (Cull et al. (1992) *PNAS USA* 89:1865-1869). This system uses a plasmid containing the LacI gene with an oligonucleotide cloning site at its 3'-end. Under the controlled induction by arabinose, a LacI-peptide fusion protein is produced. This fusion retains the natural ability of LacI to bind to a short DNA sequence known as LacO operator (LacO). By installing two copies of LacO on the expression plasmid, the LacI-peptide fusion binds tightly to the plasmid that encoded it. Because the plasmids in each cell contain only a single oligonucleotide sequence and each cell expresses only a single peptide sequence, the peptides become specifically and stably associated with the DNA sequence that directed its synthesis. The cells of the library are gently lysed and the peptide-DNA complexes are exposed to a matrix of immobilized receptor to recover the complexes containing active peptides. The associated plasmid DNA is then reintroduced into cells for amplification and DNA sequencing to determine the identity of the peptide ligands. As a demonstration of the practical utility of the method, a large random library of dodecapeptides was made and selected on a monoclonal antibody raised against the opioid peptide dynorphin B. A cohort of peptides was recovered, all related by a consensus sequence corresponding to a six-residue portion of dynorphin B. (Cull et al. (1992) *Proc. Natl. Acad. Sci. U.S.A.* 89-1869)

This scheme, sometimes referred to as peptides-on-plasmids, differs in two important ways from the phage display methods. First, the peptides are attached to the C-terminus of the fusion protein, resulting in the display of the library members as peptides having free carboxy termini. Both of the filamentous phage coat proteins, pIII and pVIII, are anchored to the phage through their C-termini, and the guest peptides are placed into the outward-extending N-terminal domains. In some designs,

the phage-displayed peptides are presented right at the amino terminus of the fusion protein. (Cwirla, et al. (1990) *Proc. Natl. Acad. Sci. U.S.A.* 87, 6378-6382) A second difference is the set of biological biases affecting the population of peptides actually present in the libraries. The LacI fusion molecules are confined to the cytoplasm of the host cells. The phage coat fusions are exposed briefly to the cytoplasm during translation but are rapidly secreted through the inner membrane into the periplasmic compartment, remaining anchored in the membrane by their C-terminal hydrophobic domains, with the N-termini, containing the peptides, protruding into the periplasm while awaiting assembly into phage particles. The peptides in the LacI and phage libraries may differ significantly as a result of their exposure to different proteolytic activities. The phage coat proteins require transport across the inner membrane and signal peptidase processing as a prelude to incorporation into phage. Certain peptides exert a deleterious effect on these processes and are underrepresented in the libraries (Gallop et al. (1994) *J. Med. Chem.* 37(9):1233-1251). These particular biases are not a factor in the LacI display system.

The number of small peptides available in recombinant random libraries is enormous. Libraries of 10^7 - 10^9 independent clones are routinely prepared. Libraries as large as 10^{11} recombinants have been created, but this size approaches the practical limit for clone libraries. This limitation in library size occurs at the step of transforming the DNA containing randomized segments into the host bacterial cells. To circumvent this limitation, an *in vitro* system based on the display of nascent peptides in polysome complexes has recently been developed. This display library method has the potential of producing libraries 3-6 orders of magnitude larger than the currently available phage/phagemid or plasmid libraries. Furthermore, the construction of the libraries, expression of the peptides, and screening, is done in an entirely cell-free format.

In one application of this method (Gallop et al. (1994) *J. Med. Chem.* 37(9):1233-1251), a molecular DNA library encoding 10^{12} decapeptides was constructed and the library expressed in an *E. coli* S30 *in vitro* coupled transcription/translation system. Conditions were chosen to stall the ribosomes on the mRNA, causing the accumulation of a substantial proportion of the RNA in

polysomes and yielding complexes containing nascent peptides still linked to their encoding RNA. The polysomes are sufficiently robust to be affinity purified on immobilized receptors in much the same way as the more conventional recombinant peptide display libraries are screened. RNA from the bound complexes is recovered, converted to cDNA, and amplified by PCR to produce a template for the next round of synthesis and screening. The polysome display method can be coupled to the phage display system. Following several rounds of screening, cDNA from the enriched pool of polysomes was cloned into a phagemid vector. This vector serves as both a peptide expression vector, displaying peptides fused to the coat proteins, and as a DNA sequencing vector for peptide identification. By expressing the polysome-derived peptides on phage, one can either continue the affinity selection procedure in this format or assay the peptides on individual clones for binding activity in a phage ELISA, or for binding specificity in a completion phage ELISA (Barret, et al. (1992) *Anal. Biochem* 204,357-364). To identify the sequences of the active peptides one sequences the DNA produced by the phagemid host.

Secondary Screening of Polypeptides and Analogs

The high through-put assays described above can be followed by secondary screens in order to identify further biological activities which will, e.g., allow one skilled in the art to differentiate agonists from antagonists. The type of a secondary screen used will depend on the desired activity that needs to be tested. For example, an assay can be developed in which the ability to inhibit an interaction between a protein of interest and its respective ligand can be used to identify antagonists from a group of peptide fragments isolated through one of the primary screens described above.

Therefore, methods for generating fragments and analogs and testing them for activity are known in the art. Once the core sequence of interest is identified, it is routine for one skilled in the art to obtain analogs and fragments.

Peptide Mimetics of *C. albicans* Polypeptides

The invention also provides for reduction of the protein binding domains of

the subject *C. albicans* polypeptides to generate mimetics, e.g. peptide or non-peptide agents. The peptide mimetics are able to disrupt binding of a polypeptide to its counter ligand, e.g., in the case of a *C. albicans* polypeptide binding to a naturally occurring ligand. The critical residues of a subject *C. albicans* polypeptide which are
5 involved in molecular recognition of a polypeptide can be determined and used to generate *C. albicans*-derived peptidomimetics which competitively or noncompetitively inhibit binding of the *C. albicans* polypeptide with an interacting polypeptide (see, for example, European patent applications EP-412,762A and EP-B31,080A).

10 For example, scanning mutagenesis can be used to map the amino acid residues of a particular *C. albicans* polypeptide involved in binding an interacting polypeptide, peptidomimetic compounds (e.g. diazepam or isoquinoline derivatives) can be generated which mimic those residues in binding to an interacting polypeptide, and which therefore can inhibit binding of a *C. albicans* polypeptide to an interacting
15 polypeptide and thereby interfere with the function of *C. albicans* polypeptide. For instance, non-hydrolyzable peptide analogs of such residues can be generated using benzodiazepine (e.g., see Freidinger et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), azepine (e.g., see Huffman et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM
20 Publisher: Leiden, Netherlands, 1988), substituted gamma lactam rings (Garvey et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), keto-methylene pseudopeptides (Ewenson et al. (1986) *J Med Chem* 29:295; and Ewenson et al. in *Peptides: Structure and Function* (Proceedings of the 9th American Peptide Symposium) Pierce Chemical Co. Rockland, IL, 1985),
25 b-turn dipeptide cores (Nagai et al. (1985) *Tetrahedron Lett* 26:647; and Sato et al. (1986) *J Chem Soc Perkin Trans* 1:1231), and b-aminoalcohols (Gordon et al. (1985) *Biochem Biophys Res Commun* 126:419; and et al. (1986) *Biochem Biophys Res Commun* 134:71).

30 Vaccine Formulations for *C. albicans* Nucleic Acids and Polypeptides

This invention also features vaccine compositions for protection against

infection by *C. albicans* or for treatment of *C. albicans* infection. In one embodiment, the vaccine compositions contain one or more immunogenic components such as a surface protein from *C. albicans*, or portion thereof, and a pharmaceutically acceptable carrier. Nucleic acids within the scope of the invention are exemplified by the nucleic acids of the invention contained in the Sequence Listing which encode *C. albicans* surface proteins. Any nucleic acid encoding an immunogenic *C. albicans* protein, or portion thereof, which is capable of expression in a cell, can be used in the present invention. These vaccines have therapeutic and prophylactic utilities.

One aspect of the invention provides a vaccine composition for protection against infection by *C. albicans* which contains at least one immunogenic fragment of a *C. albicans* protein and a pharmaceutically acceptable carrier. Preferred fragments include peptides of at least about 10 amino acid residues in length, preferably about 10-20 amino acid residues in length, and more preferably about 12-16 amino acid residues in length.

Immunogenic components of the invention can be obtained, for example, by screening polypeptides recombinantly produced from the corresponding fragment of the nucleic acid encoding the full-length *C. albicans* protein. In addition, fragments can be chemically synthesized using techniques known in the art such as conventional Merrifield solid phase f-Moc or t-Boc chemistry.

In one embodiment, immunogenic components are identified by the ability of the peptide to stimulate T cells. Peptides which stimulate T cells, as determined by, for example, T cell proliferation or cytokine secretion are defined herein as comprising at least one T cell epitope. T cell epitopes are believed to be involved in initiation and perpetuation of the immune response to the protein allergen which is responsible for the clinical symptoms of allergy. These T cell epitopes are thought to trigger early events at the level of the T helper cell by binding to an appropriate HLA molecule on the surface of an antigen presenting cell, thereby stimulating the T cell subpopulation with the relevant T cell receptor for the epitope. These events lead to T cell proliferation, lymphokine secretion, local inflammatory reactions, recruitment of additional immune cells to the site of antigen/T cell interaction, and activation of the B cell cascade, leading to the production of antibodies. A T cell epitope is the basic

element, or smallest unit of recognition by a T cell receptor, where the epitope comprises amino acids essential to receptor recognition (e.g., approximately 6 or 7 amino acid residues). Amino acid sequences which mimic those of the T cell epitopes are within the scope of this invention.

5 Screening immunogenic components can be accomplished using one or more of several different assays. For example, *in vitro*, peptide T cell stimulatory activity is assayed by contacting a peptide known or suspected of being immunogenic with an antigen presenting cell which presents appropriate MHC molecules in a T cell culture. Presentation of an immunogenic *C. albicans* peptide in association with appropriate
10 MHC molecules to T cells in conjunction with the necessary co-stimulation has the effect of transmitting a signal to the T cell that induces the production of increased levels of cytokines, particularly of interleukin-2 and interleukin-4. The culture supernatant can be obtained and assayed for interleukin-2 or other known cytokines. For example, any one of several conventional assays for interleukin-2 can be
15 employed, such as the assay described in *Proc. Natl. Acad. Sci USA*, 86: 1333 (1989) the pertinent portions of which are incorporated herein by reference. A kit for an assay for the production of interferon is also available from Genzyme Corporation (Cambridge, MA).

 Alternatively, a common assay for T cell proliferation entails measuring
20 tritiated thymidine incorporation. The proliferation of T cells can be measured *in vitro* by determining the amount of ³H-labeled thymidine incorporated into the replicating DNA of cultured cells. Therefore, the rate of DNA synthesis and, in turn, the rate of cell division can be quantified.

 Vaccine compositions of the invention containing immunogenic components
25 (e.g., *C. albicans* polypeptide or fragment thereof or nucleic acid encoding a *C. albicans* polypeptide or fragment thereof) preferably include a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier that does not cause an allergic reaction or other untoward effect in patients to whom it is administered. Suitable pharmaceutically acceptable carriers include, for example,
30 one or more of water, saline, phosphate buffered saline, dextrose, glycerol, ethanol and the like, as well as combinations thereof. Pharmaceutically acceptable carriers

may further comprise minor amounts of auxiliary substances such as wetting or emulsifying agents, preservatives or buffers, which enhance the shelf life or effectiveness of the antibody. For vaccines of the invention containing *C. albicans* polypeptides, the polypeptide is co-administered with a suitable adjuvant.

5 It will be apparent to those of skill in the art that the therapeutically effective amount of DNA or protein of this invention will depend, *inter alia*, upon the administration schedule, the unit dose of antibody administered, whether the protein or DNA is administered in combination with other therapeutic agents, the immune status and health of the patient, and the therapeutic activity of the particular protein or
10 DNA.

Vaccine compositions are conventionally administered parenterally, e.g., by injection, either subcutaneously or intramuscularly. Methods for intramuscular immunization are described by Wolff et al. (1990) *Science* 247: 1465-1468 and by Sedegah et al. (1994) *Immunology* 91: 9866-9870. Other modes of administration
15 include oral and pulmonary formulations, suppositories, and transdermal applications. Oral immunization is preferred over parenteral methods for inducing protection against infection by *C. albicans*. Cain et. al. (1993) *Vaccine* 11: 637-642. Oral formulations include such normally employed excipients as, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium
20 saccharine, cellulose, magnesium carbonate, and the like.

The vaccine compositions of the invention can include an adjuvant, including, but not limited to aluminum hydroxide; N-acetyl-muramyl--L-threonyl-D-isoglutamine (thr-MDP); N-acetyl-nor-muramyl-L-alanyl-D-isoglutamine (CGP 11637, referred to as nor-MDP); N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-
25 alanine-2-(1'-2'-dipalmitoyl-sn-glycero-3-hydroxyphosphoryloxy)-ethylamine (CGP 19835A, referred to as MTP-PE); RIBI, which contains three components from bacteria; monophosphoryl lipid A; trehalose dimycolate; cell wall skeleton (MPL + TDM + CWS) in a 2% squalene/Tween 80 emulsion; and cholera toxin. Others which may be used are non-toxic derivatives of cholera toxin, including its B subunit, and/or
30 conjugates or genetically engineered fusions of the *C. albicans* polypeptide with cholera toxin or its B subunit, procholeraenoid, fungal polysaccharides, including

schizophyllan, muramyl dipeptide, muramyl dipeptide derivatives, phorbol esters, labile toxin of *E. coli*, non-*C. albicans* fungal lysates, block polymers or saponins.

Other suitable delivery methods include biodegradable microcapsules or immuno-stimulating complexes (ISCOMs), cochleates, or liposomes, genetically engineered attenuated live vectors such as viruses or bacteria, and recombinant (chimeric) virus-like particles, e.g., bluetongue. The amount of adjuvant employed will depend on the type of adjuvant used. For example, when the mucosal adjuvant is cholera toxin, it is suitably used in an amount of 5 mg to 50 mg, for example 10 mg to 35 mg. When used in the form of microcapsules, the amount used will depend on the amount employed in the matrix of the microcapsule to achieve the desired dosage. The determination of this amount is within the skill of a person of ordinary skill in the art.

Carrier systems in humans may include enteric release capsules protecting the antigen from the acidic environment of the stomach, and including *C. albicans* polypeptide in an insoluble form as fusion proteins. Suitable carriers for the vaccines of the invention are enteric coated capsules and polylactide-glycolide microspheres. Suitable diluents are 0.2 N NaHCO₃ and/or saline.

Vaccines of the invention can be administered as a primary prophylactic agent in adults or in children, as a secondary prevention, after successful eradication of *C. albicans* in an infected host, or as a therapeutic agent in the aim to induce an immune response in a susceptible host to prevent infection by *C. albicans*. The vaccines of the invention are administered in amounts readily determined by persons of ordinary skill in the art. Thus, for adults a suitable dosage will be in the range of 10 mg to 10 g, preferably 10 mg to 100 mg. A suitable dosage for adults will also be in the range of 5 mg to 500 mg. Similar dosage ranges will be applicable for children. Those skilled in the art will recognize that the optimal dose may be more or less depending upon the patient's body weight, disease, the route of administration, and other factors. Those skilled in the art will also recognize that appropriate dosage levels can be obtained based on results with known oral vaccines such as, for example, a vaccine based on an *E. coli* lysate (6 mg dose daily up to total of 540 mg) and with an enterotoxigenic *E. coli* purified antigen (4 doses of 1 mg) (Schulman et al., *J. Urol.* 150:917-921 (1993);

Boedecker et al., *American Gastroenterological Assoc.* 999:A-222 (1993)). The number of doses will depend upon the disease, the formulation, and efficacy data from clinical trials. Without intending any limitation as to the course of treatment, the treatment can be administered over 3 to 8 doses for a primary immunization schedule
5 over 1 month (Boedecker, *American Gastroenterological Assoc.* 888:A-222 (1993)).

In a preferred embodiment, a vaccine composition of the invention can be based on a killed whole *E. coli* preparation with an immunogenic fragment of a *C. albicans* protein of the invention expressed on its surface or it can be based on an *E. coli* lysate, wherein the killed *E. coli* acts as a carrier or an adjuvant.

10 It will be apparent to those skilled in the art that some of the vaccine compositions of the invention are useful only for preventing *C. albicans* infection, some are useful only for treating *C. albicans* infection, and some are useful for both preventing and treating *C. albicans* infection. In a preferred embodiment, the vaccine composition of the invention provides protection against *C. albicans* infection by
15 stimulating humoral and/or cell-mediated immunity against *C. albicans*. It should be understood that amelioration of any of the symptoms of *C. albicans* infection is a desirable clinical goal, including a lessening of the dosage of medication used to treat *C. albicans*-caused disease, or an increase in the production of antibodies in the serum or mucous of patients.

20

Antibodies Reactive With *C. albicans* Polypeptides

The invention also includes antibodies specifically reactive with the subject *C. albicans* polypeptide. Anti-protein/anti-peptide antisera or monoclonal antibodies can be made by standard protocols (See, for example, *Antibodies: A Laboratory Manual*
25 ed. by Harlow and Lane (Cold Spring Harbor Press: 1988)). A mammal such as a mouse, a hamster or rabbit can be immunized with an immunogenic form of the peptide. Techniques for conferring immunogenicity on a protein or peptide include conjugation to carriers or other techniques well known in the art. An immunogenic portion of the subject *C. albicans* polypeptide can be administered in the presence of
30 adjuvant. The progress of immunization can be monitored by detection of antibody titers in plasma or serum. Standard ELISA or other immunoassays can be used with

the immunogen as antigen to assess the levels of antibodies.

In a preferred embodiment, the subject antibodies are immunospecific for antigenic determinants of the *C. albicans* polypeptides of the invention, e.g. antigenic determinants of a polypeptide of the invention contained in the Sequence Listing, or a
5 closely related human or non-human mammalian homolog (e.g., 90% homologous, more preferably at least about 95% homologous). In yet a further preferred embodiment of the invention, the anti-*C. albicans* antibodies do not substantially cross react (i.e., react specifically) with a protein which is for example, less than 80% percent homologous to a sequence of the invention contained in the Sequence
10 Listing. By "not substantially cross react", it is meant that the antibody has a binding affinity for a non-homologous protein which is less than 10 percent, more preferably less than 5 percent, and even more preferably less than 1 percent, of the binding affinity for a protein of the invention contained in the Sequence Listing. In a most preferred embodiment, there is no cross-reactivity between fungal and mammalian
15 antigens.

The term antibody as used herein is intended to include fragments thereof which are also specifically reactive with *C. albicans* polypeptides. Antibodies can be fragmented using conventional techniques and the fragments screened for utility in the same manner as described above for whole antibodies. For example, F(ab')₂
20 fragments can be generated by treating antibody with pepsin. The resulting F(ab')₂ fragment can be treated to reduce disulfide bridges to produce Fab' fragments. The antibody of the invention is further intended to include bispecific and chimeric molecules having an anti-*C. albicans* portion.

Both monoclonal and polyclonal antibodies (Ab) directed against *C. albicans*
25 polypeptides or *C. albicans* polypeptide variants, and antibody fragments such as Fab' and F(ab')₂, can be used to block the action of *C. albicans* polypeptide and allow the study of the role of a particular *C. albicans* polypeptide of the invention in aberrant or unwanted intracellular signaling, as well as the normal cellular function of the *C. albicans* and by microinjection of anti-*C. albicans* polypeptide antibodies of the
30 present invention.

Antibodies which specifically bind *C. albicans* epitopes can also be used in

immunohistochemical staining of tissue samples in order to evaluate the abundance and pattern of expression of *C. albicans* antigens. Anti-*C. albicans* polypeptide antibodies can be used diagnostically in immuno-precipitation and immuno-blotting to detect and evaluate *C. albicans* levels in tissue or bodily fluid as part of a clinical testing procedure. Likewise, the ability to monitor *C. albicans* polypeptide levels in an individual can allow determination of the efficacy of a given treatment regimen for an individual afflicted with such a disorder. The level of a *C. albicans* polypeptide can be measured in cells found in bodily fluid, such as in urine samples or can be measured in tissue, such as produced by gastric biopsy. Diagnostic assays using anti-*C. albicans* antibodies can include, for example, immunoassays designed to aid in early diagnosis of *C. albicans* infections. The present invention can also be used as a method of detecting antibodies contained in samples from individuals infected by this bacterium using specific *C. albicans* antigens.

Another application of anti-*C. albicans* polypeptide antibodies of the invention is in the immunological screening of cDNA libraries constructed in expression vectors such as λ gt11, λ gt18-23, λ ZAP, and λ ORF8. Messenger libraries of this type, having coding sequences inserted in the correct reading frame and orientation, can produce fusion proteins. For instance, λ gt11 will produce fusion proteins whose amino termini consist of β -galactosidase amino acid sequences and whose carboxy termini consist of a foreign polypeptide. Antigenic epitopes of a subject *C. albicans* polypeptide can then be detected with antibodies, as, for example, reacting nitrocellulose filters lifted from infected plates with anti-*C. albicans* polypeptide antibodies. Phage, scored by this assay, can then be isolated from the infected plate. Thus, the presence of *C. albicans* gene homologs can be detected and cloned from other species, and alternate isoforms (including splicing variants) can be detected and cloned.

Bio chip Technology

The nucleic acid sequences or fragments thereof of the present invention lend themselves to the detection of nucleic acid sequences or fragments thereof of *C. albicans* or other species of *Candida* using nanotechnology apparatus, compositions and methods, referred to generically herein as "bio chip" technology. Bio chips containing arrays of nucleic acid sequence can also be used to measure expression of genes of *C. albicans* or other species of *Candida*. For example, to diagnose a patient with a *C. albicans* or other *Candida* infection, a sample from a human or animal can be used as a probe on a bio chip containing an array of nucleic acid sequence from the present invention. In addition, a sample from a disease state can be compared to a sample from a non-disease state which would help identify a gene that is up-regulated or expressed in the disease state. This would provide valuable insight as to the mechanism by which the disease manifests. Changes in gene expression can also be used to identify critical pathways involved in drug transport or metabolism, and may enable the identification of novel targets involved in virulence or host cell interactions involved in maintenance of an infection. Procedures using such techniques have been described by Brown *et al.*, 1995, *Science* 270: 467-470.

Bio chip technology can also be used to monitor the genetic changes of potential therapeutic compounds including, deletions, insertions or mismatches. Once the therapeutic is added to the patient, changes to the genetic sequence can be evaluated for its efficacy. In addition, the nucleic acid sequence of the present invention can be used to determine essential genes in cell cycling. As described in Iyer *et al.*, 1999 (*Science*, 283:83-87) genes essential in the cell cycle can be identified using bio chips. Furthermore, the present invention provides nucleic acid sequences which can be used with bio chip technology to understand regulatory networks in bacteria, measure the response to environmental signals or drugs as in drug screening, and study virulence induction. (Mons *et al.*, 1998, *Nature Biotechnology*, 16: 45-48). Patents teaching this technology include U.S. Patents 5445934, 5744305, and 5800992.

Kits Containing Nucleic Acids, Polypeptides or Antibodies of the Invention

The nucleic acid, polypeptides and antibodies of the invention can be conveniently combined with other reagents and articles to form kits. Kits for diagnostic purposes typically comprise the nucleic acid, polypeptides or antibodies in vials or other suitable vessels. Kits typically comprise other reagents for performing hybridization reactions, polymerase chain reactions (PCR), or for reconstitution of lyophilized components, such as aqueous media, salts, buffers, and the like. Kits may also comprise reagents for sample processing such as detergents, chaotropic salts and the like. Kits may also comprise immobilization means such as particles, supports, wells, dipsticks and the like. Kits may also comprise labeling means such as dyes, developing reagents, radioisotopes, fluorescent agents, luminescent or chemiluminescent agents, enzymes, intercalating agents and the like. With the nucleic acid and amino acid sequence information provided herein, individuals skilled in art can readily assemble kits to serve their particular purpose. Kits further can include instructions for use.

Drug Screening Assays Using *C. albicans* Polypeptides

By making available purified and recombinant *C. albicans* polypeptides, the present invention provides assays which can be used to screen for drugs which are either agonists or antagonists of the normal cellular function, in this case, of the subject *C. albicans* polypeptides, or of their role in intracellular signaling. Such inhibitors or potentiators may be useful as new therapeutic agents to combat *C. albicans* infections in humans. A variety of assay formats will suffice and, in light of the present inventions, will be comprehended by the person skilled in the art.

In many drug screening programs which test libraries of compounds and natural extracts, high throughput assays are desirable in order to maximize the number of compounds surveyed in a given period of time. Assays which are performed in cell-free systems, such as may be derived with purified or semi-purified proteins, are often preferred as "primary" screens in that they can be generated to permit rapid development and relatively easy detection of an alteration in a molecular target which is mediated by a test compound. Moreover, the effects of cellular toxicity and/or

bioavailability of the test compound can be generally ignored in the *in vitro* system, the assay instead being focused primarily on the effect of the drug on the molecular target as may be manifest in an alteration of binding affinity with other proteins or change in enzymatic properties of the molecular target. Accordingly, in an exemplary
5 screening assay of the present invention, the compound of interest is contacted with an isolated and purified *C. albicans* polypeptide.

Screening assays can be constructed *in vitro* with a purified *C. albicans* polypeptide or fragment thereof, such as a *C. albicans* polypeptide having enzymatic activity, such that the activity of the polypeptide produces a detectable reaction
10 product. The efficacy of the compound can be assessed by generating dose response curves from data obtained using various concentrations of the test compound. Moreover, a control assay can also be performed to provide a baseline for comparison. Suitable products include those with distinctive absorption, fluorescence, or chemi-luminescence properties, for example, because detection may
15 be easily automated. A variety of synthetic or naturally occurring compounds can be tested in the assay to identify those which inhibit or potentiate the activity of the *C. albicans* polypeptide. Some of these active compounds may directly, or with chemical alterations to promote membrane permeability or solubility, also inhibit or potentiate the same activity (e.g., enzymatic activity) in whole, live *C. albicans* cells.

20

Overexpression Assays

Overexpression assays are based on the premise that overproduction of a protein would lead to a higher level of resistance to compounds that selectively interfere with the function of that protein. Overexpression assays may be used to
25 identify compounds that interfere with the function of virtually any type of protein, including without limitation enzymes, receptors, DNA- or RNA-binding proteins, or any proteins that are directly or indirectly involved in regulating cell growth.

Typically, two fungal strains are constructed. One contains a single copy of the gene of interest, and a second contains several copies of the same gene.
30 Identification of useful inhibitory compounds of this type of assay is based on a comparison of the activity of a test compound in inhibiting growth and/or viability of

the two strains. The method involves constructing a nucleic acid vector that directs high level expression of a particular target nucleic acid. The vectors are then transformed into host cells in single or multiple copies to produce strains that express low to moderate and high levels of protein encoding by the target sequence (strain A and B, respectively). Nucleic acid comprising sequences encoding the target gene
5 can, of course, be directly integrated into the host cell.

Large numbers of compounds (or crude substances which may contain active compounds) are screened for their effect on the growth of the two strains. Agents which interfere with an unrelated target equally inhibit the growth of both strains.
10 Agents which interfere with the function of the target at high concentration should inhibit the growth of both strains. It should be possible, however, to titrate out the inhibitory effect of the compound in the overexpressing strain. That is, if the compound is affecting the particular target that is being tested, it should be possible to inhibit the growth of strain A at a concentration of the compound that allows strain B
15 to grow.

Alternatively, a fungal strain is constructed that contains the gene of interest under the control of an inducible promoter. Identification of useful inhibitory agents using this type of assay is based on a comparison of the activity of a test compound in inhibiting growth and/or viability of this strain under both inducing and non-inducing
20 conditions. The method involves constructing a nucleic acid vector that directs high-level expression of a particular target nucleic acid. The vector is then transformed into host cells that are grown under both non-inducing and inducing conditions (conditions A and B, respectively).

Large numbers of compounds (or crude substances which may contain active
25 compounds) are screened for their effect on growth under these two conditions. Agents that interfere with the function of the target should inhibit growth under both conditions. It should be possible, however, to titrate out the inhibitory effect of the compound in the overexpressing strain. That is, if the compound is affecting the particular target that is being tested, it should be possible to inhibit growth under
30 condition A at a concentration that allows the strain to grow under condition B.

Ligand-binding Assays

Many of the targets according to the invention have functions that have not yet been identified. Ligand-binding assays are useful to identify inhibitor compounds that interfere with the function of a particular target, even when that function is unknown.

5 These assays are designed to detect binding of test compounds to particular targets. The detection may involve direct measurement of binding. Alternatively, indirect indications of binding may involve stabilization of protein structure or disruption of a biological function. Non-limiting examples of useful ligand-binding assays are detailed below.

10 A useful method for the detection and isolation of binding proteins is the Biomolecular Interaction Assay (BIAcore) system developed by Pharmacia Biosensor and described in the manufacturer's protocol (LKB Pharmacia, Sweden). The BIAcore system uses an affinity purified anti-GST antibody to immobilize GST-fusion proteins onto a sensor chip. The sensor utilizes surface plasmon resonance
15 which is an optical phenomenon that detects changes in refractive indices. In accordance with the practice of the invention, a protein of interest is coated onto a chip and test compounds are passed over the chip. Binding is detected by a change in the refractive index (surface plasmon resonance).

A different type of ligand-binding assay involves scintillation proximity
20 assays (SPA, described in U.S. Patent No. 4,568,649).

Another type of ligand binding assay, also undergoing development, is based on the fact that proteins containing mitochondrial targeting signals are imported into isolated mitochondria *in vitro* (Hurt *et al.*, 1985, *Embo J.* 4:2061-2068; Eilers and Schatz, *Nature*, 1986, 322:228-231). In a mitochondrial import assay, expression
25 vectors are constructed in which nucleic acids encoding particular target proteins are inserted downstream of sequences encoding mitochondrial import signals. The chimeric proteins are synthesized and tested for their ability to be imported into isolated mitochondria in the absence and presence of test compounds. A test compound that binds to the target protein should inhibit its uptake into isolated
30 mitochondria *in vitro*.

Another ligand-binding assay is the yeast two-hybrid system (Fields and Song, 1989, *Nature* 340:245-246). The yeast two-hybrid system takes advantage of the properties of the GAL4 protein of the yeast *Saccharomyces cerevisiae*. The GAL4 protein is a transcriptional activator required for the expression of genes encoding enzymes of galactose utilization. This protein consists of two separable and functionally essential domains: an N-terminal domain which binds to specific DNA sequences (UAS_G); and a C-terminal domain containing acidic regions, which is necessary to activate transcription. The native GAL4 protein, containing both domains, is a potent activator of transcription when yeast are grown on galactose media. The N-terminal domain binds to DNA in a sequence-specific manner but is unable to activate transcription. The C-terminal domain contains the activating regions but cannot activate transcription because it fails to be localized to UAS_G. In the two-hybrid system, a system of two hybrid proteins containing parts of GAL4: (1) a GAL4 DNA-binding domain fused to a protein 'X' and (2) a GAL4 activation region fused to a protein 'Y'. If X and Y can form a protein-protein complex and reconstitute proximity of the GAL4 domains, transcription of a gene regulated by UAS_G occurs. Creation of two hybrid proteins, each containing one of the interacting proteins X and Y, allows the activation region of UAS_G to be brought to its normal site of action.

The binding assay described in Fodor *et al.*, 1991, *Science* 251:767-773, which involves testing the binding affinity of test compounds for a plurality of defined polymers synthesized on a solid substrate, may also be useful.

Compounds which bind to the polypeptides of the invention are potentially useful as antifungal agents for use in therapeutic compositions.

Pharmaceutical formulations suitable for antifungal therapy comprise the antifungal agent in conjunction with one or more biologically acceptable carriers. Suitable biologically acceptable carriers include, but are not limited to, phosphate-buffered saline, saline, deionized water, or the like. Preferred biologically acceptable carriers are physiologically or pharmaceutically acceptable carriers.

The antifungal compositions include an antifungal effective amount of active agent. Antifungal effective amounts are those quantities of the antifungal agents of the present invention that afford prophylactic protection against fungal infections or which result in amelioration or cure of an existing fungal infection. This antifungal effective amount will depend upon the agent, the location and nature of the infection,

and the particular host. The amount can be determined by experimentation known in the art, such as by establishing a matrix of dosages and frequencies and comparing a group of experimental units or subjects to each point in the matrix.

5 The antifungal active agents or compositions can be formed into dosage unit forms, such as for example, creams, ointments, lotions, powders, liquids, tablets, capsules, suppositories, sprays, aerosols or the like. If the antifungal composition is formulated into a dosage unit form, the dosage unit form may contain an antifungal effective amount of active agent. Alternatively, the dosage unit form may include less than such an amount if multiple dosage unit forms or multiple dosages are to be used
10 to administer a total dosage of the active agent. Dosage unit forms can include, in addition, one or more excipient(s), diluent(s), disintegrant(s), lubricant(s), plasticizer(s), colorant(s), dosage vehicle(s), absorption enhancer(s), stabilizer(s), bactericide(s), or the like.

For general information concerning formulations, see, e.g., Gilman et al. (eds.), 1990, *Goodman and Gilman's: The Pharmacological Basis of Therapeutics*,
15 8th ed., Pergamon Press; and *Remington's Pharmaceutical Sciences*, 17th ed., 1990, Mack Publishing Co., Easton, PA; Avis et al. (eds.), 1993, *Pharmaceutical Dosage Forms: Parenteral Medications*, Dekker, New York; Lieberman et al (eds.), 1990, *Pharmaceutical Dosage Forms: Disperse Systems*, Dekker, New York.

20 The antifungal agents and compositions of the present invention are useful for preventing or treating *C. albicans* infections. Infection prevention methods incorporate a prophylactically effective amount of an antifungal agent or composition. A prophylactically effective amount is an amount effective to prevent *C. albicans* infection and will depend upon the specific fungal strain, the agent, and the host.
25 These amounts can be determined experimentally by methods known in the art and as described above.

C. albicans infection treatment methods incorporate a therapeutically effective amount of an antifungal agent or composition. A therapeutically effective amount is an amount sufficient to ameliorate or eliminate the infection. The prophylactically
30 and/or therapeutically effective amounts can be administered in one administration or over repeated administrations. Therapeutic administration can be followed by

prophylactic administration, once the initial fungal infection has been resolved.

The antifungal agents and compositions can be administered topically or systemically. Topical application is typically achieved by administration of creams, ointments, lotions, or sprays as described above. Systemic administration includes both oral and parental routes. Parental routes include, without limitation, subcutaneous, intramuscular, intraperitoneal, intravenous, transdermal, inhalation and intranasal administration.

EXEMPLIFICATION

10 Cloning and Sequencing *C. albicans* Genomic Sequence

This invention provides nucleotide sequences of the genome of *C. albicans* which thus comprises a DNA sequence library of *C. albicans* genomic DNA. The detailed description that follows provides nucleotide sequences of *C. albicans*, and also describes how the sequences were obtained and how ORFs (Open Reading Frames) and protein-coding sequences can be identified. Also described are methods of using the disclosed *C. albicans* sequences in methods including diagnostic and therapeutic applications. Furthermore, the library can be used as a database for identification and comparison of medically important sequences in this and other strains of *C. albicans* as well as other species of *Candida*.

20 Chromosomal DNA from strain SC5314 of *C. albicans* was isolated after Zymolyase digestion, sodium dodecyl sulfate lysis, potassium acetate precipitation, phenol:chloroform extraction and ethanol precipitation (Soll, D.R., T. Srikantha and S.R. Lockhart: Characterizing Developmentally Regulated Genes in *C. albicans*. In Microbial Genome Methods. K.W. Adolph, editor. CRC Press. New York. p 17-37.).

25 Genomic *C. albicans* DNA was hydrodynamically sheared in an HPLC and then separated on a standard 1% agarose gel. Fractions corresponding to 2500-3000 bp in length were excised from the gel and purified by the GeneClean procedure (Bio101, Inc.).

The purified DNA fragments were then blunt-ended using T4 DNA polymerase. The healed DNA was then ligated to unique *Bst*XI-linker adapters (5'-GTCTTCACCAACGGGG-3' and 5'-GTGGTGAAGAC-3' in 100-1000 fold molar

30

excess). These linkers are complimentary to the *Bst*XI-cut pGTC vector, while the overhang is not self-complimentary. Therefore, the linkers will not concatemerize nor will the cut-vector religate itself easily. The linker-adapted inserts were separated from the unincorporated linkers on a 1% agarose gel and purified using GeneClean.

- 5 The linker-adapted inserts were then ligated to *Bst*XI-cut vector to construct a “shotgun” subclone libraries.

Only major modifications to the protocols are highlighted. Briefly, the library was then transformed into DH5 α competent cells (Gibco/BRL, DH5 α transformation protocol). It was assessed by plating onto antibiotic plates containing ampicillin and
10 IPTG/Xgal. The plates were incubated overnight at 37°C. Transformants were then used for plating of clones and picking for sequencing. The cultures were grown overnight at 37°C. DNA was purified using a silica bead DNA preparation (Engelstein, 1996) method. In this manner, 25 μ g of DNA was obtained per clone.

These purified DNA samples were then sequenced using primarily ABI dye-terminator chemistry. All subsequent steps were based on sequencing by ABI377
15 automated DNA sequencing methods. The ABI dye terminator sequence reads were run on ABI377 machines and the data was transferred to UNIX machines following lane tracking of the gels. Base calls and quality scores were determined using the program PHRED (Ewing et al., 1998, Genome Res. 8: 175-185; Ewing and Green, 1998, Genome Res. 8: 685-734). Reads were assembled using PHRAP (P. Green,
20 Abstracts of DOE Human Genome Program Contractor-Grantee Workshop V, Jan. 1996, p.157) with default program parameters and quality scores. The initial assembly was done at 2.3-fold coverage and yielded 5821 contigs.

Finishing could follow the initial assembly. Missing mates (sequences from
25 clones that only gave reads from one end of the *Candida* DNA inserted in the plasmid) could be identified and sequenced with ABI technology to allow the identification of additional overlapping contigs.

End-sequencing of randomly picked genomic lambda was also performed. Sequencing on a both sides was done for all lambda sequences. The lambda library
30 backbone helped to verify the integrity of the assembly and allowed closure of some of the physical gaps. Primers for walking off the ends of contigs would be selected

using pick_primer (a GTC program) near the ends of the clones to facilitate gap closure. These walks could be sequenced using the selected clones and primers. These data are then reassembled with PHRAP. Additional sequencing using PCR-generated templates and screened and/or unscreened lambda templates could be done
5 in addition.

To identify *C. albicans* polypeptides the complete genomic sequence of *C. albicans* was analyzed essentially as follows: First, all possible stop-to-stop open reading frames (ORFs) greater than 180 nucleotides in all six reading frames were translated into amino acid sequences. Second, the identified ORFs were analyzed for
10 homology to known (archeabacter, prokaryotic and eukaryotic) protein sequences. Third, the coding potential of non-homologous sequences was evaluated with the program GENEMARKTM (Borodovsky and McIninch, 1993, Comp. Chem. 17:123).

Identification, Cloning and Expression of *C. albicans* Nucleic Acids

15 Expression and purification of the *C. albicans* polypeptides of the invention can be performed essentially as outlined below.

To facilitate the cloning, expression and purification of membrane and secreted proteins from *C. albicans*, a gene expression system, such as the pET System (Novagen), for cloning and expression of recombinant proteins in *E. coli*, is selected.
20 Also, a DNA sequence encoding a peptide tag, the His-Tag, is fused to the 3' end of DNA sequences of interest in order to facilitate purification of the recombinant protein products. The 3' end is selected for fusion in order to avoid alteration of any 5' terminal signal sequence.

25 PCR Amplification and Cloning of Nucleic Acids Containing ORF's Encoding Enzymes

Nucleic acids chosen (for example, from the nucleic acids set forth in SEQ ID NO: 1 - SEQ ID NO: 14103) for cloning from strain SC5314 of *C. albicans* are prepared for amplification cloning by polymerase chain reaction (PCR). Synthetic
30 oligonucleotide primers specific for the 5' and 3' ends of open reading frames (ORFs) are designed and purchased from GibcoBRL Life Technologies

(Gaithersburg, MD, USA). All forward primers (specific for the 5' end of the sequence) are designed to include an NcoI cloning site at the extreme 5' terminus. These primers are designed to permit initiation of protein translation at a methionine residue followed by a valine residue and the coding sequence for the remainder of the native *C. albicans* DNA sequence. All reverse primers (specific for the 3' end of any *C. albicans* ORF) include a EcoRI site at the extreme 5' terminus to permit cloning of each *C. albicans* sequence into the reading frame of the pET-28b. The pET-28b vector provides sequence encoding an additional 20 carboxy-terminal amino acids including six histidine residues (at the extreme C-terminus), which comprise the His-Tag.

Genomic DNA prepared from strain SC5314 of *C. albicans* is used as the source of template DNA for PCR amplification reactions (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). To amplify a DNA sequence containing an *C. albicans* ORF, genomic DNA (50 nanograms) is introduced into a reaction vial containing 2 mM MgCl₂, 1 micromolar synthetic oligonucleotide primers (forward and reverse primers) complementary to and flanking a defined *C. albicans* ORF, 0.2 mM of each deoxynucleotide triphosphate; dATP, dGTP, dCTP, dTTP and 2.5 units of heat stable DNA polymerase (Amplitaq, Roche Molecular Systems, Inc., Branchburg, NJ, USA) in a final volume of 100 microliters.

Upon completion of thermal cycling reactions, each sample of amplified DNA is washed and purified using the Qiaquick Spin PCR purification kit (Qiagen, Gaithersburg, MD, USA). All amplified DNA samples are subjected to digestion with the restriction endonucleases, e.g., NcoI and EcoRI (New England BioLabs, Beverly, MA, USA)(Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). DNA samples are then subjected to electrophoresis on 1.0 % NuSeive (FMC BioProducts, Rockland, ME USA) agarose gels. DNA is visualized by exposure to ethidium bromide and long wave uv irradiation. DNA contained in slices isolated from the agarose gel is purified using the Bio 101 GeneClean Kit protocol (Bio 101 Vista, CA, USA).

Cloning of *C. albicans* Nucleic Acids Into an Expression Vector

The pET-28b vector is prepared for cloning by digestion with restriction endonucleases, e.g., NcoI and EcoRI (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). The pET-28a vector, which
5 encodes a His-Tag that can be fused to the 5' end of an inserted gene, is prepared by digestion with appropriate restriction endonucleases.

Following digestion, DNA inserts are cloned (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994) into the previously digested pET-28b expression vector. Products of the ligation reaction are then used to
10 transform the BL21 strain of *E. coli* (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994) as described below.

Transformation Of Competent Bacteria With Recombinant Plasmids

Competent bacteria, *E. coli* strain BL21 or *E. coli* strain BL21(DE3), are
15 transformed with recombinant pET expression plasmids carrying the cloned *C. albicans* sequences according to standard methods (Current Protocols in Molecular, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). Briefly, 1 microliter of ligation reaction is mixed with 50 microliters of electrocompetent cells and subjected to a high voltage pulse, after which, samples are incubated in 0.45 milliliters SOC
20 medium (0.5% yeast extract, 2.0 % tryptone, 10 mM NaCl, 2.5 mM KCl, 10 mM MgCl₂, 10 mM MgSO₄ and 20, mM glucose) at 37°C with shaking for 1 hour. Samples are then spread on LB agar plates containing 25 microgram/ml kanamycin sulfate for growth overnight. Transformed colonies of BL21 are then picked and analyzed to evaluate cloned inserts as described below.

25

Identification Of Recombinant Expression Vectors With *C. albicans* Nucleic Acids

Individual BL21 clones transformed with recombinant pET-28b *C. albicans* ORFs are analyzed by PCR amplification of the cloned inserts using the same forward and reverse primers, specific for each *C. albicans* sequence, that were used in the
30 original PCR amplification cloning reactions. Successful amplification verifies the integration of the *C. albicans* sequences in the expression vector (Current Protocols in

Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994).

Isolation and Preparation of Nucleic Acids From Transformants

Individual clones of recombinant pET-28b vectors carrying properly cloned *C. albicans* ORFs are picked and incubated in 5 mls of LB broth plus 25 microgram/ml kanamycin sulfate overnight. The following day plasmid DNA is isolated and purified using the Qiagen plasmid purification protocol (Qiagen Inc., Chatsworth, CA, USA).

10 Expression Of Recombinant *C. albicans* Sequences In *E. coli*

The pET vector can be propagated in any *E. coli* K-12 strain e.g. HMS174, HB101, JM109, DH5, etc. for the purpose of cloning or plasmid preparation. Hosts for expression include *E. coli* strains containing a chromosomal copy of the gene for T7 RNA polymerase. These hosts are lysogens of bacteriophage DE3, a lambda derivative that carries the *lacI* gene, the *lacUV5* promoter and the gene for T7 RNA polymerase. T7 RNA polymerase is induced by addition of isopropyl-B-D-thiogalactoside (IPTG), and the T7 RNA polymerase transcribes any target plasmid, such as pET-28b, carrying its gene of interest. Strains used include: BL21(DE3) (Studier, F.W., Rosenberg, A.H., Dunn, J.J., and Dubendorff, J.W. (1990) Meth. Enzymol. 185, 60-89).

To express recombinant *C. albicans* sequences, 50 nanograms of plasmid DNA isolated as described above is used to transform competent BL21(DE3) bacteria as described above (provided by Novagen as part of the pET expression system kit). The *lacZ* gene (beta-galactosidase) is expressed in the pET-System as described for the *C. albicans* recombinant constructions. Transformed cells are cultured in SOC medium for 1 hour, and the culture is then plated on LB plates containing 25 micrograms/ml kanamycin sulfate. The following day, fungal colonies are pooled and grown in LB medium containing kanamycin sulfate (25 micrograms/ml) to an optical density at 600 nm of 0.5 to 1.0 O.D. units, at which point, 1 millimolar IPTG was added to the culture for 3 hours to induce gene expression of the *C. albicans* recombinant DNA constructions .

After induction of gene expression with IPTG, bacteria are pelleted by centrifugation in a Sorvall RC-3B centrifuge at 3500 x g for 15 minutes at 4°C. Pellets are resuspended in 50 milliliters of cold 10 mM Tris-HCl, pH 8.0, 0.1 M NaCl and 0.1 mM EDTA (STE buffer). Cells are then centrifuged at 2000 x g for 20 min at 4°C. Wet pellets are weighed and frozen at -80°C until ready for protein purification.

A variety of methodologies known in the art can be utilized to purify the isolated proteins. (Current Protocols in Protein Science, John Wiley and Sons, Inc., J. E. Coligan et al., eds., 1995). For example, the frozen cells are thawed, resuspended in buffer and ruptured by several passages through a small volume microfluidizer (Model M-110S, Microfluidics International Corporation, Newton, MA). The resultant homogenate is centrifuged to yield a clear supernatant (crude extract) and following filtration the crude extract is fractionated over columns. Fractions are monitored by absorbance at OD₂₈₀ nm. and peak fractions may analyzed by SDS-PAGE.

The concentrations of purified protein preparations are quantified spectrophotometrically using absorbance coefficients calculated from amino acid content (Perkins, S.J. 1986 Eur. J. Biochem. 157, 169-180). Protein concentrations are also measured by the method of Bradford, M.M. (1976) Anal. Biochem. 72; 248-254, and Lowry, O.H., Rosebrough, N., Farr, A.L. & Randall, R.J. (1951) J. Biol. Chem. 193, pages 265-275, using bovine serum albumin as a standard.

SDS-polyacrylamide gels of various concentrations are purchased from BioRad (Hercules, CA, USA), and stained with Coomassie blue. Molecular weight markers may include rabbit skeletal muscle myosin (200 kDa), *E. coli* β-galactosidase (116 kDa), rabbit muscle phosphorylase B (97.4 kDa), bovine serum albumin (66.2 kDa), ovalbumin (45 kDa), bovine carbonic anhydrase (31 kDa), soybean trypsin inhibitor (21.5 kDa), egg white lysozyme (14.4 kDa) and bovine aprotinin (6.5 kDa).

EQUIVALENTS

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments and methods described herein. The specific embodiments described herein are offered by

way of example only, and the invention is to limited only by the terms of the appended claims, along with the full scope of equivalents to which such claims are entitled.

TABLE 2

Contig	Orf	ntID	aaID	nt Length	aa Length	Subject Name	Blast Score	Blast Probability	Subject Taxonomy	Subject Definition
CONTIG5696	13860691_f3_8	1	14104	732	244	P15847	261	1.3(10)-22	Plasmodium falciparum	41-2 protein antigen precursor.
CONTIG5309	21953186_f2_4	2	14105	531	177	P23746	98	0.00209	Plasmodium falciparum	101 kd malaria antigen (p101) (acidic basic repeat antigen) (fragment).
CONTIG5514	11804080_c1_9	3	14106	1206	402	P31237	152	3.1(10)-8	Actinidia chinensis	l-aminocyclopropane-l-carboxylate oxidase (acc oxidase) (ethylene-forming enzyme) (etc).
CONTIG2279	22115640_f3_3	4	14107	390	130	P10990	242	1.8(10)-20	Strongylocentrotus franciscanus	actin 15a.
CONTIG5721	4001330_c2_24	5	14108	1011	337	P38673	790	3.2(10)-100	Neurospora crassa	actin-like protein (centractin).
CONTIG5565	3906531_c3_30	6	14109	1134	378	P14235	1933	8.6(10)-200	Candida albicans	actin.
CONTIG5425	10040912_c3_15	7	14110	1842	614	P46589	1451	1.0(10)-148	Candida albicans	adherence factor (adhesion and aggregation mediating surface antigen).
b1x18674.y	22456518_c2_1	8	14111	525	175	P32317	387	5.7(10)-36	Saccharomyces cerevisiae	afg1 protein.
CONTIG3076	24807836_c2_3	9	14112	717	239	P39010	148	2.1(10)-9	Saccharomyces cerevisiae	ankyrin repeat-containing protein akr1.
CONTIG3660	24876587_c1_3	10	14113	1395	465	P39010	588	2.8(10)-57	Saccharomyces cerevisiae	ankyrin repeat-containing protein akr1.
CONTIG1408	10960782_c1_5	11	14114	1278	426	P46590	1009	7.0(10)-102	Candida albicans	agglutinin-like protein precursor.
CONTIG1838	1444535_c3_5	12	14115	303	101	P46590	107	9.0(10)-5	Candida albicans	agglutinin-like protein precursor.
CONTIG2390	14954018_f3_4	13	14116	1347	449	P46590	1061	2.2(10)-107	Candida albicans	agglutinin-like protein precursor.

CONTIG2391	32677000_c2_2	14	14117	723	241	P46590	272	2.3(10)-22	Candida albicans	agglutinin-like protein precursor.
CONTIG2783	12316931_f2_3	15	14118	1506	502	P46590	1481	6.9(10)-152	Candida albicans	agglutinin-like protein precursor.
CONTIG279	12898567_f1_1	16	14119	462	154	P46590	335	4.5(10)-29	Candida albicans	agglutinin-like protein precursor.
CONTIG324	7145382_c3_3	17	14120	513	171	P46590	497	2.2(10)-46	Candida albicans	agglutinin-like protein precursor.
CONTIG3672	36038258_c2_7	18	14121	1569	523	P46590	676	1.3(10)-80	Candida albicans	agglutinin-like protein precursor.
CONTIG378	10190962_c1_2	19	14122	699	233	P46590	640	1.1(10)-61	Candida albicans	agglutinin-like protein precursor.
CONTIG4641	32609555_c2_8	20	14123	3180	1060	P46590	1374	1.5(10)-140	Candida albicans	agglutinin-like protein precursor.
CONTIG4725	26381317_c3_6	21	14124	330	110	P46590	109	5.5(10)-5	Candida albicans	agglutinin-like protein precursor.
CONTIG5089	14094431_f3_6	22	14125	1536	512	P46590	1229	3.5(10)-125	Candida albicans	agglutinin-like protein precursor.
CONTIG5089	12303906_f3_7	23	14126	1158	386	P46590	960	1.1(10)-96	Candida albicans	agglutinin-like protein precursor.
CONTIG3930	24610302_f3_3	24	14127	2034	678	P12807	2361	3.7(10)-245	Pichia angusta	peroxisomal copper amine oxidase (ec 1.4.3.6).
CONTIG4975	11923760_f2_2	25	14128	246	82	P12807	170	8.0(10)-12	Pichia angusta	peroxisomal copper amine oxidase (ec 1.4.3.6).
CONTIG1409	4331332_c1_1	26	14129	825	275	P22861	974	3.7(10)-98	Debaromyces occidentalis	glucoamylase I precursor (ec 3.2.1.3) (glucan 1,4-alpha-glucosidase) (1,4-alpha-d-glucan glucohydrolase).
CONTIG4355	860936_c3_8	27	14130	1347	449	P22861	1797	2.2(10)-185	Debaromyces occidentalis	glucoamylase I precursor (ec 3.2.1.3) (glucan 1,4-alpha-glucosidase) (1,4-alpha-d-glucan glucohydrolase).
CONTIG4543	23828132_c1_5	28	14131	1638	546	P37302	1199	5.2(10)-122	Saccharomyces cerevisiae	aminopeptidase y precursor (ec 3.4.11.-).

CONTIG1102	33487527_c2_3	29	14132	846	282	P43066	1121	9.6(10)-114	Candida albicans	d-arabinitol 2-dehydrogenase (ribulose forming) (arab) (ec 1.1.1.-).
CONTIG2679	26804052_c2_5	30	14133	2091	697	P32770	570	1.1(10)-68	Saccharomyces cerevisiae	arp protein.
CONTIG3101	4695289_c1_2	31	14134	1188	396	P51691	512	4.5(10)-88	Pseudomonas aeruginosa	arylsulfatase (ec 3.1.6.1) (aryl-sulphate sulphotriolase).
CONTIG3921	6823300_f2_1	32	14135	2088	696	Q04519	309	2.1(10)-26	Mus musculus	sphingomyelin phosphodiesterase precursor (ec 3.1.4.12) (acid sphingomyelinase).
CONTIG5771	4116286_c3_44	33	14136	2133	711	Q04519	363	1.8(10)-30	Mus musculus	sphingomyelin phosphodiesterase precursor (ec 3.1.4.12) (acid sphingomyelinase).
CONTIG4276	3380416_f3_1	34	14137	960	320	Q08853	97	0.17	Plasmodium falciparum	calcium-transporting atpase (ec 3.6.1.38) (calcium pump).
CONTIG5820	15628143_c3_88	35	14138	333	111	Q03671	353	2.2(10)-32	Candida parapsittosis	atp synthase a chain precursor (ec 3.6.1.34) (protein 6).
CONTIG5820	4037893_c3_87	36	14139	201	67	Q03671	259	2.1(10)-22	Candida parapsittosis	atp synthase a chain precursor (ec 3.6.1.34) (protein 6).
CONTIG5820	26816531_c3_86	37	14140	273	91	Q03671	113	1.7(10)-6	Candida parapsittosis	atp synthase a chain precursor (ec 3.6.1.34) (protein 6).
CONTIG2048	1377017_f2_1	38	14141	1269	423	P39960	323	1.8(10)-27	Saccharomyces cerevisiae	gipase activating protein bem2/ip12.
CONTIG5723	5901587_c2_21	39	14142	957	319	P38934	377	6.7(10)-35	Saccharomyces cerevisiae	nuclear segregation protein bfr1.
CONTIG5723	13673178_c3_26	40	14143	549	183	P38934	146	1.6(10)-9	Saccharomyces cerevisiae	nuclear segregation protein bfr1.
CONTIG5101	4085130_c3_12	41	14144	1098	366	P22506	922	1.2(10)-92	Saccharomycops is fribuligera	beta-glucosidase 1 precursor (ec 3.2.1.21) (gentiobiase) (cellobiase) (beta-d-glucoside glucohydrolase).
CONTIG5071	3908177_c1_9	42	14145	525	175	P22507	566	2.1(10)-54	Saccharomycops is fribuligera	beta-glucosidase 2 precursor (ec 3.2.1.21) (gentiobiase) (cellobiase) (beta-d-glucoside glucohydrolase).

CONTIG5101	32204500_c1_9	43	14146	939	313	P22507	495	1.3(10)-46	Saccharomycops is fibuligera	beta-glucosidase 2 precursor (ec 3.2.1.21) (gentiobiase) (cellobiase) (beta-d-glucoside glucohydrolase).
CONTIG5075	20345305_c3_10	44	14147	300	100	P07337	261	1.8(10)-21	Kluyveromyces marxianus	beta-glucosidase precursor (ec 3.2.1.21) (gentiobiase) (cellobiase) (beta-d-glucoside glucohydrolase).
CONTIG5449	26375638_f1_1	45	14148	702	234	P07337	635	3.1(10)-62	Kluyveromyces marxianus	beta-glucosidase precursor (ec 3.2.1.21) (gentiobiase) (cellobiase) (beta-d-glucoside glucohydrolase).
CONTIG5449	19660377_f1_2	46	14149	1545	515	P07337	726	1.3(10)-99	Kluyveromyces marxianus	beta-glucosidase precursor (ec 3.2.1.21) (gentiobiase) (cellobiase) (beta-d-glucoside glucohydrolase).
CONTIG1398	23629128_f3_1	47	14150	903	301	P24686	600	5.9(10)-57	Emericella nidulans	negative regulator of mitosis.
CONTIG5581	12203280_c3_17	48	14151	1629	543	P28873	2410	2.5(10)-250	Candida albicans	benomyl/methotrexate resistance protein.
CONTIG5629	15657500_c2_17	49	14152	234	78	P28873	326	6.2(10)-29	Candida albicans	benomyl/methotrexate resistance protein.
CONTIG3935	9923265_f2_4	50	14153	195	65	P80193	96	0.00029	Pseudomonas sp.	gamma-butyrobetaine,2-oxoglutarate dioxygenase (ec 1.14.11.1) (gamma-butyrobetaine hydroxylase).
CONTIG4894	31753205_f3_3	51	14154	792	264	P39969	155	5.5(10)-10	Saccharomyces cerevisiae	boi2 protein (beb1 protein).
b3x17654.y	10737800_c2_1	52	14155	288	96	P39969	188	1.7(10)-13	Saccharomyces cerevisiae	boi2 protein (beb1 protein).
CONTIG3497	6851637_c2_7	53	14156	1485	495	P48582	97	7.5(10)-7	Saccharomyces cerevisiae	bro1 protein.
CONTIG5100	1272175_f3_2	54	14157	981	327	P26448	620	1.2(10)-60	Saccharomyces cerevisiae	cell cycle arrest protein bub2.
CONTIG5769	4023377_f1_1	55	14158	3768	1256	P33314	446	3.6(10)-78	Saccharomyces cerevisiae	inhibitory regulator protein bud2/cia2.
CONTIG4354	969187_c1_6	56	14159	399	133	P25558	111	4.5(10)-5	Saccharomyces cerevisiae	bud site selection protein bud3.

CONTIG5785	20509652_c1_27	57	14160	690	230	P36581	400	2.3(10)-37	Schizosaccharo myces pombe	calnexin homolog precursor.
CONTIG4383	29859375_f3_7	58	14161	318	106	P43059	171	4.5(10)-12	Candida albicans	lysine/arginine permease (basic amino acids permease).
CONTIG2206	21504753_f2_1	59	14162	1086	362	P11356	1462	7.0(10)-150	Candida tropicalis	acyl-coenzyme a oxidase ppx-2 (ec 1.3.3.6).
CONTIG956	35678160_c3_4	60	14163	198	66	P47756	96	0.00017	Homo sapiens	f-actin capping protein beta subunit (capz).
CONTIG4105	43460811_c3_9	61	14164	1227	409	P28871	1995	2.2(10)-206	Candida albicans	candidapepsin 2 precursor (ec 3.4.23.24) (aspartate protease 2) (acp 2) (secreted aspartic protease 2).
CONTIG551	12000410_f3_2	62	14165	537	179	P43092	852	3.1(10)-85	Candida albicans	candidapepsin 3 precursor (ec 3.4.23.24) (aspartate protease 3) (acp 3) (secreted aspartic protease 3).
CONTIG4632	14554508_c3_10	63	14166	1269	423	P43094	2144	3.7(10)-222	Candida albicans	candidapepsin 5 precursor (ec 3.4.23.24) (aspartate protease 5) (acp 5) (secreted aspartic protease 5).
CONTIG4738	30711687_c1_6	64	14167	1053	351	P43095	1597	3.5(10)-164	Candida albicans	candidapepsin 6 precursor (ec 3.4.23.24) (aspartate protease 6) (acp 6) (secreted aspartic protease 6).
CONTIG1325	1345311_c3_3	65	14168	648	216	P43096	739	2.8(10)-73	Candida albicans	candidapepsin 7 precursor (ec 3.4.23.24) (aspartate protease 7) (acp 7) (secreted aspartic protease 7).
CONTIG2452	29956630_f1_1	66	14169	672	224	P43096	1116	3.2(10)-113	Candida albicans	candidapepsin 7 precursor (ec 3.4.23.24) (aspartate protease 7) (acp 7) (secreted aspartic protease 7).
CONTIG5582	29332625_f3_13	67	14170	588	196	P31225	830	6.5(10)-83	Candida albicans	corticosteroid-binding protein.

CONTIG3221	26594686_f1_1	68	14171	1011	337	P01129	130	1.5(10)-5	Schizosaccharo myces pombe	start control protein cdc10.
CONTIG4931	22462507_c1_12	69	14172	1248	416	Q09822	139	4.7(10)-6	Schizosaccharo myces pombe	cell division control protein 15.
CONTIG2190	34375931_c2_2	70	14173	1128	376	P53699	1851	4.2(10)-191	Candida albicans	cell division control protein 4.
CONTIG4308	33250391_f3_3	71	14174	213	71	P53699	360	2.5(10)-32	Candida albicans	cell division control protein 4.
CONTIG5382	3908250_c3_16	72	14175	651	217	P53699	447	6.0(10)-42	Candida albicans	cell division control protein 4.
CONTIG5233	4425683_c2_12	73	14176	1638	546	P41892	239	5.2(10)-22	Schizosaccharo myces pombe	cell division control protein 7 (ec 2.7.1.-).
CONTIG672	14460782_c1_1	74	14177	678	226	P41733	100	1.2(10)-10	Saccharomyces cerevisiae	cell division control protein 91.
b9x12n34.y	29410628_c3_2	75	14178	465	155	P41733	239	5.9(10)-20	Saccharomyces cerevisiae	cell division control protein 91.
CONTIG5371	13862507_f3_7	76	14179	255	85	P53700	327	1.3(10)-29	Candida albicans	cytochrome c heme lyase (ec 4.4.1.17) (ceh) (holocytochrome-c synthase).
CONTIG5016	25647260_f3_3	77	14180	369	123	Q09184	215	2.6(10)-17	Schizosaccharo myces pombe	curved dna-binding protein (42 kd protein).
b9x12f50.x	2390632_f1_1	78	14181	483	161	Q09184	390	2.7(10)-36	Schizosaccharo myces pombe	curved dna-binding protein (42 kd protein).
CONTIG3305	21676555_f3_5	79	14182	366	122	Q02224	100	0.0011	Homo sapiens	centromeric protein e (cenp-e protein).
CONTIG823	13776689_c1_2	80	14183	672	224	Q02224	99	0.09299	Homo sapiens	centromeric protein e (cenp-e protein).
CONTIG3114	13082811_c3_10	81	14184	1392	464	P40953	1818	1.3(10)-187	Candida albicans	chitinase 2 precursor (ec 3.2.1.14).
CONTIG5812	33706277_c2_25	82	14185	771	257	P40954	314	1.3(10)-27	Candida albicans	chitinase 3 precursor (ec 3.2.1.14).
CONTIG4261	13877232_c2_5	83	14186	393	131	P23316	581	1.6(10)-56	Candida albicans	chitin synthase 1 (ec 2.4.1.16) (chitin-udp acetyl-glucosaminyl transferase 1).

CONTIG3147	3906525_c3_8	84	14187	858	286	P30572	1122	7.5(10)-114	Candida albicans	chitin synthase 2 (ec 2.4.1.16) (chitin-udp acetyl-glucosaminyl transferase 2).
CONTIG5709	9844380_f1_2	85	14188	405	135	P30573	493	5.5(10)-46	Candida albicans	chitin synthase 3 (ec 2.4.1.16) (chitin-udp acetyl-glucosaminyl transferase 3).
CONTIG4697	22036063_f3_2	86	14189	351	117	P20486	445	4.2(10)-42	Saccharomyces cerevisiae	cyclin-dependent kinases regulatory subunit (cell division control protein cks1).
CONTIG400	25963877_c2_12	87	14190	276	92	P42916	93	0.00042	Bos taurus	collectin-43 (cl-43).
CONTIG1895	33392067_c3_3	88	14191	1377	459	P17697	93	0.2	Bos taurus	clusterin precursor (glycoprotein iii) (gpiii).
CONTIG5633	5213966_f1_1	89	14192	582	194	P32782	854	1.8(10)-85	Candida albicans	3',5'-cyclic-nucleotide phosphodiesterase (ec 3.1.4.17) (pdease).
CONTIG5314	985452_f3_8	90	14193	918	306	P54623	95	0.17999	Drosophila melanogaster	centrosomin.
CONTIG5820	22454388_f2_23	91	14194	192	64	P98001	236	3.7(10)-19	Saccharomyces douglasii	cytochrome c oxidase polypeptide i (ec 1.9.3.1).
CONTIG5820	20516937_c3_91	92	14195	363	121	P43373	508	8.8(10)-49	Candida glabrata	cytochrome c oxidase polypeptide ii (ec 1.9.3.1).
CONTIG5820	1053393_c3_90	93	14196	192	64	P43373	221	2.2(10)-18	Candida glabrata	cytochrome c oxidase polypeptide ii (ec 1.9.3.1).
CONTIG5766	4879681_c1_23	94	14197	1170	390	P16141	1479	1.1(10)-151	Candida maltosa	cytochrome p450 lia4 (alkane-inducible) (ec 1.14.14.1) (p450-alk3a) (p450-cm2).
CONTIG1622	4881561_f3_1	95	14198	309	103	P24458	282	3.2(10)-24	Candida maltosa	cytochrome p450 lia5 (alkane-inducible) (ec 1.14.14.1) (p450-alk2a) (cyp52a3-b).
CONTIG948	24632002_c2_2	96	14199	717	239	P24458	933	8.0(10)-94	Candida maltosa	cytochrome p450 lia5 (alkane-inducible) (ec 1.14.14.1) (p450-alk2a) (cyp52a3-b).
CONTIG4944	2582760_f1_3	97	14200	1998	666	P43079	2528	7.7(10)-263	Candida albicans	transcription factor cph1.

b2x11953.x	14567286_c3_2	98	14201	330	110	Q01981	120	8.6(10)-7	<i>Emmericella nidulans</i>	dna-binding protein crea.
CONTIG5461	12619012_c2_12	99	14202	1029	343	P33153	1510	5.7(10)-155	<i>Candida albicans</i>	gtp-binding rho-like protein.
CONTIG1191	22898508_c3_2	100	14203	324	108	P53707	560	2.7(10)-54	<i>Candida albicans</i>	30 kd cell surface protein (fragment).
CONTIG2359	4331511_c3_4	101	14204	672	224	P53707	1066	6.5(10)-108	<i>Candida albicans</i>	30 kd cell surface protein (fragment).
b2x13715.y	35314012_c1_1	102	14205	441	147	P38877	104	5.7(10)-6	<i>Saccharomyces cerevisiae</i>	kinetochore protein ctf8.
CONTIG5363	22345012_c1_16	103	14206	741	247	Q03100	96	0.062	<i>Dictyostelium discoideum</i>	adenylate cyclase, aggregation specific (ec 4.6.1.1) (atp pyrophosphate-lyase) (adenylate cyclase).
CONTIG5392	20160763_c2_5	104	14207	711	237	P23466	97	0.16	<i>Saccharomyces kluyveri</i>	adenylate cyclase (ec 4.6.1.1) (atp pyrophosphate-lyase) (adenylate cyclase).
CONTIG5532	36031255_c2_13	105	14208	777	259	P23466	92	0.41999	<i>Saccharomyces kluyveri</i>	adenylate cyclase (ec 4.6.1.1) (atp pyrophosphate-lyase) (adenylate cyclase).
CONTIG5820	12506285_f2_31	106	14209	345	115	P48877	436	3.7(10)-41	<i>Pichia canadensis</i>	cytochrome b (ec 1.10.2.2).
CONTIG5818	12552137_c1_31	107	14210	1194	398	P50867	1216	8.3(10)-124	<i>Emmericella nidulans</i>	cysteine synthase (ec 4.2.99.8) (o-acetylserine sulphydrylase) (o-acetylserine (thiol)-lyase) (csase).
CONTIG918	4803802_f2_2	108	14211	210	70	P28875	222	4.5(10)-18	<i>Candida albicans</i>	zinc finger protein 1.
CONTIG4794	26055406_c3_5	109	14212	621	207	Q05329	278	1.3(10)-23	<i>Homo sapiens</i>	glutamate decarboxylase, 65 kd isoform (ec 4.1.1.15) (gad-65) (65 kd glutamic acid decarboxylase).
CONTIG413	36371013_f1_1	110	14213	555	185	P31115	227	2.1(10)-18	<i>Saccharomyces cerevisiae</i>	depressed growth-rate protein deg1.
CONTIG3974	25392512_f3_2	111	14214	519	173	P31115	343	2.7(10)-31	<i>Saccharomyces cerevisiae</i>	depressed growth-rate protein deg1.

CONTIG1047	22442052_f2_3	112	14215	195	65	P50265	168	2.7(10)-12	Candida albicans	dhl1 protein.
CONTIG4729	20395443_c3_9	113	14216	432	144	P52496	296	3.6(10)-25	Candida albicans	dna ligase (ec 6.5.1.1) (poly/deoxyribonucleotide synthase (atp)).
CONTIG5311	33440656_f3_5	114	14217	2175	725	P52496	3482	0	Candida albicans	dna ligase (ec 6.5.1.1) (poly/deoxyribonucleotide synthase (atp)).
CONTIG2547	1457067_f2_2	115	14218	543	181	P33309	377	6.7(10)-35	Saccharomyces cerevisiae	dom34 protein.
CONTIG5806	22534537_c3_41	116	14219	1539	513	P52025	102	0.069	Methanococcus voltae	dna polymerase (ec 2.7.7.7).
CONTIG2772	962816_c1_5	117	14220	747	249	P33793	92	0.28999	Variola virus	dna polymerase (ec 2.7.7.7).
CONTIG5770	14460760_c3_34	118	14221	651	217	P18899	151	1.1(10)-14	Saccharomyces cerevisiae	ddt48 stress protein (dna damage- responsive protein 48) (ddrp 48) (yp 75) (flocculent specific protein).
CONTIG5802	24036003_c3_37	119	14222	291	97	P45444	130	1.2(10)-6	Emmericella nidulans	dynein heavy chain, cytosolic (dyhc).
b1x11226.y	2145390_f2_1	120	14223	687	229	P03856	1039	4.7(10)-105	Escherichia coli	protein e.
CONTIG2765	16678933_c3_4	121	14224	330	110	P54352	147	1.5(10)-9	Drosophila melanogaster	ethanolamine kinase (ec 2.7.1.82) (easily shocked protein).
CONTIG1837	24394415_c1_3	122	14225	222	74	P43084	201	1.2(10)-15	Candida albicans	probable nadph dehydrogenase (ec 1.6.99.1) (estrogen-binding protein) (ebp).
CONTIG430	47057_c3_2	123	14226	792	264	P43084	998	1.0(10)-100	Candida albicans	probable nadph dehydrogenase (ec 1.6.99.1) (estrogen-binding protein) (ebp).
CONTIG5598	13865892_f1_2	124	14227	927	309	Q07730	816	2.0(10)-81	Candida albicans	ecel protein.
CONTIG3402	22074062_c3_11	125	14228	318	106	Q06889	241	3.1(10)-20	Homo sapiens	early growth response protein 3 (egr-3) (zinc finger protein pilot).
b3x16352.y	36125311_c3_1	126	14229	657	219	P20829	96	0.031	Drosophila melanogaster	retrovirus-related env polypotein (transposon 297).

CONTIG5801	14142525_f3_19	127	14230	450	150	P30195	98	0.005	Staphylococcus epidermidis	epidermin biosynthesis protein epib.
CONTIG2399	8995963_f1_1	128	14231	939	313	P07992	237	4.5(10)-20	Homo sapiens	dna excision repair protein ercc-1.
CONTIG4000	1173500_f1_1	129	14232	1245	415	P26337	104	0.021	Trypanosoma equiperdum	putative adenylate cyclase regulatory protein.
CONTIG5532	7157067_c2_11	130	14233	1341	447	P26337	100	0.067	Trypanosoma equiperdum	putative adenylate cyclase regulatory protein.
CONTIG5145	26174017_c3_13	131	14234	882	294	P33056	90	0.34	Varioia virus	early transcription factor 70 kd subunit.
CONTIG3960	1987818_f2_1	132	14235	1599	533	P21268	116	0.0022	Saccharomyces cerevisiae	factor arrest protein.
CONTIG4071	11757652_f2_4	133	14236	945	315	P34731	1477	1.8(10)-151	Candida albicans	fatty acid synthase, subunit beta (ec 2.3.1.86) (contains: 3-hydroxypalmitoyl-[acyl-carrier-protein] dehydratase (ec 4.2.1.61); enoyl-[acyl-carrier-protein] reductase (nadh) (ec 1.3.1.9); [acyl-carrier-protein] acetyltransferase (ec 2.3.1.38); [acyl-car
CONTIG1277	16610692_f1_1	134	14237	333	111	P48630	233	2.6(10)-19	Glycine max	omega-6 fatty acid desaturase, endoplasmic reticulum isozyme 1 (ec 1.14.99.-).
CONTIG2753	4725626_c3_4	135	14238	1326	442	P46313	731	2.1(10)-72	Arabidopsis thaliana	omega-6 fatty acid desaturase, endoplasmic reticulum (ec 1.14.99.-) (delta-12 desaturase).
CONTIG4775	2164000_c2_9	136	14239	1212	404	P49842	93	0.079	Homo sapiens	g11 protein.
CONTIG5243	4425812_c1_7	137	14240	1923	641	P34116	92	0.62	Dictyostelium discoideum	cell surface glycoprotein gp138b precursor.
CONTIG3578	5126507_c2_3	138	14241	1146	382	P03351	94	0.14	Equine infectious anemia virus	gag polyprotein (contains: core proteins p15, p26, p11, p9).
CONTIG5032	24017191_c2_9	139	14242	1776	592	P32257	91	0.65	Kluyveromyces fragilis	transcription regulatory protein gall1.

CONTIG1956	4863802_c3_1	140	14243	1002	334	P27613	90	0.04599	Trichostromyces colubriformis	globin-like host-protective antigen precursor.
b9x11y68.x	5866437_c3_2	141	14244	282	94	P55143	96	4.0(10)-5	Ricinus communis	glutaredoxin.
CONTIG3232	36069567_f1_1	142	14245	408	136	Q00582	179	1.3(10)-13	Saccharomyces cerevisiae	gfp-binding protein gfr1.
CONTIG3743	24256760_c3_7	143	14246	759	253	P50505	373	1.3(10)-33	Debaryomyces occidentalis	high affinity potassium transporter.
CONTIG5247	256700_f1_1	144	14247	576	192	P50505	467	7.5(10)-44	Debaryomyces occidentalis	high affinity potassium transporter.
CONTIG3696	9776562_f1_2	145	14248	741	247	P20449	336	2.2(10)-34	Saccharomyces cerevisiae	probable atp-dependent ma helicase ca5/6.
CONTIG4636	23493942_c3_6	146	14249	249	83	P20449	273	2.2(10)-23	Saccharomyces cerevisiae	probable atp-dependent ma helicase ca5/6.
CONTIG5736	194075_c2_26	147	14250	195	65	P22414	226	1.2(10)-17	Candida tropicalis	hydrtase-dehy/drogenase-epimerase (hde).
CONTIG5736	517943_c1_18	148	14251	2472	824	P22414	3749	0	Candida tropicalis	hydrtase-dehy/drogenase-epimerase (hde).
CONTIG2897	4945130_f1_2	149	14252	474	158	P49374	294	1.8(10)-25	Kluyveromyces lacticis	high-affinity glucose transporter.
CONTIG4857	213538_f2_2	150	14253	1089	363	P49374	966	2.6(10)-97	Kluyveromyces lacticis	high-affinity glucose transporter.
CONTIG5586	4193757_f2_4	151	14254	1137	379	P49374	1050	3.2(10)-106	Kluyveromyces lacticis	high-affinity glucose transporter.
CONTIG3999	167627_f2_2	152	14255	462	154	P46973	130	4.4(10)-18	Saccharomyces cerevisiae	hit1 protein.
CONTIG4537	22304687_c3_9	153	14256	1872	624	P20050	238	8.0(10)-17	Saccharomyces cerevisiae	meiosis specific protein hop1.
CONTIG364	589040_f3_1	154	14257	279	93	P14586	97	3.1(10)-5	Plasmodium falciparum	histidine-rich protein.
CONTIG3783	14490885_c3_10	155	14258	1068	356	P25619	385	9.5(10)-36	Saccharomyces cerevisiae	30 kd heat shock protein.

CONTIG4918	10192125_f2_4	156	14259	993	331	P22121	99	0.04299	Kluyveromyces lactis	heat shock factor protein (hsf) (heat shock transcription factor) (hsf1).
CONTIG929	7036558_c3_2	157	14260	858	286	P53706	1279	1.7(10)-130	Candida albicans	atp-dependent permease hst6 (stc6 homolog).
b2x15627.y	22772062_c3_5	158	14261	348	116	P53706	527	1.6(10)-49	Candida albicans	atp-dependent permease hst6 (stc6 homolog).
b2x15627.y	4189792_c2_3	159	14262	204	68	P53706	264	1.8(10)-21	Candida albicans	atp-dependent permease hst6 (stc6 homolog).
b2x10287.y	4391406_f1_1	160	14263	498	166	P53706	792	5.2(10)-78	Candida albicans	atp-dependent permease hst6 (stc6 homolog).
b1x11761.y	234400_f3_1	161	14264	417	139	P53706	453	1.3(10)-41	Candida albicans	atp-dependent permease hst6 (stc6 homolog).
CONTIG1650	5364719_c1_2	162	14265	777	259	P53706	861	1.6(10)-85	Candida albicans	atp-dependent permease hst6 (stc6 homolog).
CONTIG4966	25625192_f2_4	163	14266	759	253	P46599	1152	5.0(10)-117	Candida albicans	serine/threonine protein kinase stc7 homolog (ec 2.7.1.-).
CONTIG5291	36135942_c2_14	164	14267	669	223	P42259	108	0.00051	Natronobacteriu m pharaonis	sensory rhodopsin ii transducer (trh- ii) (methyl-accepting phototaxis protein ii) (mmp-ii).
CONTIG1484	26605306_f1_1	165	14268	420	140	P46593	99	0.00029	Candida albicans	hyphal wall protein 1 (fragment).
CONTIG48	16890877_c2_2	166	14269	909	303	P46593	101	0.00018	Candida albicans	hyphal wall protein 1 (fragment).
CONTIG5201	29339457_f3_6	167	14270	564	188	P46593	170	7.0(10)-12	Candida albicans	hyphal wall protein 1 (fragment).
CONTIG5372	128305_c1_13	168	14271	396	132	P46593	192	3.0(10)-14	Candida albicans	hyphal wall protein 1 (fragment).
CONTIG2628	253211_f3_3	169	14272	195	65	P46591	115	9.0(10)-6	Candida albicans	hyphally regulated protein precursor.
CONTIG2694	7069056_f3_4	170	14273	873	291	P46591	338	1.3(10)-29	Candida albicans	hyphally regulated protein precursor.
CONTIG3086	12000417_f3_5	171	14274	2139	713	P46591	127	9.8(10)-5	Candida albicans	hyphally regulated protein precursor.

CONTIG3326	1214075_c1_5	172	14275	1485	495	P46591	490	5.7(10)-46	Candida albicans	hyphally regulated protein precursor.
CONTIG3270	879510_c3_7	173	14276	1821	607	P46591	553	8.4(10)-53	Candida albicans	hyphally regulated protein precursor.
CONTIG4223	24234642_c1_6	174	14277	879	293	P46591	264	1.1(10)-21	Candida albicans	hyphally regulated protein precursor.
CONTIG5648	1214055_f3_12	175	14278	855	285	P46591	291	1.3(10)-24	Candida albicans	hyphally regulated protein precursor.
CONTIG5648	29317507_f1_2	176	14279	786	262	P46591	106	0.00075	Candida albicans	hyphally regulated protein precursor.
CONTIG81	3314188_f3_2	177	14280	798	266	P46591	328	1.5(10)-28	Candida albicans	hyphally regulated protein precursor.
CONTIG825	30475963_f3_2	178	14281	696	232	P46591	224	2.1(10)-17	Candida albicans	hyphally regulated protein precursor.
b3x11288.y	437556_c2_2	179	14282	549	183	P46591	287	3.7(10)-24	Candida albicans	hyphally regulated protein precursor.
CONTIG4668	11829701_c3_7	180	14283	1989	663	P53705	3115	0	Candida albicans	integrin alpha chain-like protein.
CONTIG5178	29335005_f1_3	181	14284	2781	927	P53705	3314	0	Candida albicans	integrin alpha chain-like protein.
CONTIG5810	20335201_f1_3	182	14285	1170	390	P10621	206	1.3(10)-14	Streptomyces clavuligerus	isopenicillin n synthetase (ipns).
CONTIG5517	5212802_f3_4	183	14286	4947	1649	P46940	711	2.6(10)-87	Homo sapiens	ras gtpase-activating-like protein iggap1 (p195).
CONTIG3282	235625_c2_8	184	14287	1806	602	P47135	339	4.7(10)-28	Saccharomyces cerevisiae	jsn1 protein.
b2x12745.y	7666693_f1_1	185	14288	573	191	P47135	260	3.7(10)-21	Saccharomyces cerevisiae	jsn1 protein.
b3x14232.y	24088887_f1_1	186	14289	345	115	P52553	96	4.0(10)-5	Saccharomyces cerevisiae	protein yke2.
CONTIG839	5175282_c2_4	187	14290	183	61	P28874	193	2.1(10)-15	Candida albicans	krel protein precursor (fragment).

CONTIG5075	4739042_f3_3	188	14291	336	112	P09805	209	1.1(10)-15	Kluyveromyces lactis	killer toxin alpha and beta subunits precursor (rf2 protein) (endochitinase (ec 3.2.1.14)).
CONTIG5075	35395043_f3_4	189	14292	984	328	P09805	701	1.8(10)-68	Kluyveromyces lactis	killer toxin alpha and beta subunits precursor (rf2 protein) (endochitinase (ec 3.2.1.14)).
CONTIG4335	20954183_f1_1	190	14293	1959	653	P48012	684	2.0(10)-67	Debaryomyces occidentalis	3-isopropylmalate dehydrogenase (ec 1.1.1.85) (beta-ipm dehydrogenase) (imdh) (3-ipm-dh).
CONTIG4900	23472510_f2_4	191	14294	1149	383	P20261	91	0.34999	Candida rugosa	lipase 1 precursor (ec 3.1.1.3).
CONTIG1645	20805438_f2_1	192	14295	906	302	P25391	94	0.47999	Homo sapiens	laminin alpha-1 chain precursor (laminin a chain).
CONTIG1891	36413317_f1_1	193	14296	1575	525	P07866	493	4.5(10)-56	Saccharomyces cerevisiae	low temperature essential protein.
CONTIG1930	32042881_c3_9	194	14297	528	176	P34078	217	3.0(10)-17	Saccharomyces cerevisiae	low-temperature viability protein lvt1.
CONTIG3539	813280_f2_4	195	14298	693	231	P55080	141	5.0(10)-9	Gallus gallus	microfibrillar-associated protein 1.
CONTIG5512	554652_f1_1	196	14299	1518	506	P20484	598	5.9(10)-82	Saccharomyces cerevisiae	mak11 protein precursor.
CONTIG1224	35206700_f3_1	197	14300	378	126	P23059	97	3.1(10)-5	Saccharomyces cerevisiae	mak31 protein.
CONTIG5644	35240930_f2_7	198	14301	942	314	P23060	338	9.0(10)-31	Saccharomyces cerevisiae	mak32 protein.
CONTIG1593	2162788_f2_1	199	14302	984	328	P40850	218	6.9(10)-25	Saccharomyces cerevisiae	mkt1 protein.
CONTIG3546	19569450_c1_5	200	14303	498	166	Q06138	361	3.2(10)-33	Mus musculus	mo25 protein.
CONTIG1287	15054563_c1_1	201	14304	621	207	P53583	237	3.0(10)-19	Saccharomyces cerevisiae	mpa43 protein.
b9x13e70.x	4569682_f1_1	202	14305	432	144	P53583	145	2.7(10)-9	Saccharomyces cerevisiae	mpa43 protein.
CONTIG5115	7062777_c2_14	203	14306	1383	461	P21339	834	2.5(10)-83	Saccharomyces cerevisiae	morphogenesis-related protein (multicopy suppression of a budding defect 1).

CONTIG4502	391002_f3_2	204	14307	1635	545	P52918	995	2.2(10)-100	Saccharomyces cerevisiae	msn5 protein.
CONTIG5314	31484427_c2_14	205	14308	1968	656	P52918	779	6.0(10)-111	Saccharomyces cerevisiae	msn5 protein.
CONTIG2404	36142127_f1_1	206	14309	489	163	P09091	100	1.5(10)-5	Saccharomyces cerevisiae	mating-type protein a-1, incompletely spliced.
CONTIG2414	37517_f3_1	207	14310	849	283	P38680	311	9.5(10)-28	Neurospora crassa	n amino acid transport system protein (methyltryptophan resistance protein).
CONTIG4065	15633576_c1_6	208	14311	537	179	Q04802	899	3.2(10)-90	Candida albicans	glucosamine-6-phosphate isomerase (ec 5.3.1.10) (glucosamine-6-phosphate deaminase).
b3x10122.x	31484388_c2_3	209	14312	315	105	P52920	422	1.1(10)-39	Saccharomyces cerevisiae	nbp35 protein.
CONTIG1945	24024063_f3_3	210	14313	453	151	P42114	249	2.3(10)-21	Neurospora crassa	nadh-ubiquinone oxidoreductase 14.8 kd subunit (ec 1.6.5.3) (ec 1.6.99.3) (complex i-14.8kd) (ci-14.8kd).
CONTIG5639	10203251_c1_12	211	14314	237	79	Q02368	120	1.1(10)-7	Bos taurus	nadh-ubiquinone oxidoreductase b18 subunit (ec 1.6.5.3) (ec 1.6.99.3) (complex i-b18) (ci-b18).
CONTIG5156	19939166_c2_10	212	14315	1305	435	P38830	372	1.2(10)-49	Saccharomyces cerevisiae	nd180 protein.
CONTIG5590	808343_f2_7	213	14316	657	219	P38830	346	6.0(10)-31	Saccharomyces cerevisiae	nd180 protein.
CONTIG4140	1225637_f2_2	214	14317	1008	336	P12036	97	0.079	Homo sapiens	neurofilament triplet h protein (200 kd neurofilament protein) (nF-h).
CONTIG5109	19787840_f1_2	215	14318	195	65	P42117	121	9.0(10)-8	Neurospora crassa	nadh-ubiquinone oxidoreductase 9.5 kd subunit (ec 1.6.5.3) (ec 1.6.99.3) (complex i-9.5kd) (ci-9.5) (ubiquinone-binding protein).
CONTIG5725	447087_f1_1	216	14319	2214	738	P15296	110	0.01	Drosophila melanogaster	71 kd protein in not-1b transposable element.

CONTIG5820	23911302_c3_92	217	14320	333	111	P48901	274	5.5(10)-24	Pichia canadensis	nadh-ubiquinone oxidoreductase chain 1 (ec 1.6.5.3).
CONTIG5820	23568800_f2_29	218	14321	327	109	P48909	263	8.0(10)-23	Candida parapsilosis	nadh-ubiquinone oxidoreductase chain 3 (ec 1.6.5.3).
b3x16007.y	10593768_c2_1	219	14322	465	155	P03913	765	5.0(10)-76	Eurotium amstelodami	nadh-ubiquinone oxidoreductase chain 4 (ec 1.6.5.3).
CONTIG5820	35955252_f2_32	220	14323	228	76	P48919	251	9.6(10)-21	Candida parapsilosis	nadh-ubiquinone oxidoreductase chain 5 (ec 1.6.5.3).
CONTIG5820	4163430_f2_33	221	14324	234	78	P48919	205	9.4(10)-16	Candida parapsilosis	nadh-ubiquinone oxidoreductase chain 5 (ec 1.6.5.3).
CONTIG5820	1064800_f2_34	222	14325	957	319	P48919	1095	5.5(10)-111	Candida parapsilosis	nadh-ubiquinone oxidoreductase chain 5 (ec 1.6.5.3).
CONTIG5820	478427_c1_67	223	14326	444	148	P48923	189	5.5(10)-15	Candida parapsilosis	nadh-ubiquinone oxidoreductase chain 6 (ec 1.6.5.3).
CONTIG2096	33228382_f2_1	224	14327	666	222	P24917	802	6.2(10)-80	Neurospora crassa	nadh-ubiquinone oxidoreductase 51 kd subunit precursor (ec 1.6.5.3) (ec 1.6.99.3) (complex i-51kd) (ci-51kd).
CONTIG4848	23835843_c3_7	225	14328	375	125	P24917	342	3.3(10)-31	Neurospora crassa	nadh-ubiquinone oxidoreductase 51 kd subunit precursor (ec 1.6.5.3) (ec 1.6.99.3) (complex i-51kd) (ci-51kd).
CONTIG4889	4148275_c3_3	226	14329	360	120	P22142	525	1.3(10)-50	Neurospora crassa	nadh-ubiquinone oxidoreductase 49 kd subunit precursor (ec 1.6.5.3) (ec 1.6.99.3) (complex i-49kd) (ci-49kd).
CONTIG2672	10660657_f1_2	227	14330	303	101	P25284	124	2.7(10)-7	Neurospora crassa	nadh-ubiquinone oxidoreductase 40 kd subunit precursor (ec 1.6.5.3) (ec 1.6.99.3) (complex i-40kd) (ci-40kd).
CONTIG5373	35242916_c3_9	228	14331	966	322	P25284	670	6.0(10)-66	Neurospora crassa	nadh-ubiquinone oxidoreductase 40 kd subunit precursor (ec 1.6.5.3) (ec 1.6.99.3) (complex i-40kd) (ci-40kd).

CONTIG5591	11991308_c2_10	229	14332	528	176	Q00673	618	1.8(10)-60	Candida maltosa	probable nadh-ubiquinone oxidoreductase 30.4 kd subunit precursor (ec 1.6.5.3) (ec 1.6.99.3) (complex i-30kd) (ci-31kd) (alkane-inducible protein 1).
CONTIG5814	22381885_f3_22	230	14333	771	257	P40915	667	1.2(10)-65	Neurospora crassa	nadh-ubiquinone dehydrogenase 24 kd subunit precursor (ec 1.6.5.3) (ec 1.6.99.3).
CONTIG5490	24417937_c1_11	231	14334	627	209	P19968	289	1.3(10)-25	Neurospora crassa	nadh-ubiquinone oxidoreductase 21.3 kd subunit (ec 1.6.5.3) (ec 1.6.99.3).
CONTIG3874	196932_f1_1	232	14335	645	215	P25710	92	0.021	Neurospora crassa	nadh-ubiquinone oxidoreductase 21.3 kd subunit (ec 1.6.5.3) (ec 1.6.99.3).
CONTIG5820	11828900_f3_57	233	14336	303	101	P48929	154	2.8(10)-11	Candida parapsilosis	nadh-ubiquinone oxidoreductase chain 4l (ec 1.6.5.3).
CONTIG2465	21975640_c2_7	234	14337	1638	546	Q00402	525	8.5(10)-49	Saccharomyces cerevisiae	nuclear migration protein num1.
CONTIG555	20425012_f2_1	235	14338	510	170	Q00402	223	1.0(10)-16	Saccharomyces cerevisiae	nuclear migration protein num1.
b2x13015.y	25573505_c3_4	236	14339	654	218	Q00402	223	1.0(10)-16	Saccharomyces cerevisiae	nuclear migration protein num1.
b2x10141.y	26571942_f3_1	237	14340	450	150	Q00402	172	2.7(10)-11	Saccharomyces cerevisiae	nuclear migration protein num1.
CONTIG3947	21537801_c3_5	238	14341	528	176	P52503	149	9.6(10)-11	Mus musculus	nadh-ubiquinone oxidoreductase 13 kd-a subunit (ec 1.6.5.3) (ec 1.6.99.3) (complex i-13kd-a) (ci-13kd-a) (fragment).
CONTIG2623	4725926_f2_2	239	14342	327	109	Q03015	121	9.0(10)-8	Neurospora crassa	nadh-ubiquinone oxidoreductase 12 kd subunit precursor (ec 1.6.5.3) (ec 1.6.99.3) (complex i-12kd) (ci-12kd).
CONTIG3478	21663963_f3_3	240	14343	432	144	P21976	228	4.0(10)-19	Neurospora crassa	nadh-ubiquinone oxidoreductase 20.8 kd subunit (ec 1.6.5.3) (ec 1.6.99.3).

CONTIG1320	4816405_f2_2	241	14344	867	289	Q01969	120	8.0(10)-5	Thermotoga maritima	outer membrane protein alpha precursor.
CONTIG4181	24647750_c1_4	242	14345	1221	407	P46596	1525	1.5(10)-156	Candida albicans	opaque-phase-specific protein op4 precursor.
CONTIG1077	6672838_f2_1	243	14346	453	151	P80324	115	2.5(10)-6	Rhodotorula gracilis	d-amino acid oxidase (ec 1.4.3.3) (damox) (dao).
b9x12q69.y	1178411_c1_2	244	14347	549	183	P80324	206	2.2(10)-16	Rhodotorula gracilis	d-amino acid oxidase (ec 1.4.3.3) (damox) (dao).
CONTIG3506	24242188_f2_2	245	14348	1725	575	P54675	94	0.55	Dictyostelium discoideum	phosphatidylinositol 3-kinase 3 (ec 2.7.1.137) (pi3-kinase) (pidins-3-kinase) (pi3k) (fragment).
CONTIG5547	34094186_f2_1	246	14349	927	309	P21171	98	0.02199	Listeria monocytogenes	protein p60 precursor (invasion-associated protein).
CONTIG2585	24812505_c1_5	247	14350	1251	417	P32521	297	6.5(10)-25	Saccharomyces cerevisiae	pab-dependent poly(a)-specific ribonuclease (ec 3.1.13.4).
CONTIG3014	23603453_c1_4	248	14351	1413	471	P32521	437	7.7(10)-40	Saccharomyces cerevisiae	pab-dependent poly(a)-specific ribonuclease (ec 3.1.13.4).
CONTIG2423	2036666_f3_2	249	14352	606	202	P46463	413	1.8(10)-37	Pichia pastoris	peroxisome biosynthesis protein pas1.
b9x12387.y	26306933_c2_3	250	14353	705	235	P46463	305	6.4(10)-26	Pichia pastoris	peroxisome biosynthesis protein pas1.
CONTIG1709	6648317_f1_1	251	14354	765	255	P33289	292	1.6(10)-24	Pichia pastoris	peroxisome biosynthesis protein pas5.
CONTIG2462	6288182_c1_3	252	14355	831	277	P33289	176	5.2(10)-11	Pichia pastoris	peroxisome biosynthesis protein pas5.
CONTIG5437	21985910_f3_8	253	14356	807	269	P38759	409	5.5(10)-55	Saccharomyces cerevisiae	pep11 protein.
CONTIG1216	22687682_c1_2	254	14357	903	301	P37591	90	0.12	Salmonella typhimurium	phosphoglycerate transport regulatory protein pgic precursor.
CONTIG1009	11736666_c3_2	255	14358	1128	376	P15245	636	7.9(10)-68	Trichosporon cutaneum	phenol 2-monooxygenase (ec 1.14.13.7) (phenol hydroxylase).
CONTIG1779	21750252_c1_1	256	14359	579	193	P15245	240	2.2(10)-19	Trichosporon cutaneum	phenol 2-monooxygenase (ec 1.14.13.7) (phenol hydroxylase).

CONTIG2250	471040_c2_3	257	14360	1074	358	P15245	590	1.8(10)-57	Trichosporon cutaneum	phenol 2-monooxygenase (ec 1.14.13.7) (phenol hydroxylase).
CONTIG4933	24064692_f1_1	258	14361	3192	1064	P17442	497	1.8(10)-72	Saccharomyces cerevisiae	phosphate system positive regulatory protein pho81 (cdk inhibitor pho81).
CONTIG4933	14541562_f3_5	259	14362	591	197	P17442	116	1.1(10)-11	Saccharomyces cerevisiae	phosphate system positive regulatory protein pho81 (cdk inhibitor pho81).
CONTIG2620	6250_f3_2	260	14363	762	254	P30887	128	3.0(10)-12	Yarrowia lipolytica	acid phosphatase precursor (ec 3.1.3.2).
CONTIG5710	21679063_f1_2	261	14364	990	330	P30887	556	7.2(10)-54	Yarrowia lipolytica	acid phosphatase precursor (ec 3.1.3.2).
bix13625.x	24413917_f2_1	262	14365	237	79	P43076	314	1.2(10)-27	Candida albicans	ph responsive protein 1 precursor.
CONTIG2401	4694507_f2_3	263	14366	621	207	P54677	94	0.08	Dictyostelium discoideum	phosphatidylinositol 4-kinase (ec 2.7.1.67) (pi4-kinase) (p1dins-4-kinase) (pi4k-alpha).
CONTIG5742	2_f3_15	264	14367	1602	534	P46547	674	2.2(10)-66	Aeromonas sobria	proline iminopeptidase (ec 3.4.11.5) (prolyl aminopeptidase).
CONTIG261	1193951_c1_2	265	14368	711	237	Q03178	344	2.1(10)-31	Saccharomyces cerevisiae	pir1 protein precursor.
CONTIG321	20900277_f2_1	266	14369	537	179	Q03178	275	4.2(10)-24	Saccharomyces cerevisiae	pir1 protein precursor.
CONTIG2674	24641526_c1_4	267	14370	753	251	Q03180	150	4.2(10)-9	Saccharomyces cerevisiae	pir3 protein precursor.
CONTIG4408	900312_c2_5	268	14371	276	92	Q03180	316	1.8(10)-28	Saccharomyces cerevisiae	pir3 protein precursor.
CONTIG5438	23550277_f1_3	269	14372	927	309	Q03180	151	1.3(10)-9	Saccharomyces cerevisiae	pir3 protein precursor.
CONTIG2663	195900_c1_6	270	14373	906	302	P14262	226	6.7(10)-19	Bacillus cereus	1-phosphatidylinositol phosphodiesterase precursor (ec 3.1.4.10) (phosphatidylinositol-specific phospholipase c) (pi-plc).

CONTIG4729	1960002_c2_8	271	14374	768	256	P14262	211	3.2(10)-17	Bacillus cereus	l-phosphatidylinositol phosphodiesterase precursor (ec 3.1.4.10) (phosphatidylinositol-specific phospholipase c) (pi-pltc).
CONTIG5819	9953410_c2_51	272	14375	912	304	P08954	251	1.5(10)-21	Bacillus thuringiensis	l-phosphatidylinositol phosphodiesterase precursor (ec 3.1.4.10) (phosphatidylinositol-specific phospholipase c) (pi-pltc).
CONTIG2658	20878327_f3_4	273	14376	621	207	Q07066	117	1.2(10)-5	Rattus norvegicus	22 kd peroxisomal membrane protein.
CONTIG4228	9953916_f2_2	274	14377	1158	386	P19881	505	1.8(10)-48	Saccharomyces cerevisiae	4-nitrophenylphosphatase (ec 3.1.3.41) (pnppase).
CONTIG5607	2743761_f2_3	275	14378	978	326	P19881	499	7.9(10)-48	Saccharomyces cerevisiae	4-nitrophenylphosphatase (ec 3.1.3.41) (pnppase).
CONTIG4086	24257827_f1_1	276	14379	1794	598	P27401	271	5.2(10)-20	Simian foamy virus	pol polyprotein (contains: protease (ec 3.4.23.-); reverse transcriptase (ec 2.7.7.49); endonuclease).
CONTIG3273	23549091_c1_3	277	14380	1227	409	P11976	134	1.8(10)-5	Dictyostelium discoideum	prestalk protein precursor.
CONTIG4135	4391000_c3_14	278	14381	750	250	P43078	633	5.0(10)-62	Candida albicans	probable protein-tyrosine phosphatase (ec 3.1.3.48).
CONTIG3462	6051688_f1_1	279	14382	738	246	P46030	1046	8.5(10)-106	Candida albicans	peptide transporter ptr2.
CONTIG3462	35397630_f1_2	280	14383	447	149	P46030	660	6.9(10)-65	Candida albicans	peptide transporter ptr2.
CONTIG5662	22063750_c2_11	281	14384	798	266	P46030	969	1.2(10)-97	Candida albicans	peptide transporter ptr2.
CONTIG5277	12121001_f1_1	282	14385	1455	485	P21304	1116	3.2(10)-113	Saccharomyces cerevisiae	periodic tryptophan protein 1.
CONTIG5277	35160930_f2_5	283	14386	471	157	P21304	314	1.3(10)-27	Saccharomyces cerevisiae	periodic tryptophan protein 1.
CONTIG4400	20367130_c2_7	284	14387	2481	827	P25635	2564	1.2(10)-266	Saccharomyces cerevisiae	periodic tryptophan protein 2.

CONTIG4400	11212511_c2_6	285	14388	255	85	P25635	233	2.2(10)-18	Saccharomyces cerevisiae	periodic tryptophan protein 2.
CONTIG5805	4565937_c3_44	286	14389	1350	450	P32747	851	3.8(10)-85	Schizosaccharomyces pombe	dihydroorotate dehydrogenase precursor (ec 1.3.3.1) (dihydroorotate oxidase) (dhodetase).
CONTIG3991	24625633_c2_10	287	14390	462	154	P38230	112	4.4(10)-6	Saccharomyces cerevisiae	putative quinone oxidoreductase (ec 1.6.5.5) (nadph:quinone reductase).
CONTIG1000	14641562_f3_2	288	14391	798	266	P43123	486	1.8(10)-46	Saccharomyces cerevisiae	hypothetical 53.5 kd protein in pho2-pol3 intergenic region.
CONTIG722	15104049_c1_1	289	14392	708	236	P43123	614	5.0(10)-60	Saccharomyces cerevisiae	hypothetical 53.5 kd protein in pho2-pol3 intergenic region.
CONTIG3961	19941377_c1_4	290	14393	861	287	P43124	307	1.7(10)-27	Saccharomyces cerevisiae	hypothetical 46.1 kd protein in pho2-pol3 intergenic region.
CONTIG3081	26771927_f2_2	291	14394	1776	592	P10563	145	1.6(10)-6	Emericella nidulans	quinic acid utilization activator.
CONTIG5205	24648263_c1_3	292	14395	654	218	P15325	91	0.11	Emericella nidulans	quinate permease (quinate transporter).
CONTIG5535	875380_c3_26	293	14396	1314	438	P15325	777	2.7(10)-77	Emericella nidulans	quinate permease (quinate transporter).
CONTIG4158	21959653_f2_1	294	14397	1389	463	Q00799	106	0.035	Plasmodium vivax	reticulocyte binding protein 2 (fragment).
CONTIG4231	35979552_f1_2	295	14398	798	266	Q09823	91	0.28999	Schizosaccharomyces pombe	meiotic recombination protein rec10.
CONTIG1116	4323388_f2_1	296	14399	357	119	P06615	484	3.1(10)-46	Escherichia coli	resolvase (protein d).
CONTIG4168	23494750_c3_6	297	14400	792	264	P25560	281	3.6(10)-38	Saccharomyces cerevisiae	rer1 protein.
CONTIG4253	21564705_f3_3	298	14401	873	291	P13830	92	0.003	Plasmodium falciparum	ring-infected erythrocyte surface antigen precursor.
CONTIG89	480205_f3_1	299	14402	564	188	P13830	98	0.019	Plasmodium falciparum	ring-infected erythrocyte surface antigen precursor.
CONTIG2501	25672306_f3_3	300	14403	297	99	P39083	171	1.0(10)-11	Saccharomyces cerevisiae	rho-type gtpase activating protein rga1/dbm1.

CONTIG3656	30195212_c3_8	301	14404	1827	609	P16664	119	2.6(10)-9	Saccharomyces cerevisiae	reduced growth phenotype protein (tgp1 protein).
CONTIG5773	26603932_f3_17	302	14405	2133	711	P16664	101	0.097	Saccharomyces cerevisiae	reduced growth phenotype protein (tgp1 protein).
CONTIG5255	25426061_f1_1	303	14406	495	165	P32445	129	1.3(10)-8	Saccharomyces cerevisiae	mitochondrial single-stranded dna-binding protein rim1 precursor.
b1x13632.x	4297187_c2_2	304	14407	486	162	P11894	96	7.5(10)-5	Pisum sativum	50s ribosomal protein l9, chloroplast precursor (cl13).
CONTIG4506	24222750_c1_14	305	14408	321	107	P35996	133	4.7(10)-9	Saccharomyces cerevisiae	mitochondrial 60s ribosomal protein 138 (ym138).
CONTIG2246	25578538_f3_1	306	14409	726	242	Q03586	90	0.20999	Thermoplasma acidophilum	dna-directed ma polymerase subunit a" (ec 2.7.7.6).
CONTIG5115	32603135_c2_15	307	14410	1611	537	P14248	100	0.23999	Plasmodium falciparum	dna-directed ma polymerase ii largest subunit (ec 2.7.7.6).
CONTIG5699	34382302_f2_13	308	14411	336	112	P40422	224	1.1(10)-18	Saccharomyces cerevisiae	dna-directed ma polymerases i, ii, and iii 7.7 kd polypeptide (abc10-alpha).
CONTIG4406	12581969_c1_3	309	14412	612	204	P43332	290	1.1(10)-25	Drosophila melanogaster	u1 small nuclear ribonucleoprotein a (u1 snrnp a protein) (sex determination protein snf).
CONTIG3563	12679588_c3_12	310	14413	192	64	P22470	120	1.5(10)-6	Saccharomyces cerevisiae	san1 protein.
CONTIG1198	6644592_c1_2	311	14414	882	294	P43612	195	2.7(10)-14	Saccharomyces cerevisiae	slt4-associating protein sap155.
CONTIG904	16484682_c2_3	312	14415	744	248	P40856	97	0.062	Saccharomyces cerevisiae	slt4-associating protein sap185.
CONTIG5203	29859687_f1_2	313	14416	912	304	P34732	1361	3.6(10)-139	Candida albicans	vesicular-fusion protein sec18.
CONTIG4696	4741260_c3_10	314	14417	1266	422	P40075	335	1.8(10)-30	Saccharomyces cerevisiae	scs2 protein.
CONTIG5771	26798553_c1_35	315	14418	2652	884	P53009	480	5.7(10)-64	Saccharomyces cerevisiae	scy1 protein.
CONTIG5771	4842_c3_45	316	14419	249	83	P53009	106	6.9(10)-5	Saccharomyces cerevisiae	scy1 protein.

CONTIG1564	16460150_c3_7	317	14420	1245	415	P11075	1003	6.0(10)-100	Saccharomyces cerevisiae	protein transport protein sec7.
CONTIG4576	23836088_f1_1	318	14421	1476	492	P11075	593	1.2(10)-99	Saccharomyces cerevisiae	protein transport protein sec7.
b9x13e73.x	23828931_c1_2	319	14422	699	233	P11075	497	5.0(10)-46	Saccharomyces cerevisiae	protein transport protein sec7.
CONTIG622	22267763_c2_1	320	14423	657	219	P07856	100	0.0071	Bombyx mori	sericin precursor.
CONTIG4510	5937751_f1_1	321	14424	372	124	P43682	123	5.5(10)-8	Saccharomyces cerevisiae	sft1 protein (p14).
CONTIG2934	15678317_f3_1	322	14425	705	235	P51534	194	2.6(10)-14	Saccharomyces cerevisiae	sft4 protein.
CONTIG3277	25394788_f1_1	323	14426	1458	486	P51534	220	2.0(10)-16	Saccharomyces cerevisiae	sft4 protein.
CONTIG5610	10547257_f3_6	324	14427	2658	886	P40537	479	2.2(10)-42	Saccharomyces cerevisiae	smt4 protein.
CONTIG4849	23650260_c2_6	325	14428	210	70	P40204	147	1.6(10)-10	Saccharomyces cerevisiae	small nuclear ribonucleoprotein e homolog snp2.
CONTIG2959	29382327_f1_1	326	14429	597	199	P54705	91	0.13	Dictyostelium discoideum	snwa protein.
CONTIG5167	14093817_c3_18	327	14430	978	326	P24706	117	1.1(10)-6	Onchocerca volvulus	superoxide dismutase (cu-zn) (ec 1.15.1.1).
b1x17876.y	25578211_c2_2	328	14431	516	172	P08866	836	1.5(10)-83	Escherichia coli	sopa protein (protein a).
b1x11226.x	21540701_c2_6	329	14432	483	161	P08866	715	1.0(10)-70	Escherichia coli	sopa protein (protein a).
b1x11226.x	32619052_c1_5	330	14433	309	103	P08867	436	3.7(10)-41	Escherichia coli	sopb protein (protein b).
CONTIG5433	14570176_c2_10	331	14434	1107	369	Q10088	763	8.3(10)-76	Schizosaccharomyces pombe	putative agmatinase precursor (ec 3.5.3.11) (agmatine ureohydrolase) (aah).
CONTIG5672	26251313_c2_19	332	14435	1269	423	Q10088	663	3.2(10)-65	Schizosaccharomyces pombe	putative agmatinase precursor (ec 3.5.3.11) (agmatine ureohydrolase) (aah).
CONTIG3618	24509438_f2_2	333	14436	1065	355	P38789	410	2.1(10)-38	Saccharomyces cerevisiae	sft1 protein.
CONTIG5811	13836588_f2_12	334	14437	1437	479	P25344	290	2.7(10)-25	Saccharomyces cerevisiae	sft50 protein.

CONTIG4795	23718818_c2_5	335	14438	1380	460	P15705	1349	6.7(10)-138	Saccharomyces cerevisiae	heat shock protein stt1.
CONTIG5567	14158153_3_7	336	14439	1653	551	P33300	809	1.1(10)-80	Saccharomyces cerevisiae	sur1 protein.
CONTIG5164	2535912_c2_12	337	14440	588	196	P35189	362	2.6(10)-33	Saccharomyces cerevisiae	transcription initiation factor tff1f small subunit (transcription factor g 30 kd subunit) (anc1 protein).
CONTIG3505	554676_c3_5	338	14441	837	279	P50273	106	0.00689	Saccharomyces cerevisiae	tcn10 protein.
CONTIG2133	24414693_f2_2	339	14442	591	197	P35691	618	1.8(10)-60	Saccharomyces cerevisiae	translationally controlled tumor protein homolog (tcp).
CONTIG2919	12276817_c1_6	340	14443	1074	358	P43072	1461	9.0(10)-150	Candida albicans	transcription factor ttiib 70 kd subunit (tfiib) (b-related factor) (brf).
CONTIG909	14648575_c2_4	341	14444	435	145	P43072	507	1.1(10)-48	Candida albicans	transcription factor ttiib 70 kd subunit (tfiib) (b-related factor) (brf).
CONTIG5805	33594561_c1_28	342	14445	849	283	Q07141	97	0.07499	Rattus norvegicus	transducin-like enhancer protein 4 (esp2 protein).
CONTIG3813	1375450_f2_1	343	14446	813	271	P50616	93	0.05099	Homo sapiens	lob protein.
CONTIG1976	1054752_c1_2	344	14447	765	255	P54006	357	8.8(10)-33	Cochliobolus carbonum	tox2 protein.
CONTIG4613	35803575_f3_2	345	14448	2082	694	P52494	3512	0	Candida albicans	neutral trehalase (ec 3.2.1.28) (alpha, alpha-trehalase) (alpha, alpha-trehalose glucohydrolase).
blx18142.y	12131382_c1_3	346	14449	426	142	P52494	378	6.2(10)-34	Candida albicans	neutral trehalase (ec 3.2.1.28) (alpha, alpha-trehalase) (alpha, alpha-trehalose glucohydrolase).
CONTIG4017	5164063_f1_1	347	14450	276	92	P05476	162	4.0(10)-12	Kluyveromyces fragilis	dna-binding protein trf1 (terminal region recognition factor 1).
blx11191.x	24062515_c1_1	348	14451	585	195	P43075	864	1.7(10)-86	Candida albicans	trna ligase (ec 6.5.1.3).

CONTIG1170	6837803_f2_2	349	14452	381	127	P43073	495	2.1(10)-47	Candida albicans	n-(5'-phosphoribosyl)anthranilate isomerase (ec 5.3.1.24) (prai).
CONTIG2981	13065655_f2_2	350	14453	471	157	P43073	552	1.8(10)-53	Candida albicans	n-(5'-phosphoribosyl)anthranilate isomerase (ec 5.3.1.24) (prai).
CONTIG2310	12344063_c1_1	351	14454	1083	361	P38069	452	7.5(10)-43	Saccharomyces cerevisiae	tip1 protein.
CONTIG3129	15785956_f2_1	352	14455	1242	414	P38069	382	4.7(10)-35	Saccharomyces cerevisiae	tip1 protein.
CONTIG3321	4117760_c2_4	353	14456	699	233	P38069	105	0.0038	Saccharomyces cerevisiae	tip1 protein.
CONTIG4184	22453500_c1_3	354	14457	1791	597	P38069	614	5.0(10)-60	Saccharomyces cerevisiae	tip1 protein.
CONTIG5269	36363428_c2_10	355	14458	1776	592	P38069	608	2.2(10)-59	Saccharomyces cerevisiae	tip1 protein.
b3x17645.y	22861952_f2_1	356	14459	504	168	P38069	238	2.8(10)-19	Saccharomyces cerevisiae	tip1 protein.
CONTIG5026	4172555_f3_5	357	14460	1965	655	P36629	200	7.5(10)-13	Schizosaccharomyces pombe	splicing factor u2af large subunit.
CONTIG1886	390875_c2_4	358	14461	852	284	P48777	670	6.0(10)-66	Emericella nidulans	purine permease.
CONTIG4810	24491437_c1_5	359	14462	1269	423	P50101	602	1.2(10)-57	Saccharomyces cerevisiae	putative ubiquitin carboxyl-terminal hydrolase ym9952.06 (ec 3.1.2.15) (ubiquitin thiolesterase) (ubiquitin-specific processing protease) (deubiquitinating enzyme).
CONTIG5048	6683068_c2_8	360	14463	1866	622	P50101	312	2.7(10)-33	Saccharomyces cerevisiae	putative ubiquitin carboxyl-terminal hydrolase ym9952.06 (ec 3.1.2.15) (ubiquitin thiolesterase) (ubiquitin-specific processing protease) (deubiquitinating enzyme).

CONTIG574	33492067_f2_1	361	14464	465	155	P50101	280	3.2(10)-23	Saccharomyces cerevisiae	putative ubiquitin carboxyl-terminal hydrolase ym9952.06 (ec 3.1.2.15) (ubiquitin thiolesterase) (ubiquitin-specific processing protease) (deubiquitinating enzyme).
CONTIG67	23907956_c2_5	362	14465	753	251	P50101	215	2.7(10)-16	Saccharomyces cerevisiae	putative ubiquitin carboxyl-terminal hydrolase ym9952.06 (ec 3.1.2.15) (ubiquitin thiolesterase) (ubiquitin-specific processing protease) (deubiquitinating enzyme).
b9x1ln21.y	511450_f2_1	363	14466	600	200	P50101	703	1.6(10)-68	Saccharomyces cerevisiae	putative ubiquitin carboxyl-terminal hydrolase ym9952.06 (ec 3.1.2.15) (ubiquitin thiolesterase) (ubiquitin-specific processing protease) (deubiquitinating enzyme).
CONTIG1897	24492177_c3_3	364	14467	600	200	P53874	476	9.5(10)-45	Saccharomyces cerevisiae	putative ubiquitin carboxyl-terminal hydrolase ynl186w (ec 3.1.2.15) (ubiquitin thiolesterase) (ubiquitin-specific processing protease) (deubiquitinating enzyme).
CONTIG1897	25601635_c2_2	365	14468	708	236	P53874	555	1.1(10)-53	Saccharomyces cerevisiae	putative ubiquitin carboxyl-terminal hydrolase ynl186w (ec 3.1.2.15) (ubiquitin thiolesterase) (ubiquitin-specific processing protease) (deubiquitinating enzyme).
CONTIG3015	36125410_f3_3	366	14469	228	76	P37299	131	7.7(10)-9	Saccharomyces cerevisiae	ubiquinol-cytochrome c reductase complex 8.5 kd protein (ec 1.10.2.2) (complex iii polypeptide x).

CONTIG493	32119080_c3_5	367	14470	798	266	P21374	170	5.7(10)-13	Saccharomyces cerevisiae	utr3 protein (unknown transcript 3 protein).
CONTIG4116	12542632_f3_2	368	14471	942	314	P40389	288	1.8(10)-25	Schizosaccharo myces pombe	uv-induced protein uviz22.
CONTIG5568	14570138_c2_15	369	14472	1782	594	Q01222	90	0.59999	Vaccinia virus	protein b18.
CONTIG4594	34454133_c2_8	370	14473	1743	581	P03739	96	0.016	coliphage T4	receptor recognizing protein (protein gp38).
CONTIG5422	6678576_c3_21	371	14474	1752	584	Q00154	90	0.45	Ictalurid herpesvirus 1	hypothetical gene 66 protein.
CONTIG5558	20001260_f2_4	372	14475	813	271	P28968	100	0.00479	Equine herpesvirus 1	glycoprotein x precursor.
CONTIG5313	20504025_c1_9	373	14476	369	123	P02845	111	5.2(10)-5	Gallus gallus	vitellogenin ii precursor (contains: lipovitellin, phosvitin).
CONTIG4187	22384417_c2_9	374	14477	414	138	P48836	225	8.5(10)-19	Saccharomyces cerevisiae	vacuolar atp synthase subunit m16 (ec 3.6.1.34) (v-atpase 13 kd subunit).
CONTIG2626	24023287_f2_1	375	14478	231	77	P43074	161	5.2(10)-12	Candida albicans	white colony protein wh11.
CONTIG2482	14462501_f2_1	376	14479	570	190	P12611	239	1.3(10)-19	Saccharomyces cerevisiae	growth regulation protein.
CONTIG4814	245650_f3_8	377	14480	1227	409	P34761	372	1.1(10)-33	Saccharomyces cerevisiae	whi3 protein.
CONTIG3043	2243837_c3_12	378	14481	921	307	Q09697	103	0.014	Schizosaccharo myces pombe	hypothetical 88.2 kd protein c217.18c in chromosome i.
blx17717.y	1206528_f3_1	379	14482	600	200	Q09710	92	0.07199	Schizosaccharo myces pombe	hypothetical 49.6 kd protein c18b11.03c in chromosome i.
CONTIG5676	12192155_c3_24	380	14483	909	303	Q09725	162	1.3(10)-8	Schizosaccharo myces pombe	hypothetical 180.2 kd protein c31a2.05c in chromosome i.
CONTIG3055	281425_c3_4	381	14484	1500	500	Q09731	317	5.4(10)-26	Schizosaccharo myces pombe	hypothetical trp-asp repeats containing protein c31a2.14 in chromosome i.
CONTIG3735	13792302_f2_5	382	14485	783	261	Q09739	126	2.2(10)-6	Schizosaccharo myces pombe	hypothetical 24.2 kd protein c13a11.03 in chromosome i.

CONTIG2846	6127280_f1_1	383	14486	1143	381	Q09764	389	4.5(10)-35	Schizosaccharo myces pombe	hypothetical 107.1 kd protein c24h6.11c in chromosome i.
CONTIG3265	4860177_c1_1	384	14487	1281	427	Q09766	553	4.4(10)-66	Schizosaccharo myces pombe	hypothetical 98.4 kd protein c24h6.13 in chromosome i.
b1x11338.x	22396043_f1_1	385	14488	807	269	Q09766	560	9.0(10)-54	Schizosaccharo myces pombe	hypothetical 98.4 kd protein c24h6.13 in chromosome i.
CONTIG4316	26370187_c3_8	386	14489	1815	605	Q09778	187	5.9(10)-11	Schizosaccharo myces pombe	hypothetical 103.4 kd protein c22f3.13 in chromosome i.
CONTIG3575	11734755_c3_8	387	14490	1533	511	Q09795	458	1.7(10)-43	Schizosaccharo myces pombe	hypothetical protein c22g7.01c in chromosome i (fragment).
CONTIG5448	14656328_c3_20	388	14491	1137	379	P31381	274	1.8(10)-33	Saccharomyces cerevisiae	hypothetical 58.3 kd protein in pml2-ccr4 intergenic region.
CONTIG4740	19546930_c1_12	389	14492	2001	667	P39730	1076	1.5(10)-114	Saccharomyces cerevisiae	112.3 kd protein in pyk1-snc1 intergenic region.
b3x19243.x	12144380_f3_3	390	14493	888	296	P39730	496	1.6(10)-46	Saccharomyces cerevisiae	112.3 kd protein in pyk1-snc1 intergenic region.
CONTIG5803	32454376_c2_27	391	14494	1773	591	Q09833	610	1.3(10)-59	Schizosaccharo myces pombe	hypothetical 59.6 kd protein c4g8.07c in chromosome i.
CONTIG5514	30111260_f1_1	392	14495	954	318	P39731	208	5.4(10)-17	Saccharomyces cerevisiae	hypothetical 33.2 kd protein in pyk1-snc1 intergenic region.
CONTIG2478	3925307_c2_5	393	14496	1023	341	P39727	560	2.7(10)-54	Saccharomyces cerevisiae	hypothetical 46.3 kd protein in pta1- cdc24 intergenic region.
CONTIG5040	2382188_f1_3	394	14497	642	214	P39727	319	9.4(10)-29	Saccharomyces cerevisiae	hypothetical 46.3 kd protein in pta1- cdc24 intergenic region.
CONTIG5405	26367963_f2_1	395	14498	240	80	P39727	249	5.7(10)-21	Saccharomyces cerevisiae	hypothetical 46.3 kd protein in pta1- cdc24 intergenic region.
CONTIG4366	32225063_f1_1	396	14499	1542	514	P39722	1001	2.7(10)-145	Saccharomyces cerevisiae	hypothetical 75.2 kd protein in acs1- gev3 intergenic region.
CONTIG3023	35156567_c2_3	397	14500	657	219	P39721	621	9.3(10)-61	Saccharomyces cerevisiae	hypothetical 27.1 kd protein in acs1- gev3 intergenic region.
CONTIG3635	993925_c3_5	398	14501	756	252	P39721	642	5.5(10)-63	Saccharomyces cerevisiae	hypothetical 27.1 kd protein in acs1- gev3 intergenic region.
CONTIG5064	7056255_f3_3	399	14502	1503	501	P39719	759	5.7(10)-88	Saccharomyces cerevisiae	hypothetical 87.5 kd protein in acs1- gev3 intergenic region.

CONTIG5747	4507828_c1_32	400	14503	4209	1403	Q09863	132	7.5(10)-15	Schizosaccharo myces pombe	hypothetical 122.9 kd protein c29e6.10c in chromosome i.
CONTIG5058	25431575_c1_4	401	14504	837	279	Q09875	205	5.7(10)-22	Schizosaccharo myces pombe	hypothetical 35.8 kd protein c12g12.12 in chromosome i.
CONTIG4920	21883432_c3_12	402	14505	711	237	Q09876	329	2.0(10)-28	Schizosaccharo myces pombe	hypothetical 143.3 kd trp-aspar peptide containing protein c12g12.13c in chromosome i.
CONTIG612	35253213_c2_3	403	14506	915	305	P39705	104	0.00719	Saccharomyces cerevisiae	hypothetical 59.0 kd protein in tlc3- rfa1 intergenic region.
CONTIG1201	3257650_f2_1	404	14507	852	284	Q09885	548	5.0(10)-53	Schizosaccharo myces pombe	hypothetical 43.0 kd protein c8a4.09c in chromosome i.
CONTIG4243	10632925_f2_1	405	14508	1122	374	Q09887	690	4.5(10)-68	Schizosaccharo myces pombe	hypothetical amino-acid permease c8a4.11.
CONTIG5363	24259527_c2_21	406	14509	1647	549	P27637	138	6.9(10)-11	Saccharomyces cerevisiae	hypothetical 78.3 kd protein in rfa1- adel intergenic region.
CONTIG3920	23476535_f3_2	407	14510	702	234	P46683	354	1.8(10)-32	Saccharomyces cerevisiae	ankyrin repeat-containing protein yarl.
CONTIG4130	14100652_c1_7	408	14511	1275	425	Q10138	165	1.3(10)-9	Schizosaccharo myces pombe	hypothetical 51.5 kd protein c3h8.02 in chromosome i.
CONTIG5576	10970251_c2_19	409	14512	1830	610	P18634	120	0.00044	Saccharomyces cerevisiae	hypothetical 24.4 kd protein in ap10 region.
CONTIG5790	2109436_f3_15	410	14513	732	244	Q10154	184	1.8(10)-14	Schizosaccharo myces pombe	hypothetical 27.1 kd protein c1d4.09c in chromosome i.
CONTIG3744	4875077_f3_5	411	14514	225	75	Q10167	159	8.4(10)-12	Schizosaccharo myces pombe	hypothetical 8.2 kd protein c26a3.14c in chromosome i.
CONTIG1323	2239550_c3_8	412	14515	1098	366	Q10168	114	0.0006	Schizosaccharo myces pombe	hypothetical 60.7 kd protein c26a3.15c in chromosome i.
CONTIG5342	1069015_c2_19	413	14516	534	178	Q10191	242	2.2(10)-20	Schizosaccharo myces pombe	hypothetical 44.5 kd protein c3f10.17 in chromosome i.
CONTIG5042	10554561_f1_1	414	14517	744	248	Q10193	92	0.00048	Schizosaccharo myces pombe	hypothetical protein c13f4.01c in chromosome i (fragment).
CONTIG68	24081533_f3_1	415	14518	333	111	Q10220	91	0.00013	Schizosaccharo myces pombe	hypothetical 10.1 kd protein c4h3.13 in chromosome i.

CONTIG5080	21675012_f2_3	416	14519	321	107	Q10225	145	2.5(10)-9	Schizosaccharo myces pombe	hypothetical 60.5 kd protein c13d6.04c in chromosome i.
b2x17307.y	24398337_f2_1	417	14520	498	166	P38281	154	9.1(10)-11	Saccharomyces cerevisiae	hypothetical 35.8 kd protein in ysw1-rib7 intergenic region.
b9x13n27.y	11191300_f1_1	418	14521	819	273	P38285	119	7.2(10)-5	Saccharomyces cerevisiae	hypothetical 62.7 kd protein in rpb5-cdc28 intergenic region.
CONTIG2095	22298932_c1_2	419	14522	1110	370	P38288	286	3.6(10)-50	Saccharomyces cerevisiae	hypothetical 48.0 kd protein in cdc28-ar1 intergenic region precursor.
b1x14474.y	4900756_f2_1	420	14523	342	114	P38288	163	2.2(10)-11	Saccharomyces cerevisiae	hypothetical 48.0 kd protein in cdc28-ar1 intergenic region precursor.
CONTIG5404	3939136_f2_4	421	14524	717	239	P38289	129	7.0(10)-6	Saccharomyces cerevisiae	hypothetical 67.6 kd protein in cdc28-ar1 intergenic region.
CONTIG5404	24064718_f3_5	422	14525	1230	410	P38289	378	1.1(10)-34	Saccharomyces cerevisiae	hypothetical 67.6 kd protein in cdc28-ar1 intergenic region.
CONTIG498	14554632_f1_1	423	14526	540	180	P38291	187	9.0(10)-15	Saccharomyces cerevisiae	hypothetical 15.8 kd protein in tyr1- sse2 intergenic region.
CONTIG5571	6915705_f1_3	424	14527	447	149	P38293	343	2.7(10)-31	Saccharomyces cerevisiae	hypothetical 16.8 kd protein in smv2-rps101 intergenic region.
CONTIG5613	4861502_c3_23	425	14528	1296	432	P38295	573	1.1(10)-55	Saccharomyces cerevisiae	hypothetical 51.3 kd protein in smv2-rps101 intergenic region.
CONTIG4141	4296930_f1_1	426	14529	2109	703	P38297	1015	5.5(10)-113	Saccharomyces cerevisiae	hypothetical 97.8 kd protein in smv2-rps101 intergenic region.
CONTIG4848	10172502_c2_6	427	14530	969	323	P38301	497	1.3(10)-47	Saccharomyces cerevisiae	hypothetical 30.3 kd protein in mba1-rps13 intergenic region.
CONTIG1093	4085177_c3_4	428	14531	732	244	P38304	263	8.0(10)-23	Saccharomyces cerevisiae	hypothetical 25.3 kd protein in rim2-msl1 intergenic region.
CONTIG2021	55413_c1_3	429	14532	381	127	P38310	183	1.6(10)-13	Saccharomyces cerevisiae	hypothetical 51.5 kd protein in ktr3- dur1.2 intergenic region.
CONTIG2021	43235792_c1_2	430	14533	300	100	P38310	292	1.3(10)-25	Saccharomyces cerevisiae	hypothetical 51.5 kd protein in ktr3- dur1.2 intergenic region.
CONTIG3770	14853256_f1_1	431	14534	1560	520	P38310	539	4.9(10)-62	Saccharomyces cerevisiae	hypothetical 51.5 kd protein in ktr3- dur1.2 intergenic region.

CONTIG4869	36379191_fl_1	432	14535	1890	630	P38314	748	3.2(10)-74	Saccharomyces cerevisiae	hypothetical 57.2 kd protein in met8-hpc2 intergenic region.
CONTIG5078	10253375_fl_2	433	14536	1374	458	P38315	220	3.7(10)-28	Saccharomyces cerevisiae	hypothetical 77.7 kd protein in hpc2-pyc2 intergenic region.
CONTIG5078	10972792_c2_9	434	14537	501	167	P38316	210	3.2(10)-17	Saccharomyces cerevisiae	hypothetical 21.1 kd protein in hpc2-pyc2 intergenic region.
CONTIG2756	4081257_c1_3	435	14538	849	283	P38318	516	1.2(10)-49	Saccharomyces cerevisiae	hypothetical 63.0 kd protein in pyc2-pdb1 intergenic region.
CONTIG5462	23632937_c1_9	436	14539	909	303	P38324	371	1.2(10)-39	Saccharomyces cerevisiae	hypothetical 35.9 kd protein in pcs60-abd1 intergenic region.
CONTIG5481	34567136_c3_17	437	14540	1038	346	P38326	261	1.3(10)-22	Saccharomyces cerevisiae	hypothetical 34.3 kd protein in pcs60-abd1 intergenic region.
CONTIG4802	1432318_fl_1	438	14541	1200	400	P38355	954	4.7(10)-96	Saccharomyces cerevisiae	hypothetical 47.5 kd protein in ape3-apm3 intergenic region.
CONTIG5783	33367952_c2_32	439	14542	1341	447	P38355	1025	1.3(10)-103	Saccharomyces cerevisiae	hypothetical 47.5 kd protein in ape3-apm3 intergenic region.
CONTIG4478	26363125_f2_3	440	14543	261	87	P38331	174	2.2(10)-13	Saccharomyces cerevisiae	hypothetical 27.6 kd protein in prp5-alg7 intergenic region.
CONTIG4214	1190687_c3_12	441	14544	1080	360	P38332	479	4.9(10)-68	Saccharomyces cerevisiae	hypothetical 43.3 kd protein in alg7-enp1 intergenic region.
CONTIG5028	24885077_c2_13	442	14545	1323	441	P38335	211	3.3(10)-14	Saccharomyces cerevisiae	hypothetical 79.0 kd protein in srb6-rib5 intergenic region.
CONTIG5469	33753201_c1_9	443	14546	327	109	P38336	129	4.0(10)-8	Saccharomyces cerevisiae	hypothetical 32.9 kd protein in rib5-shm1 intergenic region.
CONTIG3946	34085811_f2_1	444	14547	825	275	P38337	93	0.00389	Saccharomyces cerevisiae	hypothetical 16.4 kd protein in rib5-shm1 intergenic region.
CONTIG3003	14148263_fl_2	445	14548	723	241	P38339	329	5.4(10)-29	Saccharomyces cerevisiae	hypothetical 74.6 kd protein in rib5-shm1 intergenic region.
CONTIG3946	36620632_c1_4	446	14549	510	170	P38339	279	1.3(10)-23	Saccharomyces cerevisiae	hypothetical 74.6 kd protein in rib5-shm1 intergenic region.
CONTIG3946	34687_c3_5	447	14550	939	313	P38339	229	1.0(10)-24	Saccharomyces cerevisiae	hypothetical 74.6 kd protein in rib5-shm1 intergenic region.
CONTIG4811	16900307_fl_1	448	14551	735	245	P38340	660	6.9(10)-65	Saccharomyces cerevisiae	hypothetical 26.1 kd protein in rib5-shm1 intergenic region.

CONTIG5801	4297816_c1_26	449	14552	969	323	P38342	458	1.7(10)-43	Saccharomyces cerevisiae	hypothetical 36.0 kd protein in shm1-mrp137 intergenic region.
CONTIG2744	7159681_f1_1	450	14553	1356	452	P38344	558	4.4(10)-54	Saccharomyces cerevisiae	34.7 kd protein in shm1-mrp137 intergenic region.
CONTIG5819	4406952_f3_18	451	14554	420	140	P38345	226	6.7(10)-19	Saccharomyces cerevisiae	hypothetical 14.6 kd protein in mrp137-rif1 intergenic region.
CONTIG4670	898581_f1_3	452	14555	1053	351	P38348	114	0.00071	Saccharomyces cerevisiae	hypothetical 55.5 kd protein in mrp137-rif1 intergenic region.
CONTIG3998	34022010_f1_1	453	14556	1290	430	P38349	331	5.0(10)-30	Saccharomyces cerevisiae	hypothetical 50.0 kd protein in mrp137-rif1 intergenic region.
CONTIG5423	10839692_c1_8	454	14557	183	61	P38149	147	3.2(10)-9	Saccharomyces cerevisiae	hypothetical trp-asp repeats containing protein in paf1-mrp127 intergenic region.
CONTIG5423	556313_c2_13	455	14558	285	95	P38149	106	7.7(10)-5	Saccharomyces cerevisiae	hypothetical trp-asp repeats containing protein in paf1-mrp127 intergenic region.
CONTIG5423	25584437_c3_14	456	14559	1038	346	P38149	568	1.2(10)-54	Saccharomyces cerevisiae	hypothetical trp-asp repeats containing protein in paf1-mrp127 intergenic region.
CONTIG5423	19550376_c1_7	457	14560	1857	619	P38149	276	8.5(10)-43	Saccharomyces cerevisiae	hypothetical trp-asp repeats containing protein in paf1-mrp127 intergenic region.
CONTIG1240	6642128_f1_1	458	14561	969	323	P35194	229	2.1(10)-17	Saccharomyces cerevisiae	hypothetical 287.5 kd protein in pdf3-hna2 intergenic region.
CONTIG3591	189089_f1_1	459	14562	1788	596	P35194	697	3.7(10)-67	Saccharomyces cerevisiae	hypothetical 287.5 kd protein in pdf3-hna2 intergenic region.
CONTIG5173	24423500_c3_5	460	14563	3699	1233	P35194	2065	4.2(10)-243	Saccharomyces cerevisiae	hypothetical 287.5 kd protein in pdf3-hna2 intergenic region.
CONTIG3222	24414042_c2_10	461	14564	1089	363	P38207	531	3.2(10)-51	Saccharomyces cerevisiae	hypothetical 59.4 kd protein in rfi1-pep1 intergenic region.
CONTIG4194	26370812_c1_6	462	14565	996	332	P38201	160	2.5(10)-9	Saccharomyces cerevisiae	hypothetical 42.6 kd protein in aac2-rp119 intergenic region.
CONTIG3680	33214025_f3_4	463	14566	807	269	P38197	596	4.2(10)-58	Saccharomyces cerevisiae	hypothetical 29.1 kd protein in ura7-poll2 intergenic region.

blx18501.y	23719125_c2_2	464	14567	483	161		P39519	382	2.0(10)-35	Saccharomyces cerevisiae	hypothetical protein in bdf1 5'region (orf1) (fragment).
CONTIG3776	26298305_c3_7	465	14568	1425	475		P34216	284	1.1(10)-22	Saccharomyces cerevisiae	hypothetical 150.8 kd protein in sec17-qcr1 intergenic region.
CONTIG5621	14475260_c1_15	466	14569	1335	445		P34216	621	1.5(10)-59	Saccharomyces cerevisiae	hypothetical 150.8 kd protein in sec17-qcr1 intergenic region.
CONTIG5677	1382888_c2_23	467	14570	435	145		P34216	200	1.3(10)-14	Saccharomyces cerevisiae	hypothetical 150.8 kd protein in sec17-qcr1 intergenic region.
CONTIG2781	4331300_c3_3	468	14571	726	242		P38191	191	3.3(10)-15	Saccharomyces cerevisiae	hypothetical 16.1 kd protein in sec17-qcr1 intergenic region.
CONTIG2936	20370436_f3_8	469	14572	1050	350		P34217	284	4.0(10)-24	Saccharomyces cerevisiae	hypothetical 73.8 kd protein in shp1-sec17 intergenic region.
b9x12233.y	5313175_c2_1	470	14573	525	175		P34222	282	7.7(10)-25	Saccharomyces cerevisiae	hypothetical 23.1 kd protein in shp1-sec17 intergenic region.
CONTIG5255	35406261_c1_6	471	14574	402	134		P38182	463	5.2(10)-44	Saccharomyces cerevisiae	hypothetical 13.6 kd protein in nup170-lis1 intergenic region.
CONTIG3087	33414832_c2_5	472	14575	1026	342		P38177	103	1.7(10)-9	Saccharomyces cerevisiae	hypothetical 52.0 kd protein in rpl17a-bob1 intergenic region.
CONTIG3872	13678753_f2_3	473	14576	603	201		P38175	139	1.1(10)-9	Saccharomyces cerevisiae	hypothetical 20.4 kd protein in map2-tel1 intergenic region.
CONTIG1584	11171932_f3_4	474	14577	525	175		P53716	208	5.4(10)-17	Candida albicans	hypothetical protein in whs11 5'region (fragment).
CONTIG4974	26550_c1_11	475	14578	1983	661		P38170	358	1.3(10)-60	Saccharomyces cerevisiae	hypothetical 83.0 kd protein in atp1-rox3 intergenic region.
CONTIG4344	34581312_c2_9	476	14579	1443	481		P38169	1094	7.0(10)-111	Saccharomyces cerevisiae	hypothetical 52.4 kd protein in atp1-rox3 intergenic region precursor.
CONTIG3397	1415962_c1_3	477	14580	762	254		P38167	128	2.6(10)-5	Saccharomyces cerevisiae	hypothetical 119.3 kd protein in sft2-ap1 intergenic region.
CONTIG717	24251437_c3_3	478	14581	213	71		P38167	128	4.4(10)-7	Saccharomyces cerevisiae	hypothetical 119.3 kd protein in sft2-ap1 intergenic region.
CONTIG5740	9765625_f1_5	479	14582	1719	573		P38164	357	5.5(10)-46	Saccharomyces cerevisiae	hypothetical 104.7 kd protein in pkc1-rtg3 intergenic region.

CONTIG4783	34432691_f2_2	480	14583	1338	446	P38163	410	2.8(10)-37	Saccharomyces cerevisiae	hypothetical 111.7 kd protein in pkl 5 region.
b3x16024.y	25985783_c2_4	481	14584	588	196	P38163	192	6.0(10)-14	Saccharomyces cerevisiae	hypothetical 111.7 kd protein in pkl 5 region.
CONTIG5780	4429752_f3_22	482	14585	555	185	P38162	212	2.0(10)-17	Saccharomyces cerevisiae	hypothetical 23.0 kd protein in pkl 5 region.
CONTIG2040	32476457_f2_2	483	14586	393	131	P38211	238	1.2(10)-19	Saccharomyces cerevisiae	hypothetical 50.8 kd protein in coq1-hhf1 intergenic region precursor.
CONTIG2045	19565750_c1_2	484	14587	729	243	P38212	231	2.0(10)-19	Saccharomyces cerevisiae	hypothetical 23.9 kd protein in coq1-hhf1 intergenic region.
CONTIG1288	23558305_c2_2	485	14588	603	201	P38213	93	0.00012	Saccharomyces cerevisiae	hypothetical 82.4 kd protein in coq1-hhf1 intergenic region.
CONTIG5357	2460390_c1_17	486	14589	564	188	P38218	191	1.3(10)-25	Saccharomyces cerevisiae	hypothetical 19.9 kd protein in fur4-chs3 intergenic region.
CONTIG334	4884687_c2_1	487	14590	801	267	P38219	819	9.6(10)-82	Saccharomyces cerevisiae	hypothetical 44.2 kd protein in sco2-mrf1 intergenic region.
CONTIG5653	10946932_c1_14	488	14591	1227	409	P38222	249	4.5(10)-19	Saccharomyces cerevisiae	hypothetical 62.6 kd protein in cds1-rpl2 intergenic region.
b9x11364.x	157830_c2_1	489	14592	594	198	P38235	121	1.0(10)-11	Saccharomyces cerevisiae	hypothetical 40.3 kd protein in reb1-tyr2 intergenic region.
CONTIG4967	24296902_c1_9	490	14593	585	195	P38239	169	7.4(10)-13	Saccharomyces cerevisiae	hypothetical 13.2 kd protein in orc2-tip1 intergenic region.
CONTIG5566	2346901_c1_24	491	14594	927	309	P38241	213	3.6(10)-17	Saccharomyces cerevisiae	hypothetical 40.9 kd protein in orc2-tip1 intergenic region.
CONTIG5501	4788913_c3_33	492	14595	828	276	P38244	278	4.7(10)-37	Saccharomyces cerevisiae	hypothetical 47.8 kd protein in hsp26-sec18 intergenic region.
CONTIG2050	21964140_c3_8	493	14596	624	208	P38245	173	1.8(10)-12	Saccharomyces cerevisiae	hypothetical 51.6 kd protein in hsp26-sec18 intergenic region.
CONTIG215	26611657_c3_6	494	14597	561	187	P38245	109	0.0002	Saccharomyces cerevisiae	hypothetical 51.6 kd protein in hsp26-sec18 intergenic region.
CONTIG5460	30553265_c1_18	495	14598	306	102	P38245	98	0.00024	Saccharomyces cerevisiae	hypothetical 51.6 kd protein in hsp26-sec18 intergenic region.

CONTIG5687	10632066_c1_16	496	14599	645	215	P38245	140	2.3(10)-11	Saccharomyces cerevisiae	hypothetical 51.6 kd protein in hsp26-sec18 intergenic region.
CONTIG4124	12207001_f1_2	497	14600	1158	386	P38249	517	7.5(10)-78	Saccharomyces cerevisiae	hypothetical 110.3 kd protein in hsp26-sec18 intergenic region.
CONTIG4124	24650176_f2_4	498	14601	918	306	P38249	210	6.7(10)-16	Saccharomyces cerevisiae	hypothetical 110.3 kd protein in hsp26-sec18 intergenic region.
CONTIG2716	24648467_c3_6	499	14602	750	250	P38249	239	5.4(10)-19	Saccharomyces cerevisiae	hypothetical 110.3 kd protein in hsp26-sec18 intergenic region.
CONTIG424	10973926_c3_3	500	14603	780	260	P38254	570	2.3(10)-55	Saccharomyces cerevisiae	hypothetical 86.4 kd protein in pho5-vps15 intergenic region.
CONTIG3278	3916250_c3_6	501	14604	783	261	P38256	395	8.3(10)-37	Saccharomyces cerevisiae	hypothetical 27.1 kd protein in pho5-vps15 intergenic region.
CONTIG3786	26679002_c2_2	502	14605	423	141	P38260	108	9.1(10)-6	Saccharomyces cerevisiae	hypothetical 32.6 kd protein in vps15-ymc2 intergenic region.
CONTIG3316	26428175_c3_4	503	14606	1848	616	P38261	223	2.8(10)-25	Saccharomyces cerevisiae	hypothetical 85.5 kd protein in vps15-ymc2 intergenic region.
CONTIG4278	22351430_f3_5	504	14607	1428	476	P38263	222	2.2(10)-20	Saccharomyces cerevisiae	hypothetical 41.2 kd protein in ymc2-cmd1 intergenic region.
CONTIG3715	9866261_c3_6	505	14608	597	199	P38264	563	1.3(10)-54	Saccharomyces cerevisiae	hypothetical 21.1 kd protein in ymc2-cmd1 intergenic region.
CONTIG4986	477290_f3_5	506	14609	225	75	P38276	158	1.1(10)-11	Saccharomyces cerevisiae	hypothetical 20.5 kd protein in csr1-iral intergenic region.
CONTIG3089	9765718_f3_2	507	14610	753	251	P38278	388	4.5(10)-36	Saccharomyces cerevisiae	hypothetical 38.5 kd protein in iral-mak5 intergenic region.
CONTIG2092	2734652_f1_1	508	14611	1020	340	P38279	617	2.5(10)-60	Saccharomyces cerevisiae	hypothetical 33.5 kd protein in mps9-ysw1 intergenic region.
CONTIG4650	23648387_c2_9	509	14612	1068	356	P38279	226	5.2(10)-28	Saccharomyces cerevisiae	hypothetical 33.5 kd protein in mps9-ysw1 intergenic region.
CONTIG1652	6664067_f1_1	510	14613	297	99	P25559	117	1.1(10)-6	Saccharomyces cerevisiae	hypothetical 35.8 kd protein in nls1-bud3 intergenic region.
CONTIG3851	12531386_f1_3	511	14614	498	166	P25559	115	1.8(10)-5	Saccharomyces cerevisiae	hypothetical 35.8 kd protein in nls1-bud3 intergenic region.
CONTIG5085	4697052_f3_5	512	14615	870	290	P25368	391	2.2(10)-36	Saccharomyces cerevisiae	hypothetical 34.5 kd protein in ste50-his4 intergenic region.

CONTIG5025	5267050_f3_4	513	14616	1410	470	P25369	177	4.7(10)-13	Saccharomyces cerevisiae	hypothetical 23.6 kd protein in glk1-sie50 intergenic region.
CONTIG4432	393750_c3_13	514	14617	1131	377	P25370	254	9.4(10)-35	Saccharomyces cerevisiae	hypothetical 64.9 kd protein in glk1-sie50 intergenic region.
CONTIG5231	5159507_f1_2	515	14618	945	315	P25370	205	2.2(10)-18	Saccharomyces cerevisiae	hypothetical 64.9 kd protein in glk1-sie50 intergenic region.
CONTIG4053	13867194_c1_5	516	14619	1176	392	P25573	106	0.0064	Saccharomyces cerevisiae	hypothetical 47.2 kd protein in pdi1 5'region.
blx12128.x	10650307_f1_1	517	14620	537	179	P25586	796	2.7(10)-79	Saccharomyces cerevisiae	hypothetical 37.2 kd protein in chl-apa1/dtp intergenic region.
CONTIG1235	30367630_c3_5	518	14621	285	95	P25600	127	8.4(10)-8	Saccharomyces cerevisiae	transposon ty5-1 34.5 kd hypothetical protein.
CONTIG4104	26571875_f2_5	519	14622	591	197	P25614	537	7.4(10)-52	Saccharomyces cerevisiae	very hypothetical 22.8 kd protein in pgk1 region.
CONTIG2428	25839455_c3_7	520	14623	771	257	P25616	194	2.7(10)-15	Saccharomyces cerevisiae	hypothetical 36.3 kd protein in pol4-srd1 intergenic region.
CONTIG2517	19569002_f2_1	521	14624	1107	369	P25618	956	3.0(10)-96	Saccharomyces cerevisiae	hypothetical 107.9 kd protein in pol4-srd1 intergenic region.
b3x19615.x	26289182_f3_2	522	14625	822	274	P25618	321	8.9(10)-28	Saccharomyces cerevisiae	hypothetical 107.9 kd protein in pol4-srd1 intergenic region.
CONTIG4131	9805133_c2_8	523	14626	927	309	P25353	216	1.0(10)-16	Saccharomyces cerevisiae	hypothetical 84.9 kd protein in pml-rim1 intergenic region.
CONTIG5716	12265875_f2_5	524	14627	1179	393	P25359	297	2.6(10)-47	Saccharomyces cerevisiae	hypothetical 44.1 kd protein in gns1-rbk1 intergenic region.
CONTIG453	569427_c3_3	525	14628	354	118	P25625	158	3.5(10)-15	Saccharomyces cerevisiae	hypothetical 42.5 kd protein in tsml-arel intergenic region.
CONTIG5633	9970281_c1_11	526	14629	717	239	P25625	325	2.2(10)-29	Saccharomyces cerevisiae	hypothetical 42.5 kd protein in tsml-arel intergenic region.
CONTIG5573	2117811_c3_17	527	14630	717	239	P25631	329	8.1(10)-30	Saccharomyces cerevisiae	hypothetical 24.7 kd protein in are1-thr4 intergenic region.
CONTIG5366	2032593_c2_5	528	14631	1554	518	P25355	237	1.1(10)-23	Saccharomyces cerevisiae	hypothetical 65.2 kd protein in thr4-pwp2 intergenic region.
CONTIG1960	25491692_f3_4	529	14632	411	137	P25637	239	2.7(10)-20	Saccharomyces cerevisiae	hypothetical 29.0 kd protein in pwp2-sup61 intergenic region.

CONTIG1960	4964437_f1_1	530	14633	366	122	P25637	191	3.3(10)-15	Saccharomyces cerevisiae	hypothetical 29.0 kd protein in pwp2-sup61 intergenic region.
b4x10153.x	36510253_f1_1	531	14634	645	215	P25639	180	5.0(10)-13	Saccharomyces cerevisiae	hypothetical 65.0 kd protein in pwp2-sup61 intergenic region.
CONTIG2339	35445252_f3_1	532	14635	888	296	P25363	324	2.7(10)-29	Saccharomyces cerevisiae	hypothetical 13.8 kd protein in pwp2-sup61 intergenic region.
CONTIG3075	22032568_f2_1	533	14636	438	146	P25642	141	6.7(10)-10	Saccharomyces cerevisiae	hypothetical 13.6 kd protein in cpr4-sol2 intergenic region.
CONTIG2389	9786562_c2_2	534	14637	1038	346	P25646	316	6.7(10)-41	Saccharomyces cerevisiae	hypothetical 48.5 kd protein in ers1-srb8 intergenic region.
CONTIG5343	3915637_f3_9	535	14638	774	258	P25651	139	1.7(10)-9	Saccharomyces cerevisiae	hypothetical 21.7 kd protein in tup1-abp1 intergenic region.
CONTIG4878	13707750_c3_6	536	14639	612	204	P25654	212	2.0(10)-17	Saccharomyces cerevisiae	hypothetical 20.7 kd protein in kin82 5'region.
CONTIG5585	13953186_f1_3	537	14640	483	161	P25656	306	2.2(10)-27	Saccharomyces cerevisiae	hypothetical 45.0 kd protein in not1/cdc39-hmr intergenic region.
CONTIG5585	4767162_f3_13	538	14641	804	268	P25656	621	9.3(10)-61	Saccharomyces cerevisiae	hypothetical 45.0 kd protein in not1/cdc39-hmr intergenic region.
CONTIG5697	4803755_f3_7	539	14642	1290	430	P25366	214	6.4(10)-20	Saccharomyces cerevisiae	hypothetical 41.6 kd protein in hmr 5'region.
CONTIG2699	10737811_f3_3	540	14643	834	278	Q10235	181	4.4(10)-23	Schizosaccharo myces pombe	hypothetical 26.7 kd protein c4g9.01 in chromosome i.
CONTIG847	859567_f1_1	541	14644	801	267	Q10236	629	1.3(10)-61	Schizosaccharo myces pombe	hypothetical 36.8 kd protein c4g9.02 in chromosome i.
CONTIG3654	1064780_f1_1	542	14645	1230	410	Q10250	570	2.8(10)-79	Schizosaccharo myces pombe	hypothetical 170.7 kd protein c5618.02 in chromosome i.
CONTIG3654	24650300_f2_2	543	14646	858	286	Q10250	455	9.8(10)-42	Schizosaccharo myces pombe	hypothetical 170.7 kd protein c5618.02 in chromosome i.
CONTIG4736	35318780_c1_9	544	14647	951	317	Q10250	257	1.2(10)-20	Schizosaccharo myces pombe	hypothetical 170.7 kd protein c5618.02 in chromosome i.
CONTIG5596	23609626_f1_3	545	14648	1500	500	Q10299	558	4.4(10)-54	Schizosaccharo myces pombe	hypothetical 50.5 kd protein c2n10.05c in chromosome i.
CONTIG5587	4689135_f2_7	546	14649	1494	498	P38961	878	5.4(10)-88	Saccharomyces cerevisiae	hypothetical 47.2 kd protein in pdc2-af1 intergenic region.

CONTIG2667	1961627_c1_4	547	14650	837	279	P38962	124	2.3(10)-13	Saccharomyces cerevisiae	hypothetical 23.1 kd protein in pdc2-af1 intergenic region.
CONTIG1729	20523262_f2_1	548	14651	873	291	P35178	362	2.6(10)-33	Saccharomyces cerevisiae	hypothetical 33.2 kd protein in sss1-slu7 intergenic region.
CONTIG5257	2910127_c3_10	549	14652	1551	517	P38966	126	4.2(10)-9	Saccharomyces cerevisiae	hypothetical 18.9 kd protein in slu7 3'region.
CONTIG4200	24422805_f3_4	550	14653	678	226	Q02354	213	7.2(10)-17	Saccharomyces cerevisiae	hypothetical 52.2 kd protein in ada2 3'region.
b2x15202.y	4332253_c3_2	551	14654	531	177	Q10354	204	1.3(10)-16	Schizosaccharo myces pombe	hypothetical protein c22e12.01 in chromosome i (fragment).
b2x14806.x	9957175_c3_2	552	14655	528	176	P48569	259	2.1(10)-22	Saccharomyces cerevisiae	hypothetical 37.0 kd protein in rpl41a-inh1 intergenic region.
CONTIG3986	19566052_c2_9	553	14656	468	156	Q10448	96	0.00048	Schizosaccharo myces pombe	hypothetical 16.9 kd protein c12b10.15c in chromosome i.
CONTIG4653	31266406_f1_4	554	14657	696	232	Q10449	224	6.7(10)-18	Schizosaccharo myces pombe	hypothetical 57.2 kd protein c12b10.16c in chromosome i.
CONTIG4684	5352182_c2_6	555	14658	1305	435	Q10449	950	1.3(10)-95	Schizosaccharo myces pombe	hypothetical 57.2 kd protein c12b10.16c in chromosome i.
b2x14975.x	15814068_f1_1	556	14659	798	266	Q10495	92	0.28999	Schizosaccharo myces pombe	hypothetical 111.4 kd protein c26f1.08c in chromosome i.
CONTIG4094	25567802_f2_4	557	14660	411	137	P32643	121	3.6(10)-7	Saccharomyces cerevisiae	hypothetical 34.8 kd protein in rad24-bmh1 intergenic region.
CONTIG5442	883577_c2_15	558	14661	375	125	P32643	218	4.7(10)-18	Saccharomyces cerevisiae	hypothetical 34.8 kd protein in rad24-bmh1 intergenic region.
CONTIG1671	24645437_f2_2	559	14662	462	154	P40098	164	2.5(10)-12	Saccharomyces cerevisiae	hypothetical 27.7 kd protein in isc10 3'region.
CONTIG4226	21907010_c2_10	560	14663	660	220	P40098	164	2.5(10)-12	Saccharomyces cerevisiae	hypothetical 27.7 kd protein in isc10 3'region.
CONTIG4923	24414193_c1_7	561	14664	975	325	P40098	252	1.2(10)-21	Saccharomyces cerevisiae	hypothetical 27.7 kd protein in isc10 3'region.
CONTIG237	12189437_f3_1	562	14665	420	140	P40006	92	0.00032	Saccharomyces cerevisiae	hypothetical 25.0 kd protein in wbp1-nmn1 intergenic region precursor.

CONTIG4491	12304650_c3_5	563	14666	483	161	P40006	106	8.5(10)-6	Saccharomyces cerevisiae	hypothetical 25.0 kd protein in wbp1-mm1 intergenic region precursor.
CONTIG4412	6694056_f3_2	564	14667	408	136	P40005	170	5.7(10)-13	Saccharomyces cerevisiae	hypothetical 14.3 kd protein in gen4-wbp1 intergenic region.
CONTIG4862	23525308_f2_3	565	14668	816	272	P40002	283	1.1(10)-28	Saccharomyces cerevisiae	hypothetical 72.5 kd protein in gen4-wbp1 intergenic region.
CONTIG1147	22445186_c2_5	566	14669	753	251	P39968	798	1.6(10)-79	Saccharomyces cerevisiae	hypothetical 64.0 kd protein in mm21-ubc8 intergenic region.
CONTIG3040	191556_c1_3	567	14670	864	288	P39998	183	1.3(10)-19	Saccharomyces cerevisiae	hypothetical 61.3 kd protein in mm21-ubc8 intergenic region.
CONTIG4603	24070302_f3_6	568	14671	1293	431	P39997	468	1.5(10)-44	Saccharomyces cerevisiae	hypothetical 57.4 kd protein in mm21-ubc8 intergenic region.
CONTIG5740	26344178_c2_19	569	14672	1242	414	P39992	370	7.0(10)-70	Saccharomyces cerevisiae	hypothetical 78.3 kd protein in rip1-ura3 intergenic region.
CONTIG5740	1259633_c1_14	570	14673	441	147	P39992	288	1.6(10)-24	Saccharomyces cerevisiae	hypothetical 78.3 kd protein in rip1-ura3 intergenic region.
CONTIG4276	4296937_c1_2	571	14674	1164	388	P39988	492	4.4(10)-47	Saccharomyces cerevisiae	hypothetical 35.6 kd protein in mcm3-vma3 intergenic region.
CONTIG2682	16509687_c1_5	572	14675	648	216	P32618	91	0.23	Saccharomyces cerevisiae	hypothetical 106.1 kd protein in gly1-gda1 intergenic region.
CONTIG248	32314768_f2_1	573	14676	258	86	P32617	232	1.6(10)-19	Saccharomyces cerevisiae	hypothetical 18.5 kd protein in gly1-gda1 intergenic region.
CONTIG5058	2520166_f2_2	574	14677	459	153	P32617	255	5.7(10)-22	Saccharomyces cerevisiae	hypothetical 18.5 kd protein in gly1-gda1 intergenic region.
CONTIG5797	21500125_f1_2	575	14678	1665	555	P32614	775	4.5(10)-77	Saccharomyces cerevisiae	hypothetical 50.8 kd protein in pau2-gly1 intergenic region.
CONTIG4125	24433500_c2_10	576	14679	1101	367	P39985	222	3.0(10)-20	Saccharomyces cerevisiae	hypothetical 115.9 kd protein in pcm1-rpl15b intergenic region.
CONTIG4125	23485912_c2_9	577	14680	735	245	P39985	118	0.00017	Saccharomyces cerevisiae	hypothetical 115.9 kd protein in pcm1-rpl15b intergenic region.
CONTIG4125	182912_c2_8	578	14681	951	317	P39985	194	1.3(10)-27	Saccharomyces cerevisiae	hypothetical 115.9 kd protein in pcm1-rpl15b intergenic region.

CONTIG2947	36224092_c1_7	579	14682	630	210	P39979	344	2.1(10)-31	Saccharomyces cerevisiae	hypothetical 20.7 kd protein in hxt8-can1 intergenic region.
CONTIG4619	24786376_f1_2	580	14683	966	322	P39975	99	4.7(10)-7	Saccharomyces cerevisiae	hypothetical 26.8 kd protein in hxt8 5' region.
CONTIG3418	10736090_c3_2	581	14684	540	180	P40007	342	3.3(10)-31	Saccharomyces cerevisiae	hypothetical 26.9 kd protein in mml1-pmi40 intergenic region.
CONTIG5678	10650812_c3_16	582	14685	750	250	P40011	550	3.1(10)-53	Saccharomyces cerevisiae	hypothetical 25.6 kd protein in mtf2-srp1 intergenic region.
CONTIG1606	21485925_f3_1	583	14686	759	253	P40015	412	1.3(10)-38	Saccharomyces cerevisiae	hypothetical 53.9 kd protein in afg3-seb2 intergenic region.
b9x13d54.x	2228442_f2_1	584	14687	552	184	P40015	534	1.5(10)-51	Saccharomyces cerevisiae	hypothetical 53.9 kd protein in afg3-seb2 intergenic region.
CONTIG1396	35162537_c2_3	585	14688	285	95	P40018	131	7.7(10)-9	Saccharomyces cerevisiae	hypothetical 22.4 kd protein in gal83-ypt8 intergenic region.
CONTIG3465	23945377_c3_4	586	14689	591	197	P40019	112	8.0(10)-7	Saccharomyces cerevisiae	hypothetical 18.3 kd protein in gal83-ypt8 intergenic region.
CONTIG1149	33790917_c3_2	587	14690	450	150	P25992	95	0.00129	Drosophila melanogaster	yemanuclin-alpha.
CONTIG3595	24645926_f3_3	588	14691	480	160	P25992	90	0.00459	Drosophila melanogaster	yemanuclin-alpha.
CONTIG5289	24804687_f1_1	589	14692	498	166	P40030	397	5.0(10)-37	Saccharomyces cerevisiae	hypothetical 17.1 kd protein in sah1-me14 intergenic region.
CONTIG4774	34663177_f3_3	590	14693	1446	482	P39955	115	0.002	Saccharomyces cerevisiae	hypothetical 100.3 kd protein in me14-caj1 intergenic region.
CONTIG2302	26460063_c3_9	591	14694	309	103	P40032	183	2.8(10)-13	Saccharomyces cerevisiae	hypothetical 74.0 kd protein in caj1-hom3 intergenic region.
CONTIG2302	9787682_c2_7	592	14695	1422	474	P40032	896	6.7(10)-90	Saccharomyces cerevisiae	hypothetical 74.0 kd protein in caj1-hom3 intergenic region.
CONTIG2013	35273405_c3_6	593	14696	888	296	P40034	211	5.2(10)-21	Saccharomyces cerevisiae	hypothetical 56.5 kd protein in caj1-hom3 intergenic region.
CONTIG4315	22478433_f2_4	594	14697	819	273	P40041	234	8.4(10)-24	Saccharomyces cerevisiae	hypothetical 56.6 kd protein in gep2-ic11 intergenic region.
CONTIG4019	15648937_f3_3	595	14698	288	96	P40046	171	4.5(10)-13	Saccharomyces cerevisiae	hypothetical 14.4 kd protein in mri1-ald3 intergenic region.

blx15658.x	24219818_c3_2	596	14699	564	188	P40050	145	3.7(10)-9	Saccharomyces cerevisiae	hypothetical 79.5 kd protein in rps24ea-1lv1 intergenic region.
CONTIG4767	24425938_c3_6	597	14700	633	211	P40053	487	1.5(10)-46	Saccharomyces cerevisiae	hypothetical 72.4 kd protein in rps24ea-1lv1 intergenic region.
CONTIG5081	10157813_f3_6	598	14701	630	210	P40053	199	5.2(10)-15	Saccharomyces cerevisiae	hypothetical 72.4 kd protein in rps24ea-1lv1 intergenic region.
CONTIG5805	917040_f3_19	599	14702	1632	544	P40055	1483	4.2(10)-152	Saccharomyces cerevisiae	hypothetical 62.3 kd protein in rps24ea-1lv1 intergenic region.
CONTIG5805	20484767_c3_45	600	14703	948	316	P40056	110	0.00069	Saccharomyces cerevisiae	hypothetical 33.9 kd protein in rps24ea-1lv1 intergenic region.
CONTIG4712	26343942_c1_5	601	14704	2478	826	P40061	443	3.2(10)-48	Saccharomyces cerevisiae	hypothetical 164.4 kd protein in met6-pup3 intergenic region.
CONTIG4758	23457193_c3_7	602	14705	915	305	P40071	617	2.5(10)-60	Saccharomyces cerevisiae	hypothetical 81.5 kd protein in uss1-beb1 intergenic region.
CONTIG5744	10571050_f1_6	603	14706	801	267	P40078	1127	2.2(10)-114	Saccharomyces cerevisiae	hypothetical 29.7 kd protein in rsp5-pak1 intergenic region.
b3x16061.y	33625061_f1_1	604	14707	300	100	P40078	310	8.4(10)-28	Saccharomyces cerevisiae	hypothetical 29.7 kd protein in rsp5-pak1 intergenic region.
CONTIG5744	36205142_c2_24	605	14708	1257	419	P40079	406	5.7(10)-38	Saccharomyces cerevisiae	hypothetical 40.8 kd protein in rsp5-pak1 intergenic region.
CONTIG1683	6662635_f3_1	606	14709	624	208	P40080	122	7.7(10)-11	Saccharomyces cerevisiae	hypothetical 23.5 kd protein in rsp5-pak1 intergenic region.
CONTIG197	6662635_c1_1	607	14710	375	125	P40080	126	2.6(10)-8	Saccharomyces cerevisiae	hypothetical 23.5 kd protein in rsp5-pak1 intergenic region.
CONTIG4059	19804043_c3_4	608	14711	1656	552	P32634	272	3.2(10)-35	Saccharomyces cerevisiae	hypothetical 195.4 kd protein in rps26b-glc7 intergenic region.
CONTIG5596	6125175_c3_29	609	14712	558	186	P40081	314	3.2(10)-28	Saccharomyces cerevisiae	hypothetical 20.4 kd protein in glc7-gdi1 intergenic region.
CONTIG4470	4022126_f2_1	610	14713	456	152	P40083	112	8.0(10)-7	Saccharomyces cerevisiae	hypothetical 16.6 kd protein in gdi1-cox15 intergenic region.
CONTIG5806	10752150_f2_10	611	14714	900	300	P40084	154	1.7(10)-14	Saccharomyces cerevisiae	hypothetical 26.2 kd protein in gdi1-cox15 intergenic region.
CONTIG5806	23878186_c3_42	612	14715	2064	688	P40085	615	2.3(10)-64	Saccharomyces cerevisiae	hypothetical 64.8 kd protein in gdi1-cox15 intergenic region.

CONTIG3542	6753888_g2_8	613	14716	243	81	P40087	146	1.3(10)-9	Saccharomyces cerevisiae	hypothetical 47.4 kd protein in mag1-ubp5 intergenic region.
CONTIG3193	30583281_f3_5	614	14717	657	219	P40088	586	4.7(10)-57	Saccharomyces cerevisiae	hypothetical 45.7 kd protein in ubp5-spt15 intergenic region.
CONTIG4266	783432_f3_3	615	14718	753	251	P40088	736	6.0(10)-73	Saccharomyces cerevisiae	hypothetical 45.7 kd protein in ubp5-spt15 intergenic region.
CONTIG4827	4803182_c1_9	616	14719	366	122	P40088	395	8.3(10)-37	Saccharomyces cerevisiae	hypothetical 45.7 kd protein in ubp5-spt15 intergenic region.
CONTIG5193	22461088_c1_5	617	14720	213	71	P40088	94	0.00054	Saccharomyces cerevisiae	hypothetical 45.7 kd protein in ubp5-spt15 intergenic region.
CONTIG4547	9975078_f1_1	618	14721	1170	390	P10356	885	9.9(10)-89	Saccharomyces cerevisiae	hypothetical 49.5 kd protein in ubp3-pet122 intergenic region.
CONTIG579	10312507_f3_1	619	14722	867	289	P10356	596	4.2(10)-58	Saccharomyces cerevisiae	hypothetical 49.5 kd protein in ubp3-pet122 intergenic region.
CONTIG1031	203790_f3_2	620	14723	210	70	P40093	208	9.0(10)-17	Saccharomyces cerevisiae	hypothetical 38.2 kd protein in bem2-spt2 intergenic region.
CONTIG1657	20503405_c1_2	621	14724	1113	371	P40094	365	1.3(10)-39	Saccharomyces cerevisiae	hypothetical 92.5 kd protein in bem2-spt2 intergenic region.
CONTIG3413	24647192_f1_1	622	14725	534	178	P43585	380	3.0(10)-34	Saccharomyces cerevisiae	hypothetical 95.4 kd protein in sec4-msh4 intergenic region.
CONTIG2625	2944467_c1_4	623	14726	1059	353	P43584	345	1.6(10)-31	Saccharomyces cerevisiae	hypothetical 28.8 kd protein in smc1-sec4 intergenic region.
CONTIG4411	3207837_c1_8	624	14727	534	178	P43583	200	1.8(10)-14	Saccharomyces cerevisiae	hypothetical 207.6 kd protein in smc1-sec4 intergenic region.
CONTIG4411	25598900_c1_7	625	14728	2469	823	P43583	689	2.1(10)-86	Saccharomyces cerevisiae	hypothetical 207.6 kd protein in smc1-sec4 intergenic region.
CONTIG4411	1458318_c1_6	626	14729	777	259	P43583	253	4.0(10)-20	Saccharomyces cerevisiae	hypothetical 207.6 kd protein in smc1-sec4 intergenic region.
CONTIG737	10242915_f3_2	627	14730	1230	410	P43583	336	6.0(10)-29	Saccharomyces cerevisiae	hypothetical 78.8 kd protein in hsp12-hxt10 intergenic region.
CONTIG5119	34412805_c1_5	628	14731	1074	358	P43579	239	1.8(10)-26	Saccharomyces cerevisiae	hypothetical 18.1 kd protein in snp2-mdj1 intergenic region.
CONTIG4849	32134430_f2_3	629	14732	468	156	P43577	320	7.2(10)-29	Saccharomyces cerevisiae	hypothetical 18.1 kd protein in snp2-mdj1 intergenic region.

CONTIG5773	16829826_c2_29	630	14733	2268	756	P43572	307	1.2(10)-44	Saccharomyces cerevisiae	hypothetical 96.7 kd protein in ste2-frs2 intergenic region.
CONTIG1740	6728457_c3_5	631	14734	888	296	P43570	113	0.00042	Saccharomyces cerevisiae	hypothetical 57.6 kd protein in cak1-ste2 intergenic region.
CONTIG3935	31484410_c3_9	632	14735	1071	357	P43570	113	3.2(10)-5	Saccharomyces cerevisiae	hypothetical 57.6 kd protein in cak1-ste2 intergenic region.
CONTIG5007	2117067_f2_1	633	14736	2271	757	P43564	1132	1.5(10)-136	Saccharomyces cerevisiae	hypothetical 119.5 kd protein in rp041-hac1 intergenic region.
CONTIG3136	87801_f2_2	634	14737	945	315	P43563	762	1.1(10)-75	Saccharomyces cerevisiae	hypothetical 30.1 kd protein in rp041-hac1 intergenic region.
CONTIG3527	14629387_c1_5	635	14738	1014	338	P43558	423	8.9(10)-40	Saccharomyces cerevisiae	hypothetical 33.5 kd protein in sec53-act1 intergenic region.
CONTIG4698	9774142_c3_6	636	14739	495	165	P43557	431	1.3(10)-40	Saccharomyces cerevisiae	hypothetical 24.0 kd protein in emp47-sec53 intergenic region.
CONTIG4417	31490962_c1_7	637	14740	1812	604	P43556	156	8.1(10)-8	Saccharomyces cerevisiae	hypothetical 82.2 kd protein in emp47-sec53 intergenic region.
CONTIG5679	24410411_c3_21	638	14741	2727	909	P43556	1002	3.5(10)-113	Saccharomyces cerevisiae	hypothetical 82.2 kd protein in emp47-sec53 intergenic region.
CONTIG5734	4331313_c3_20	639	14742	699	233	P43543	648	1.3(10)-63	Saccharomyces cerevisiae	hypothetical 25.2 kd protein in thi5 5'region and in rp043 5'region.
CONTIG5811	19531250_c2_33	640	14743	279	93	P43586	91	0.00033	Saccharomyces cerevisiae	hypothetical 23.6 kd protein in deg1-nic96 intergenic region.
CONTIG5811	36136312_c3_39	641	14744	210	70	P43586	185	1.5(10)-14	Saccharomyces cerevisiae	hypothetical 23.6 kd protein in deg1-nic96 intergenic region.
CONTIG5104	4953287_c1_7	642	14745	384	128	P43587	145	2.6(10)-10	Saccharomyces cerevisiae	hypothetical 18.2 kd protein in nic96-mpr1 intergenic region.
CONTIG3151	10938578_c2_5	643	14746	504	168	P43597	277	6.7(10)-23	Saccharomyces cerevisiae	hypothetical 137.7 kd protein in ugs1-fab1 intergenic region.
CONTIG5105	23437500_c3_16	644	14747	2706	902	P43597	277	1.6(10)-20	Saccharomyces cerevisiae	hypothetical 137.7 kd protein in ugs1-fab1 intergenic region.
CONTIG4942	34098376_c1_18	645	14748	1362	454	P43601	310	4.0(10)-26	Saccharomyces cerevisiae	hypothetical 55.1 kd protein in fab1-pea4 intergenic region.
CONTIG5385	6663901_c3_13	646	14749	1137	379	P43601	332	4.0(10)-52	Saccharomyces cerevisiae	hypothetical 55.1 kd protein in fab1-pea4 intergenic region.

CONTIG5385	3162756_c1_10	647	14750	492	164	P43601	326	3.0(10)-29	Saccharomyces cerevisiae	hypothetical 55.1 kd protein in fab1-pe54 intergenic region.
CONTIG4937	4876638_f2_2	648	14751	792	264	P43605	319	9.4(10)-29	Saccharomyces cerevisiae	hypothetical 31.8 kd protein in his2-cdc14 intergenic region.
CONTIG5120	4876635_f2_2	649	14752	792	264	P43605	321	5.7(10)-29	Saccharomyces cerevisiae	hypothetical 31.8 kd protein in his2-cdc14 intergenic region.
CONTIG5749	1457775_c2_20	650	14753	2367	789	P43606	282	2.2(10)-40	Saccharomyces cerevisiae	hypothetical 76.3 kd protein in cdc14-met10 intergenic region.
CONTIG3584	5355206_c1_5	651	14754	867	289	P43607	146	8.5(10)-14	Saccharomyces cerevisiae	hypothetical 31.9 kd protein in rpl5b-qcr6 intergenic region.
CONTIG4260	21602157_f3_3	652	14755	1479	493	P43616	1705	1.3(10)-175	Saccharomyces cerevisiae	hypothetical 52.9 kd protein in sap155-ym31 intergenic region.
CONTIG2711	33486292_f1_1	653	14756	504	168	P43620	104	8.9(10)-5	Saccharomyces cerevisiae	hypothetical 75.9 kd protein in sap155-ym31 intergenic region.
b9x13e61.x	601375_c1_2	654	14757	366	122	P43620	246	5.0(10)-20	Saccharomyces cerevisiae	hypothetical 75.9 kd protein in sap155-ym31 intergenic region.
CONTIG5393	3906630_f1_4	655	14758	693	231	P53200	272	9.0(10)-24	Saccharomyces cerevisiae	hypothetical 22.2 kd protein in pmc1-tfg2 intergenic region.
b9x10b27.y	3129561_c1_3	656	14759	309	103	P53201	139	9.5(10)-9	Saccharomyces cerevisiae	hypothetical 55.2 kd protein in pmc1-tfg2 intergenic region.
CONTIG5688	878137_f3_11	657	14760	267	89	P53203	103	7.0(10)-5	Saccharomyces cerevisiae	hypothetical 52.9 kd protein in pmc1-tfg2 intergenic region.
CONTIG1105	35807791_f1_1	658	14761	984	328	P53207	148	1.3(10)-7	Saccharomyces cerevisiae	hypothetical 71.4 kd protein in sec9-msb2 intergenic region.
CONTIG4835	390687_f1_1	659	14762	570	190	P53210	162	9.4(10)-12	Saccharomyces cerevisiae	hypothetical 34.7 kd protein in msb2-uga1 intergenic region.
CONTIG3627	13093786_c1_6	660	14763	1188	396	P53214	104	0.014	Saccharomyces cerevisiae	hypothetical 57.5 kd protein in vma7-rps31a intergenic region.
CONTIG2939	22443767_c2_7	661	14764	879	293	P53215	646	2.1(10)-63	Saccharomyces cerevisiae	hypothetical 27.8 kd protein in vma7-rps31a intergenic region.
CONTIG2811	9853430_f2_1	662	14765	792	264	P53217	172	4.7(10)-13	Saccharomyces cerevisiae	hypothetical 33.3 kd protein in vma7-rps31a intergenic region.
CONTIG4609	24251567_c3_19	663	14766	408	136	P53219	268	2.3(10)-23	Saccharomyces cerevisiae	hypothetical 38.5 kd protein in erv1-gls2 intergenic region.

CONTIG3168	784761_c2_3	664	14767	495	165	P53220	207	6.9(10)-17	Saccharomyces cerevisiae	hypothetical 27.2 kd protein in gls2-rp126b intergenic region.
CONTIG1693	21644025_f3_2	665	14768	747	249	P53223	280	1.3(10)-24	Saccharomyces cerevisiae	hypothetical 27.6 kd protein in rp126b-acb1 intergenic region.
b3x19755.y	14881550_c3_2	666	14769	672	224	P53224	365	1.2(10)-33	Saccharomyces cerevisiae	hypothetical 25.2 kd protein in acb1-kss1 intergenic region.
CONTIG3063	26204932_c1_4	667	14770	900	300	P53230	253	1.2(10)-21	Saccharomyces cerevisiae	hypothetical 44.2 kd protein in rme1-ffc4 intergenic region.
CONTIG4403	6817152_c3_18	668	14771	1443	481	P53235	664	9.6(10)-82	Saccharomyces cerevisiae	hypothetical 71.3 kd protein in scm4-mup1 intergenic region.
CONTIG3899	25439825_c3_11	669	14772	1134	378	P53236	414	8.8(10)-38	Saccharomyces cerevisiae	hypothetical 106.7 kd protein in mup1-spr3 intergenic region.
CONTIG3899	25478382_c1_6	670	14773	1281	427	P53236	650	1.1(10)-63	Saccharomyces cerevisiae	hypothetical 106.7 kd protein in mup1-spr3 intergenic region.
CONTIG3812	14882056_c1_5	671	14774	819	273	P53237	127	9.9(10)-14	Saccharomyces cerevisiae	hypothetical 28.6 kd protein in mup1-spr3 intergenic region.
CONTIG2127	11836180_c3_8	672	14775	1038	346	P53252	948	2.1(10)-95	Saccharomyces cerevisiae	hypothetical 38.3 kd protein in rp116b-pdc6 intergenic region.
CONTIG5575	4328376_c1_12	673	14776	936	312	P53252	1038	6.0(10)-105	Saccharomyces cerevisiae	hypothetical 38.3 kd protein in rp116b-pdc6 intergenic region.
CONTIG1333	24353387_f1_1	674	14777	528	176	P53254	181	1.2(10)-12	Saccharomyces cerevisiae	hypothetical 140.5 kd protein in ctt1-prp31 intergenic region.
CONTIG4138	24407561_f3_2	675	14778	1086	362	P53254	657	1.5(10)-63	Saccharomyces cerevisiae	hypothetical 140.5 kd protein in ctt1-prp31 intergenic region.
CONTIG4138	34550010_f2_1	676	14779	1737	579	P53254	1120	3.3(10)-145	Saccharomyces cerevisiae	hypothetical 140.5 kd protein in ctt1-prp31 intergenic region.
CONTIG5586	12673377_f3_13	677	14780	1509	503	P53255	681	4.0(10)-67	Saccharomyces cerevisiae	hypothetical 58.2 kd protein in dbf2-vas1 intergenic region.
b1x18864.x	11020455_f3_1	678	14781	414	138	P53256	136	4.9(10)-9	Saccharomyces cerevisiae	hypothetical 28.3 kd protein in vas1-ask10 intergenic region.
CONTIG5811	11728431_f3_14	679	14782	987	329	P53259	443	6.7(10)-42	Saccharomyces cerevisiae	hypothetical 38.8 kd protein in mic1-srb5 intergenic region.
CONTIG5789	10744037_f2_9	680	14783	501	167	P53260	123	5.5(10)-8	Saccharomyces cerevisiae	hypothetical 20.8 kd protein in mic1-srb5 intergenic region.

CONTIG5789	29319426_f3_14	681	14784	1737	579	P53261	970	7.0(10)-145	Saccharomyces cerevisiae	hypothetical 69.9 kd protein in mcl-srb5 intergenic region.
CONTIG1910	1196902_c3_6	682	14785	900	300	P53264	303	4.7(10)-27	Saccharomyces cerevisiae	hypothetical 52.0 kd protein in clb6-spt6 intergenic region.
CONTIG3957	24501663_c1_5	683	14786	1203	401	P53264	235	8.0(10)-38	Saccharomyces cerevisiae	hypothetical 52.0 kd protein in clb6-spt6 intergenic region.
CONTIG5726	25553192_f1_3	684	14787	1416	472	P53264	627	2.2(10)-61	Saccharomyces cerevisiae	hypothetical 52.0 kd protein in clb6-spt6 intergenic region.
b9x12862.x	14163125_c2_3	685	14788	519	173	P53265	113	1.3(10)-11	Saccharomyces cerevisiae	hypothetical 46.7 kd protein in clb6-spt6 intergenic region.
CONTIG5805	1382056_f1_1	686	14789	777	259	P53266	456	2.7(10)-43	Saccharomyces cerevisiae	hypothetical 45.1 kd protein in clb6-spt6 intergenic region.
CONTIG3478	12117316_f1_1	687	14790	813	271	P53271	96	0.01499	Saccharomyces cerevisiae	hypothetical 31.8 kd protein in nup57-mep1 intergenic region.
CONTIG1322	25992067_c1_3	688	14791	843	281	P53273	368	9.6(10)-33	Saccharomyces cerevisiae	hypothetical 117.0 kd protein in asn2-phb1 intergenic region.
b9x11v18.x	433257_f1_1	689	14792	264	88	P53273	175	4.0(10)-12	Saccharomyces cerevisiae	hypothetical 117.0 kd protein in asn2-phb1 intergenic region.
b9x11v18.x	896883_f1_2	690	14793	402	134	P53273	387	8.9(10)-35	Saccharomyces cerevisiae	hypothetical 117.0 kd protein in asn2-phb1 intergenic region.
CONTIG4839	22460927_f1_2	691	14794	330	110	P53275	164	6.7(10)-12	Saccharomyces cerevisiae	hypothetical 35.7 kd protein in asn2-phb1 intergenic region.
CONTIG5498	26376953_f3_4	692	14795	552	184	P53275	155	6.7(10)-11	Saccharomyces cerevisiae	hypothetical 35.7 kd protein in asn2-phb1 intergenic region.
CONTIG5140	35798416_c3_11	693	14796	1431	477	P53276	236	9.6(10)-17	Saccharomyces cerevisiae	hypothetical 80.2 kd protein in asn2-phb1 intergenic region.
CONTIG4916	35197837_f3_4	694	14797	2475	825	P53280	322	3.2(10)-25	Saccharomyces cerevisiae	hypothetical 128.8 kd protein in pas2-prs5 intergenic region.
CONTIG3062	24746053_c1_4	695	14798	1245	415	P53285	839	7.4(10)-84	Saccharomyces cerevisiae	hypothetical 54.5 kd protein in obf2-skl1 intergenic region.
CONTIG4419	932_c1_7	696	14799	2271	757	P48234	1655	1.3(10)-196	Saccharomyces cerevisiae	hypothetical 81.7 kd protein in mol1-mat2 intergenic region.
CONTIG3140	19921961_c3_5	697	14800	342	114	P48236	180	2.7(10)-13	Saccharomyces cerevisiae	hypothetical 51.6 kd protein in rpl30b-rsr1 intergenic region.

CONTIG5415	4085330_c3_18	698	14801	741	247	P48236	453	5.9(10)-43	Saccharomyces cerevisiae	hypothetical 51.6 kd protein in rpl30b-rsr1 intergenic region.
CONTIG4736	26589027_f3_5	699	14802	1737	579	P48237	155	3.2(10)-17	Saccharomyces cerevisiae	hypothetical 101.4 kd protein in rpl30b-rsr1 intergenic region.
CONTIG1495	4020005_f1_1	700	14803	681	227	P53289	114	1.6(10)-6	Saccharomyces cerevisiae	hypothetical 29.3 kd protein in nsr1-tif631 intergenic region.
CONTIG4106	24031312_c2_8	701	14804	1152	384	P53290	982	8.5(10)-106	Saccharomyces cerevisiae	hypothetical 38.6 kd protein in tif631-kre11 intergenic region.
CONTIG2374	3938811_f2_1	702	14805	516	172	P53292	199	1.1(10)-15	Saccharomyces cerevisiae	hypothetical 39.6 kd protein in tif631-kre11 intergenic region.
CONTIG2163	24020392_c3_13	703	14806	645	215	P53297	263	6.5(10)-32	Saccharomyces cerevisiae	hypothetical 78.8 kd protein in erg1-mr4 intergenic region.
CONTIG5528	19648387_c3_16	704	14807	1581	527	P53301	626	2.7(10)-61	Saccharomyces cerevisiae	hypothetical 52.8 kd protein in bub1-hi1 intergenic region.
CONTIG5731	14270312_c1_17	705	14808	1389	463	P53301	861	3.3(10)-86	Saccharomyces cerevisiae	hypothetical 52.8 kd protein in bub1-hi1 intergenic region.
CONTIG4320	20742136_c1_7	706	14809	1176	392	P42826	676	1.3(10)-66	Saccharomyces cerevisiae	hypothetical 68.3 kd protein in pdx1-sng1 intergenic region.
CONTIG4562	9796938_f2_1	707	14810	645	215	P42826	211	2.3(10)-16	Saccharomyces cerevisiae	hypothetical 68.3 kd protein in pdx1-sng1 intergenic region.
CONTIG1773	23647503_c1_2	708	14811	1059	353	P46951	141	1.6(10)-6	Saccharomyces cerevisiae	hypothetical 95.4 kd protein in sng1-pnt6 intergenic region.
CONTIG2260	21929700_c1_3	709	14812	897	299	P42935	646	2.1(10)-63	Saccharomyces cerevisiae	hypothetical trp-asp repeats containing protein in pnt6-pct1 intergenic region.
CONTIG4027	4787686_f3_5	710	14813	915	305	P42935	614	5.0(10)-60	Saccharomyces cerevisiae	hypothetical trp-asp repeats containing protein in pnt6-pct1 intergenic region.
b9x13p32.y	25586700_c2_3	711	14814	627	209	P42938	167	1.1(10)-18	Saccharomyces cerevisiae	hypothetical 33.3 kd protein in ade3-ser2 intergenic region.
CONTIG5354	54807_c3_10	712	14815	471	157	P42942	192	2.7(10)-26	Saccharomyces cerevisiae	hypothetical 45.2 kd gip-binding protein in trx1-rtal intergenic region.

CONTIG372	24006652_c2_3	713	14816	1035	345	P53303	934	6.2(10)-94	Saccharomyces cerevisiae	hypothetical 55.1 kd protein in trx1-rtal intergenic region.
CONTIG5241	14720402_f3_4	714	14817	327	109	P53305	149	9.6(10)-11	Saccharomyces cerevisiae	hypothetical 12.4 kd protein in nab1a-crm1 intergenic region.
CONTIG2537	195812_f1_1	715	14818	729	243	P50079	146	1.5(10)-9	Saccharomyces cerevisiae	hypothetical 51.2 kd protein in pe154-die2 intergenic region.
CONTIG2537	4900305_f3_5	716	14819	756	252	P50079	256	1.3(10)-21	Saccharomyces cerevisiae	hypothetical 51.2 kd protein in pe154-die2 intergenic region.
CONTIG5563	14240928_f2_7	717	14820	453	151	P50086	207	6.9(10)-17	Saccharomyces cerevisiae	hypothetical 25.6 kd protein in sm11-pho81 intergenic region.
CONTIG4370	1427005_f2_3	718	14821	444	148	P50087	92	0.00479	Saccharomyces cerevisiae	hypothetical 26.9 kd protein in yhb1-pfk1 intergenic region.
CONTIG658	14144410_c1_5	719	14822	639	213	P50087	124	2.8(10)-6	Saccharomyces cerevisiae	hypothetical 26.9 kd protein in yhb1-pfk1 intergenic region.
CONTIG3329	13797751_c3_6	720	14823	639	213	P50089	122	4.0(10)-5	Saccharomyces cerevisiae	hypothetical 89.2 kd protein in yhb1-pfk1 intergenic region.
CONTIG4481	2087750_f3_7	721	14824	1971	657	P50090	800	1.0(10)-79	Saccharomyces cerevisiae	hypothetical 100.0 kd protein in yhb1-pfk1 intergenic region.
CONTIG2919	2376505_c1_7	722	14825	534	178	P53313	345	4.2(10)-41	Saccharomyces cerevisiae	hypothetical 86.6 kd protein in pfk1-tds4 intergenic region.
CONTIG4371	4079643_f1_1	723	14826	651	217	P53313	486	6.0(10)-46	Saccharomyces cerevisiae	hypothetical 86.6 kd protein in pfk1-tds4 intergenic region.
b3x16281.x	31910000_f1_1	724	14827	774	258	P53313	920	1.8(10)-92	Saccharomyces cerevisiae	hypothetical 86.6 kd protein in pfk1-tds4 intergenic region.
CONTIG5580	6146938_f2_4	725	14828	744	248	P53314	166	1.5(10)-24	Saccharomyces cerevisiae	hypothetical 26.7 kd protein in tds4-mgal intergenic region.
CONTIG3849	19703452_c3_13	726	14829	498	166	P53317	100	2.7(10)-5	Saccharomyces cerevisiae	hypothetical 22.3 kd protein in mgal-rgn4 intergenic region.
CONTIG4091	25797125_c1_6	727	14830	1104	368	P53320	620	1.2(10)-60	Saccharomyces cerevisiae	putative mitochondrial carrier ygr257c.
CONTIG1658	29304217_c3_5	728	14831	654	218	P53324	95	0.039	Saccharomyces cerevisiae	hypothetical 48.5 kd protein in apl6-mes1 intergenic region.
CONTIG2484	3907500_f2_1	729	14832	1122	374	P53324	123	6.7(10)-5	Saccharomyces cerevisiae	hypothetical 48.5 kd protein in apl6-mes1 intergenic region.

CONTIG3380	21760000_c1_4	730	14833	1152	384	P53324	190	2.3(10)-12	Saccharomyces cerevisiae	hypothetical 48.5 kd protein in apl6-mes1 intergenic region.
CONTIG4490	23472215_f3_3	731	14834	1287	429	P53324	181	3.7(10)-11	Saccharomyces cerevisiae	hypothetical 48.5 kd protein in apl6-mes1 intergenic region.
CONTIG5554	9806587_f1_4	732	14835	1254	418	P53324	180	4.4(10)-11	Saccharomyces cerevisiae	hypothetical 48.5 kd protein in apl6-mes1 intergenic region.
CONTIG5727	6040627_f2_6	733	14836	1071	357	P53324	177	6.7(10)-11	Saccharomyces cerevisiae	hypothetical 48.5 kd protein in apl6-mes1 intergenic region.
CONTIG2072	4296877_f2_3	734	14837	963	321	P53326	509	6.9(10)-49	Saccharomyces cerevisiae	hypothetical 81.2 kd protein in mes1-foi2 intergenic region.
CONTIG3749	5119828_f1_1	735	14838	654	218	P53326	318	9.5(10)-28	Saccharomyces cerevisiae	hypothetical 81.2 kd protein in mes1-foi2 intergenic region.
CONTIG3849	4100692_f1_1	736	14839	396	132	P40325	109	2.5(10)-6	Saccharomyces cerevisiae	hypothetical 22.4 kd protein in foi2-ya7 intergenic region.
CONTIG1015	16414137_f2_1	737	14840	867	289	P53327	601	4.2(10)-57	Saccharomyces cerevisiae	hypothetical 22.4 kd protein in ya7-taf145 intergenic region.
CONTIG1720	10725802_f2_1	738	14841	1008	336	P53327	1356	4.5(10)-138	Saccharomyces cerevisiae	hypothetical 22.4 kd protein in ya7-taf145 intergenic region.
CONTIG2182	4000876_f3_1	739	14842	810	270	P53327	389	1.5(10)-34	Saccharomyces cerevisiae	hypothetical 22.4 kd protein in ya7-taf145 intergenic region.
CONTIG4896	35187912_c1_7	740	14843	2811	937	P53327	3340	0	Saccharomyces cerevisiae	hypothetical 22.4 kd protein in ya7-taf145 intergenic region.
CONTIG3655	12922150_f3_3	741	14844	237	79	P53328	102	9.3(10)-6	Saccharomyces cerevisiae	hypothetical 17.9 kd protein in ya7-taf145 intergenic region.
CONTIG3655	912553_f3_4	742	14845	477	159	P53328	168	9.4(10)-13	Saccharomyces cerevisiae	hypothetical 17.9 kd protein in ya7-taf145 intergenic region.
CONTIG4340	15042160_f1_2	743	14846	1341	447	P53331	358	1.3(10)-32	Saccharomyces cerevisiae	hypothetical 62.8 kd protein in taf145-yor1 intergenic region.
CONTIG5048	9859381_f3_4	744	14847	1005	335	P53332	366	9.8(10)-34	Saccharomyces cerevisiae	hypothetical 34.3 kd protein in taf145-yor1 intergenic region.
CONTIG4274	31672540_f1_1	745	14848	1236	412	P53334	653	3.7(10)-64	Saccharomyces cerevisiae	hypothetical 40.2 kd protein in taf145-yor1 intergenic region.
CONTIG5393	35192158_c3_20	746	14849	189	63	P53335	178	8.1(10)-14	Saccharomyces cerevisiae	hypothetical 31.3 kd protein in taf145-yor1 intergenic region.

CONTIG3351	20320250_f2_2	747	14850	948	316	P53337	505	1.8(10)-48	Saccharomyces cerevisiae	hypothetical 35.0 kd protein in bgl2-zuo1 intergenic region.
CONTIG5245	22437652_f2_6	748	14851	702	234	P53193	191	3.3(10)-15	Saccharomyces cerevisiae	hypothetical 21.8 kd protein in ckb1-ate1 intergenic region.
CONTIG5245	30272885_f1_5	749	14852	375	125	P53192	119	3.2(10)-7	Saccharomyces cerevisiae	hypothetical 27.1 kd protein in alk1-ckb1 intergenic region.
CONTIG1957	22437936_c1_3	750	14853	993	331	P53189	725	8.9(10)-72	Saccharomyces cerevisiae	hypothetical 56.4 kd protein in rpl32-cwh41 intergenic region precursor.
CONTIG5688	1366302_f2_8	751	14854	534	178	P53188	154	2.8(10)-11	Saccharomyces cerevisiae	hypothetical 14.4 kd protein in rpl32-cwh41 intergenic region.
CONTIG5795	2831532_c1_32	752	14855	1881	627	P53179	221	1.7(10)-17	Saccharomyces cerevisiae	hypothetical 29.4 kd protein in sug1-mal5 intergenic region.
CONTIG4495	9859830_f2_1	753	14856	861	287	P53177	517	9.8(10)-50	Saccharomyces cerevisiae	hypothetical 30.8 kd protein in ole1-tif4632 intergenic region.
CONTIG4395	23626552_f2_4	754	14857	411	137	P53173	429	2.1(10)-40	Saccharomyces cerevisiae	hypothetical 15.9 kd protein in ole1-tif4632 intergenic region.
CONTIG4558	29306687_c1_8	755	14858	714	238	P53169	97	0.04399	Saccharomyces cerevisiae	hypothetical 73.1 kd protein in pyc1-ubc2 intergenic region.
CONTIG5171	12753942_c3_12	756	14859	1521	507	P53165	217	2.2(10)-26	Saccharomyces cerevisiae	hypothetical 72.9 kd protein in rpb9-alg2 intergenic region.
CONTIG1209	23605012_c3_1	757	14860	537	179	P53164	160	3.2(10)-11	Saccharomyces cerevisiae	hypothetical 43.5 kd protein in rpb9-alg2 intergenic region.
CONTIG2381	24067761_f2_3	758	14861	318	106	P53164	101	8.8(10)-5	Saccharomyces cerevisiae	hypothetical 43.5 kd protein in rpb9-alg2 intergenic region.
CONTIG4883	35802_f2_3	759	14862	495	165	P53157	357	8.8(10)-33	Saccharomyces cerevisiae	hypothetical 15.0 kd protein in scy1-hnm1 intergenic region.
CONTIG4386	9971000_c3_8	760	14863	1230	410	P53154	1188	7.7(10)-121	Saccharomyces cerevisiae	hypothetical 65.3 kd protein in mad1-scy1 intergenic region.
CONTIG4386	19728427_c3_7	761	14864	606	202	P53154	310	3.5(10)-27	Saccharomyces cerevisiae	hypothetical 65.3 kd protein in mad1-scy1 intergenic region.
CONTIG1247	23941552_c2_3	762	14865	741	247	P53153	366	9.8(10)-34	Saccharomyces cerevisiae	hypothetical 32.1 kd protein in mad1-scy1 intergenic region.

CONTIG4360	5104135_f2_1	763	14866	1911	637	P53148	285	1.1(10)-21	Saccharomyces cerevisiae	hypothetical 104.8 kd protein in pan2-nup145 intergenic region.
CONTIG4954	4020162_f3_7	764	14867	2064	688	P53145	1597	1.1(10)-178	Saccharomyces cerevisiae	hypothetical gip-binding protein in seh1-prp20 intergenic region.
CONTIG4126	24882202_f1_3	765	14868	897	299	P43343	90	0.033	Serratia marcescens	hypothetical 17.8 kd protein in rpod 3'region.
CONTIG4478	2814032_f2_2	766	14869	705	235	P53144	352	3.0(10)-32	Saccharomyces cerevisiae	hypothetical 25.3 kd protein in cyh2-seh1 intergenic region.
CONTIG4787	24642158_c3_12	767	14870	1371	457	P53137	312	3.1(10)-45	Saccharomyces cerevisiae	hypothetical 72.0 kd protein in taf60-g4p1 intergenic region.
CONTIG5761	6837777_f3_14	768	14871	1224	408	P53136	192	3.8(10)-20	Saccharomyces cerevisiae	hypothetical 51.9 kd protein in taf60-g4p1 intergenic region.
CONTIG4476	4775285_c1_8	769	14872	1197	399	P53135	93	0.28	Saccharomyces cerevisiae	hypothetical 77.3 kd protein in snf4-taf60 intergenic region.
CONTIG2551	16422132_f1_1	770	14873	1365	455	P53134	645	2.7(10)-63	Saccharomyces cerevisiae	hypothetical 80.0 kd protein in snf4-taf60 intergenic region.
blx18334.y	35277300_c3_2	771	14874	348	116	P53134	280	1.3(10)-23	Saccharomyces cerevisiae	hypothetical 80.0 kd protein in snf4-taf60 intergenic region.
CONTIG5294	4453436_c2_11	772	14875	1929	643	P53129	411	1.3(10)-36	Saccharomyces cerevisiae	hypothetical 73.5 kd protein in sec3-sup44 intergenic region.
CONTIG3383	21909427_f2_1	773	14876	1059	353	Q01163	242	6.4(10)-20	Saccharomyces cerevisiae	hypothetical 55.6 kd protein in cegl-soh1 intergenic region.
CONTIG4824	2386468_f2_3	774	14877	816	272	P53127	327	3.7(10)-28	Saccharomyces cerevisiae	hypothetical 163.2 kd protein in ssm1b-cegl1 intergenic region.
CONTIG4824	12343933_f3_6	775	14878	1500	500	P53127	246	1.6(10)-25	Saccharomyces cerevisiae	hypothetical 163.2 kd protein in ssm1b-cegl1 intergenic region.
CONTIG5110	10945140_c3_10	776	14879	849	283	P53127	179	8.9(10)-11	Saccharomyces cerevisiae	hypothetical 163.2 kd protein in ssm1b-cegl1 intergenic region.
CONTIG5110	21516391_c2_9	777	14880	243	81	P53127	103	0.00027	Saccharomyces cerevisiae	hypothetical 163.2 kd protein in ssm1b-cegl1 intergenic region.
CONTIG2152	9980192_f2_1	778	14881	744	248	P53125	136	7.5(10)-8	Saccharomyces cerevisiae	hypothetical 145.6 kd protein in ssm1b-cegl1 intergenic region.
CONTIG4593	22548377_f3_2	779	14882	1182	394	P53123	169	2.7(10)-10	Saccharomyces cerevisiae	hypothetical 37.4 kd protein in sec27-ssm1b intergenic region.

CONTIG2011	782252_c3_3	780	14883	1044	348	P53121	957	2.2(10)-96	Saccharomyces cerevisiae	hypothetical 90.8 kd protein in mrf1-sec27 intergenic region.
CONTIG4571	24020176_c3_8	781	14884	387	129	P30777	136	3.0(10)-8	Saccharomyces cerevisiae	hypothetical 72.6 kd protein in mrf1-sec27 intergenic region.
CONTIG4571	23929025_c2_6	782	14885	219	73	P30777	105	6.2(10)-5	Saccharomyces cerevisiae	hypothetical 72.6 kd protein in mrf1-sec27 intergenic region.
CONTIG5602	26587777_f2_6	783	14886	2253	751	P53118	1220	3.1(10)-124	Saccharomyces cerevisiae	hypothetical 78.1 kd protein in tip20-mrf1 intergenic region.
CONTIG5768	10157032_f2_9	784	14887	1131	377	P53110	279	1.6(10)-24	Saccharomyces cerevisiae	hypothetical 41.6 kd protein in sut1-rck1 intergenic region.
CONTIG4642	985817_f3_5	785	14888	531	177	P53108	184	3.3(10)-14	Saccharomyces cerevisiae	hypothetical 34.8 kd protein in sut1-rck1 intergenic region.
b9x11g30.y	26375317_f2_1	786	14889	585	195	P53107	198	9.3(10)-26	Saccharomyces cerevisiae	hypothetical 50.3 kd protein in ace1-rad54 intergenic region.
CONTIG4768	10805312_c1_10	787	14890	2559	853	P53094	259	1.1(10)-34	Saccharomyces cerevisiae	hypothetical 167.1 kd protein in emp24-gen1 intergenic region.
CONTIG2954	36582072_c1_5	788	14891	699	233	P53088	535	3.0(10)-56	Saccharomyces cerevisiae	hypothetical 21.9 kd protein in vam7-ypt32 intergenic region.
CONTIG2816	15026907_c3_11	789	14892	798	266	P53078	507	1.1(10)-48	Saccharomyces cerevisiae	hypothetical 32.0 kd protein in gog5-clg1 intergenic region.
CONTIG5752	14948801_c2_19	790	14893	600	200	P53073	260	1.7(10)-22	Saccharomyces cerevisiae	hypothetical 21.5 kd protein in sec15-sap4 intergenic region.
CONTIG5752	4375000_f3_10	791	14894	864	288	P53072	447	2.6(10)-42	Saccharomyces cerevisiae	hypothetical 33.6 kd protein in sec15-sap4 intergenic region.
CONTIG4535	5109703_f2_2	792	14895	303	101	P53070	112	1.3(10)-5	Saccharomyces cerevisiae	hypothetical 75.4 kd protein in hap2-ade5,6 intergenic region.
CONTIG5017	25985663_c1_5	793	14896	231	77	P53067	151	1.3(10)-9	Saccharomyces cerevisiae	hypothetical 113.9 kd protein in pdel-cse1 intergenic region.
CONTIG5402	14179201_f2_3	794	14897	708	236	P53067	318	2.1(10)-27	Saccharomyces cerevisiae	hypothetical 113.9 kd protein in pdel-cse1 intergenic region.
CONTIG5402	12320142_f1_2	795	14898	2028	676	P53067	574	6.5(10)-65	Saccharomyces cerevisiae	hypothetical 113.9 kd protein in pdel-cse1 intergenic region.
CONTIG4913	81891_f2_2	796	14899	627	209	P53066	412	1.3(10)-38	Saccharomyces cerevisiae	hypothetical 20.1 kd protein in pdel-cse1 intergenic region.

CONTIG4301	29323575_f3_8	797	14900	573	191	P53065	237	1.1(10)-19	Saccharomyces cerevisiae	hypothetical 45.9 kd protein in pde1-ese1 intergenic region.
CONTIG1060	4064135_f1_1	798	14901	699	233	P53063	481	6.4(10)-46	Saccharomyces cerevisiae	hypothetical 44.5 kd protein in pde1-ese1 intergenic region.
CONTIG4790	13876625_c2_11	799	14902	1026	342	P53063	164	1.5(10)-9	Saccharomyces cerevisiae	hypothetical 44.5 kd protein in pde1-ese1 intergenic region.
CONTIG4126	5114032_c2_10	800	14903	933	311	P53062	186	1.2(10)-14	Saccharomyces cerevisiae	hypothetical 22.8 kd protein in pde1-ese1 intergenic region.
CONTIG5815	2063950_f1_7	801	14904	1224	408	P38887	890	2.8(10)-89	Saccharomyces cerevisiae	hypothetical 69.0 kd protein in ppx1-rps7a intergenic region.
CONTIG5815	24300062_f2_16	802	14905	588	196	P38887	180	5.4(10)-13	Saccharomyces cerevisiae	hypothetical 69.0 kd protein in ppx1-rps7a intergenic region.
CONTIG5154	24226087_c1_11	803	14906	612	204	P38890	251	8.3(10)-21	Saccharomyces cerevisiae	hypothetical 60.5 kd protein in skn7-twt1 intergenic region.
CONTIG5442	4102137_c2_14	804	14907	555	185	P38892	319	9.4(10)-29	Saccharomyces cerevisiae	hypothetical 33.8 kd protein in twt1-pho12 intergenic region.
b1x19728.x	36335306_f1_1	805	14908	618	206	P38892	108	0.00042	Saccharomyces cerevisiae	hypothetical 33.8 kd protein in twt1-pho12 intergenic region.
b3x14382.x	23831557_f3_1	806	14909	411	137	P35649	177	1.1(10)-12	Eikenella corrodens	hypothetical 66.3 kd protein in hag2 5'region.
CONTIG3285	23703430_f1_2	807	14910	1158	386	P38753	657	1.3(10)-64	Saccharomyces cerevisiae	hypothetical 51.2 kd protein in lag1-rpl14b intergenic region.
CONTIG3035	23472677_f2_2	808	14911	1215	405	P38749	215	6.5(10)-16	Saccharomyces cerevisiae	hypothetical 38.0 kd protein in prps4-sie20 intergenic region.
CONTIG5394	1347212_f1_2	809	14912	1248	416	P38749	215	8.0(10)-16	Saccharomyces cerevisiae	hypothetical 38.0 kd protein in prps4-sie20 intergenic region.
CONTIG5817	24792087_c2_51	810	14913	1479	493	P38748	385	3.8(10)-66	Saccharomyces cerevisiae	hypothetical 67.5 kd protein in prps4-sie20 intergenic region.
CONTIG5817	3938825_c3_61	811	14914	354	118	P38748	122	8.8(10)-7	Saccharomyces cerevisiae	hypothetical 67.5 kd protein in prps4-sie20 intergenic region.
CONTIG4867	33594062_f1_3	812	14915	1023	341	P38747	491	5.5(10)-47	Saccharomyces cerevisiae	hypothetical 36.1 kd protein in ylt2-prps4 intergenic region.
CONTIG2148	5895657_c3_8	813	14916	789	263	P23180	216	4.0(10)-17	Saccharomyces cerevisiae	hypothetical 53.1 kd protein in spo11-opi1 intergenic region.

CONTIG5234	6829777_c3_19	814	14917	1260	420	P38742	163	2.5(10)-22	Saccharomyces cerevisiae	hypothetical 130.0 kd protein in snf6-spo11 intergenic region.
CONTIG5598	15630010_f3_13	815	14918	1707	569	P38741	420	8.0(10)-39	Saccharomyces cerevisiae	hypothetical 80.1 kd protein in snf6-spo11 intergenic region.
CONTIG5079	29487677_c3_9	816	14919	1119	373	P38738	171	4.7(10)-21	Saccharomyces cerevisiae	hypothetical 77.8 kd protein in gut1-rim1 intergenic region.
CONTIG5683	210937_f1_6	817	14920	1119	373	P38738	146	3.0(10)-15	Saccharomyces cerevisiae	hypothetical 77.8 kd protein in gut1-rim1 intergenic region.
CONTIG5035	32610175_f1_1	818	14921	420	140	P38737	98	0.00889	Saccharomyces cerevisiae	hypothetical 210.4 kd protein in gut1-rim1 intergenic region.
CONTIG5683	19567257_c1_16	819	14922	1359	453	P38737	438	8.8(10)-40	Saccharomyces cerevisiae	hypothetical 210.4 kd protein in gut1-rim1 intergenic region.
blx10655.y	1178830_c1_4	820	14923	891	297	P38737	627	6.5(10)-60	Saccharomyces cerevisiae	hypothetical 210.4 kd protein in gut1-rim1 intergenic region.
CONTIG5155	10972531_c1_12	821	14924	681	227	P38736	340	5.5(10)-31	Saccharomyces cerevisiae	hypothetical 25.4 kd protein in gut1-rim1 intergenic region.
CONTIG3715	19538927_f3_1	822	14925	1758	586	P38732	565	8.0(10)-55	Saccharomyces cerevisiae	hypothetical 67.5 kd protein in cbp2 5' region.
CONTIG2855	12140933_c3_4	823	14926	909	303	P38757	240	8.5(10)-40	Saccharomyces cerevisiae	hypothetical 50.6 kd protein in rpl14b-gpa1 intergenic region.
CONTIG4553	137_f1_1	824	14927	1080	360	P38758	278	4.5(10)-44	Saccharomyces cerevisiae	hypothetical 57.0 kd protein in sod2-rpl27 intergenic region.
CONTIG2218	29416405_f2_1	825	14928	927	309	P41907	120	8.5(10)-5	Saccharomyces douglasii	hypothetical 44.4 kd protein in spo13-arg4 intergenic region.
CONTIG5342	24414687_c1_14	826	14929	978	326	P38768	331	5.0(10)-30	Saccharomyces cerevisiae	hypothetical 39.5 kd protein in put2-pu2 intergenic region.
CONTIG5174	24430287_f3_3	827	14930	1107	369	P38770	105	0.0061	Saccharomyces cerevisiae	hypothetical 53.4 kd protein in sh2-pu2 intergenic region.
CONTIG3828	3134635_c3_6	828	14931	1023	341	P45417	98	0.029	Erwinia chrysanthemi	hypothetical 36.0 kd protein in kdgk 5' region (kl orf).
CONTIG3991	2928552_c1_7	829	14932	831	277	P38772	130	6.7(10)-10	Saccharomyces cerevisiae	hypothetical 42.3 kd protein in put2-srb2 intergenic region.
CONTIG5727	12320437_c3_30	830	14933	1419	473	P38775	184	6.2(10)-19	Saccharomyces cerevisiae	hypothetical 62.7 kd protein in dog1-aap1 intergenic region.

CONTIG1837	24226377_fl_1	831	14934	453	151	P38779	139	6.2(10)-9	Saccharomyces cerevisiae	hypothetical 42.5 kd protein in cox6-cup1 intergenic region.
CONTIG3857	11754662_c1_6	832	14935	558	186	P38786	112	1.3(10)-13	Saccharomyces cerevisiae	hypothetical 32.2 kd protein in vma22-trp3 intergenic region.
CONTIG2317	802018_fl_1	833	14936	819	273	P38788	679	6.7(10)-67	Saccharomyces cerevisiae	heat shock protein 70 homolog yhm064c.
CONTIG4019	34621093_c2_8	834	14937	549	183	P38790	138	3.8(10)-9	Saccharomyces cerevisiae	hypothetical 33.1 kd protein in ssf1-dys1 intergenic region.
CONTIG1881	36507697_c3_3	835	14938	816	272	P38792	798	2.3(10)-91	Saccharomyces cerevisiae	hypothetical 39.4 kd protein in dys1-erg7 intergenic region.
CONTIG5727	468826_fl_2	836	14939	930	310	P38794	133	3.8(10)-7	Saccharomyces cerevisiae	hypothetical 26.5 kd protein in dys1-erg7 intergenic region.
CONTIG5718	23728436_fl_3	837	14940	2148	716	P38795	2641	8.1(10)-275	Saccharomyces cerevisiae	hypothetical 80.7 kd protein in erg7-nmd2 intergenic region.
CONTIG5718	9876910_c1_12	838	14941	1107	369	P38796	403	1.2(10)-37	Saccharomyces cerevisiae	hypothetical 44.9 kd protein in erg7-nmd2 intergenic region.
CONTIG3841	31453213_13_3	839	14942	672	224	P38797	557	5.5(10)-54	Saccharomyces cerevisiae	hypothetical 41.2 kd protein in erg7-nmd2 intergenic region.
CONTIG5364	12923450_c1_9	840	14943	2217	739	P38800	520	9.0(10)-49	Saccharomyces cerevisiae	hypothetical 149.7 kd protein in ire1-ksp1 intergenic region.
CONTIG149	4098277_c3_4	841	14944	651	217	P38801	144	3.2(10)-10	Saccharomyces cerevisiae	hypothetical 21.0 kd protein in ire1-ksp1 intergenic region.
CONTIG1515	4313882_13_5	842	14945	855	285	P38803	209	1.5(10)-25	Saccharomyces cerevisiae	hypothetical 37.9 kd protein in site12-nam8 intergenic region.
CONTIG5603	22456507_fl_3	843	14946	402	134	P38804	151	5.9(10)-11	Saccharomyces cerevisiae	hypothetical 12.0 kd protein in nam8-gar1 intergenic region.
CONTIG5314	25836002_c3_15	844	14947	924	308	P38805	808	1.3(10)-80	Saccharomyces cerevisiae	hypothetical 35.1 kd protein in nam8-gar1 intergenic region.
CONTIG2603	19565967_12_2	845	14948	300	100	P38806	242	1.3(10)-20	Saccharomyces cerevisiae	hypothetical 32.1 kd protein in gar1-msr1 intergenic region.
CONTIG1503	35287809_c1_2	846	14949	501	167	P38809	121	5.4(10)-7	Saccharomyces cerevisiae	hypothetical 40.7 kd protein in hxi5-nrk1 intergenic region.
CONTIG5260	21595180_13_5	847	14950	2763	921	P38810	764	3.8(10)-112	Saccharomyces cerevisiae	hypothetical 104.0 kd protein in hxi5-nrk1 intergenic region.

CONTIG1273	9820388_f2_1	848	14951	1224	408	P38811	725	7.4(10)-70	Saccharomyces cerevisiae	hypothetical 433.2 kd protein in hxl5-nrk1 intergenic region.
CONTIG1273	4493903_f3_3	849	14952	192	64	P38811	103	0.00077	Saccharomyces cerevisiae	hypothetical 433.2 kd protein in hxl5-nrk1 intergenic region.
CONTIG5146	2932950_f1_3	850	14953	345	115	P38811	196	1.1(10)-13	Saccharomyces cerevisiae	hypothetical 433.2 kd protein in hxl5-nrk1 intergenic region.
CONTIG2684	975752_f3_2	851	14954	768	256	P38811	442	8.1(10)-40	Saccharomyces cerevisiae	hypothetical 433.2 kd protein in hxl5-nrk1 intergenic region.
CONTIG2684	22289681_f3_3	852	14955	414	138	P38811	247	4.0(10)-19	Saccharomyces cerevisiae	hypothetical 433.2 kd protein in hxl5-nrk1 intergenic region.
CONTIG2684	4790927_f1_1	853	14956	642	214	P38811	479	9.5(10)-44	Saccharomyces cerevisiae	hypothetical 433.2 kd protein in hxl5-nrk1 intergenic region.
CONTIG3275	31753138_c1_5	854	14957	1392	464	P38811	1744	3.7(10)-178	Saccharomyces cerevisiae	hypothetical 433.2 kd protein in hxl5-nrk1 intergenic region.
CONTIG5146	35208393_f3_8	855	14958	1824	608	P38811	1291	1.2(10)-154	Saccharomyces cerevisiae	hypothetical 433.2 kd protein in hxl5-nrk1 intergenic region.
CONTIG5146	24850936_c3_17	856	14959	402	134	P38812	322	4.5(10)-29	Saccharomyces cerevisiae	hypothetical 20.9 kd protein in hxl5-nrk1 intergenic region.
CONTIG5146	34072262_c3_16	857	14960	276	92	P38812	164	2.5(10)-12	Saccharomyces cerevisiae	hypothetical 20.9 kd protein in hxl5-nrk1 intergenic region.
CONTIG2312	25551701_f2_1	858	14961	1644	548	P38814	114	0.0032	Saccharomyces cerevisiae	hypothetical 96.4 kd protein in nrk1-cdc12 intergenic region.
CONTIG4805	33400307_f3_3	859	14962	507	169	P38815	127	2.6(10)-8	Saccharomyces cerevisiae	hypothetical 24.6 kd protein in nrk1-cdc12 intergenic region.
CONTIG3625	11025278_f3_1	860	14963	966	322	P38817	819	9.6(10)-82	Saccharomyces cerevisiae	hypothetical 64.3 kd protein in cdc12-orc6 intergenic region.
CONTIG4231	595950_c3_14	861	14964	681	227	P38817	263	5.5(10)-22	Saccharomyces cerevisiae	hypothetical 64.3 kd protein in cdc12-orc6 intergenic region.
CONTIG3444	4381300_f2_4	862	14965	822	274	P38818	99	1.7(10)-5	Saccharomyces cerevisiae	hypothetical 68.3 kd protein in cdc12-orc6 intergenic region.
CONTIG1329	970327_c2_3	863	14966	1101	367	P38822	222	1.8(10)-17	Saccharomyces cerevisiae	hypothetical 71.2 kd protein in cdc12-orc6 intergenic region.
CONTIG2212	14571875_c1_2	864	14967	648	216	P38822	433	1.1(10)-40	Saccharomyces cerevisiae	hypothetical 71.2 kd protein in cdc12-orc6 intergenic region.

CONTIG3703	3909375_f3_4	865	14968	492	164	P38824	220	2.8(10)-18	Saccharomyces cerevisiae	hypothetical 17.3 kd protein in cdc12-ore6 intergenic region.
CONTIG5029	4332753_f3_6	866	14969	687	229	P38829	362	5.2(10)-37	Saccharomyces cerevisiae	hypothetical 25.7 kd protein in msh1-ep1 intergenic region.
CONTIG5332	23476587_c1_8	867	14970	477	159	Q03000	167	4.0(10)-12	Saccharomyces kluyveri	hypothetical protein in his3 3'region (fragment).
CONTIG4899	25562760_f2_3	868	14971	1557	519	P38835	379	4.9(10)-39	Saccharomyces cerevisiae	hypothetical 95.1 kd protein in act5-yck1 intergenic region.
CONTIG5061	25943801_f2_6	869	14972	678	226	P38836	179	3.6(10)-13	Saccharomyces cerevisiae	hypothetical 49.8 kd protein in act3-yck1 intergenic region precursor.
CONTIG5061	33492053_f1_2	870	14973	486	162	P38836	469	1.2(10)-44	Saccharomyces cerevisiae	hypothetical 49.8 kd protein in act3-yck1 intergenic region precursor.
CONTIG5616	3964061_c2_32	871	14974	930	310	P38838	310	8.4(10)-28	Saccharomyces cerevisiae	hypothetical 30.6 kd protein in act5-yck1 intergenic region.
CONTIG3240	93777_f1_1	872	14975	432	144	P38841	103	7.2(10)-6	Saccharomyces cerevisiae	hypothetical 12.8 kd protein in yck1-sps100 intergenic region precursor.
CONTIG4506	128_c1_l3	873	14976	777	259	P38842	199	4.9(10)-16	Saccharomyces cerevisiae	hypothetical 27.0 kd protein in sps100-rpl44 intergenic region.
CONTIG3496	869052_f3_4	874	14977	855	285	P38843	571	1.8(10)-55	Saccharomyces cerevisiae	hypothetical 34.9 kd protein in rpl44-dcd1 intergenic region.
CONTIG5538	13782952_f1_1	875	14978	1197	399	P38848	167	3.7(10)-16	Saccharomyces cerevisiae	hypothetical 66.1 kd protein in mrp6-spo12 intergenic region.
CONTIG5538	23834385_f2_7	876	14979	624	208	P38848	193	2.0(10)-14	Saccharomyces cerevisiae	hypothetical 66.1 kd protein in mrp6-spo12 intergenic region.
CONTIG3910	9970912_f1_1	877	14980	1671	557	P38849	310	8.3(10)-29	Saccharomyces cerevisiae	hypothetical 59.8 kd protein in mrp6-spo12 intergenic region.
CONTIG2384	24711087_c2_5	878	14981	795	265	P38852	102	1.3(10)-6	Saccharomyces cerevisiae	hypothetical 40.4 kd protein in spo16-rec104 intergenic region.
CONTIG5795	26270192_f1_1	879	14982	549	183	P38853	112	2.0(10)-11	Saccharomyces cerevisiae	hypothetical 131.1 kd protein in rec104-sol3 intergenic region.

CONTIG5584	4803175_f1_1	880	14983	1656	552	P38860	834	2.5(10)-83	Saccharomyces cerevisiae	hypothetical 55.5 kd gtp-binding protein in cdc23-nmd3 intergenic region.
CONTIG5333	20671805_f3_3	881	14984	1896	632	P38862	1280	1.3(10)-130	Saccharomyces cerevisiae	hypothetical 71.4 kd protein in nmd3-eno2 intergenic region.
CONTIG5333	14235882_f3_4	882	14985	1761	587	P38863	449	1.0(10)-41	Saccharomyces cerevisiae	hypothetical 96.8 kd protein in nmd3-eno2 intergenic region.
CONTIG2653	16656413_f3_7	883	14986	300	100	P38869	202	2.2(10)-16	Saccharomyces cerevisiae	hypothetical 26.3 kd protein in oye2-gnd1 intergenic region.
CONTIG4499	14475780_c1_10	884	14987	3549	1183	P38873	1475	2.2(10)-289	Saccharomyces cerevisiae	hypothetical 175.8 kd protein in gnd1-erg9 intergenic region.
CONTIG4215	1953125_c3_8	885	14988	783	261	P38874	420	1.8(10)-39	Saccharomyces cerevisiae	hypothetical 35.2 kd protein in gnd1-erg9 intergenic region.
CONTIG3026	4964451_c3_4	886	14989	975	325	P38875	689	5.7(10)-68	Saccharomyces cerevisiae	hypothetical 67.8 kd protein in gnd1-erg9 intergenic region.
CONTIG4215	2386450_f2_2	887	14990	852	284	P38875	520	4.7(10)-50	Saccharomyces cerevisiae	hypothetical 67.8 kd protein in gnd1-erg9 intergenic region.
CONTIG1004	12931425_c1_3	888	14991	474	158	P38880	351	1.2(10)-31	Saccharomyces cerevisiae	hypothetical 66.7 kd protein in egd2-sun1 intergenic region.
CONTIG5696	10735952_f1_3	889	14992	1851	617	P38880	250	2.5(10)-33	Saccharomyces cerevisiae	hypothetical 66.7 kd protein in egd2-sun1 intergenic region.
CONTIG5786	6831313_f1_6	890	14993	1416	472	P38880	956	3.0(10)-96	Saccharomyces cerevisiae	hypothetical 66.7 kd protein in egd2-sun1 intergenic region.
CONTIG840	24617137_f3_1	891	14994	1086	362	P38883	215	1.1(10)-17	Saccharomyces cerevisiae	hypothetical 86.7 kd protein in egd2-sun1 intergenic region.
CONTIG5772	0_c2_35	892	14995	744	248	P38884	293	6.5(10)-37	Saccharomyces cerevisiae	hypothetical 36.5 kd protein in egd2-sun1 intergenic region.
CONTIG5080	19719002_f2_4	893	14996	1152	384	P40560	276	1.3(10)-23	Saccharomyces cerevisiae	hypothetical 59.7 kd protein in bet1-pan1 intergenic region.
CONTIG3418	21878768_f3_1	894	14997	1095	365	P40558	791	9.0(10)-79	Saccharomyces cerevisiae	hypothetical 31.9 kd protein in bet1-pan1 intergenic region.
CONTIG5305	14225302_f1_3	895	14998	726	242	P40555	268	2.3(10)-23	Saccharomyces cerevisiae	hypothetical 24.8 kd protein in faa3-bet1 intergenic region.

CONTIG5305	24824087_c2_12	896	14999	321	107	P40554	300	9.6(10)-27	Saccharomyces cerevisiae	hypothetical 11.0 kd protein in faa3-bel intergenic region.
CONTIG943	4882893_c3_4	897	15000	654	218	P40553	347	1.0(10)-31	Saccharomyces cerevisiae	hypothetical 24.1 kd protein in pdrl1-faa3 intergenic region.
CONTIG5137	24397087_c1_11	898	15001	960	320	P40546	350	6.0(10)-44	Saccharomyces cerevisiae	hypothetical 38.9 kd protein in rpb3-rp15a intergenic region.
CONTIG5137	31360692_f1_1	899	15002	885	295	P40545	730	2.6(10)-72	Saccharomyces cerevisiae	hypothetical 29.6 kd protein in rpb3-rp15a intergenic region.
CONTIG4095	24491562_f1_1	900	15003	1524	508	P40533	1000	6.4(10)-101	Saccharomyces cerevisiae	hypothetical 54.9 kd protein in cbr5-not3 intergenic region.
CONTIG4049	2400285_f3_2	901	15004	576	192	P40531	240	2.2(10)-20	Saccharomyces cerevisiae	36.7 kd protein in cbr5-not3 intergenic region.
CONTIG4902	3990802_c2_5	902	15005	1128	376	P40531	223	5.5(10)-17	Saccharomyces cerevisiae	36.7 kd protein in cbr5-not3 intergenic region.
CONTIG5387	23828211_f1_2	903	15006	825	275	P40526	237	4.5(10)-20	Saccharomyces cerevisiae	hypothetical 30.3 kd protein in gpl1-syl1 intergenic region.
CONTIG4685	24666006_f1_1	904	15007	900	300	P40522	146	2.0(10)-7	Saccharomyces cerevisiae	hypothetical 71.4 kd protein in snp1-gpp1 intergenic region.
CONTIG5529	24413182_f3_7	905	15008	1431	477	P25040	511	4.2(10)-49	Saccharomyces cerevisiae	hypothetical protein in ifm1 3'region (fragment).
CONTIG4987	25973417_c1_4	906	15009	633	211	P40518	332	3.8(10)-30	Saccharomyces cerevisiae	hypothetical 17.1 kd protein in mr3-snp1 intergenic region.
CONTIG4301	3939552_f2_6	907	15010	534	178	P40515	282	7.7(10)-25	Saccharomyces cerevisiae	hypothetical 17.7 kd protein in mr3-snp1 intergenic region.
CONTIG4536	79432_f3_5	908	15011	1491	497	P40514	959	1.3(10)-96	Saccharomyces cerevisiae	hypothetical 75.5 kd protein in sec6-mr3 intergenic region.
CONTIG4270	22375806_c2_6	909	15012	861	287	P40513	306	2.2(10)-27	Saccharomyces cerevisiae	hypothetical 30.1 kd protein in hop1-rps24eb intergenic region.
CONTIG4285	3929050_c3_9	910	15013	1863	621	P40511	394	9.5(10)-34	Saccharomyces cerevisiae	hypothetical 102.4 kd protein in sen3-hop1 intergenic region.
CONTIG4331	21683430_c2_6	911	15014	1077	359	P40506	874	1.3(10)-87	Saccharomyces cerevisiae	hypothetical 41.9 kd protein in sds3-ths1 intergenic region.
CONTIG5478	21673306_c1_10	912	15015	936	312	P40496	532	2.5(10)-51	Saccharomyces cerevisiae	hypothetical 30.5 kd protein in sgsl-sds3 intergenic region.

CONTIG5084	21988181_c2_12	913	15016	1104	368	P40493	539	4.5(10)-52	Saccharomyces cerevisiae	hypothetical 39.4 kd protein in sgal-sds3 intergenic region.
CONTIG5084	6829650_f2_4	914	15017	1080	360	P40492	164	8.9(10)-22	Saccharomyces cerevisiae	hypothetical 59.9 kd protein in sgal-sds3 intergenic region.
CONTIG5326	22298317_f3_5	915	15018	1497	499	P40489	158	6.9(10)-11	Saccharomyces cerevisiae	hypothetical 72.7 kd protein in pfk26-sgal intergenic region.
CONTIG5169	4694051_f1_4	916	15019	945	315	P40487	1041	2.8(10)-105	Saccharomyces cerevisiae	hypothetical 48.3 kd protein in pfk26-sgal intergenic region.
CONTIG5169	35959676_f1_5	917	15020	279	93	P40487	345	1.6(10)-31	Saccharomyces cerevisiae	hypothetical 48.3 kd protein in pfk26-sgal intergenic region.
CONTIG5169	4890750_c2_9	918	15021	1593	531	P40486	883	1.6(10)-88	Saccharomyces cerevisiae	hypothetical 59.2 kd protein in pfk26-sgal intergenic region.
CONTIG4700	29331302_c3_10	919	15022	870	290	P40484	492	4.4(10)-47	Saccharomyces cerevisiae	hypothetical 27.4 kd protein in pfk26-sgal intergenic region.
CONTIG4688	10727160_c3_9	920	15023	2238	746	P40483	1041	3.8(10)-112	Saccharomyces cerevisiae	hypothetical zinc metalloproteinase yll108w (ec 3.4.24.-).
CONTIG5768	10001527_c2_23	921	15024	2328	776	P40482	1576	5.9(10)-162	Saccharomyces cerevisiae	hypothetical 103.6 kd protein in cox5b-pfk26 intergenic region.
CONTIG3740	796890_f1_1	922	15025	741	247	P40481	224	2.3(10)-18	Saccharomyces cerevisiae	hypothetical 42.5 kd protein in cox5b-pfk26 intergenic region.
CONTIG5386	25953452_f2_3	923	15026	3399	1133	P40480	314	3.1(10)-24	Saccharomyces cerevisiae	hypothetical 123.6 kd protein in nup159-cox5b intergenic region.
CONTIG1610	16287535_c2_3	924	15027	1035	345	P40468	252	8.0(10)-43	Saccharomyces cerevisiae	hypothetical 269.9 kd protein in fkh1-sth1 intergenic region.
CONTIG4136	16460202_c3_7	925	15028	3318	1106	P40468	1864	1.8(10)-192	Saccharomyces cerevisiae	hypothetical 269.9 kd protein in fkh1-sth1 intergenic region.
CONTIG4486	9923387_c1_5	926	15029	1830	610	P40468	563	2.0(10)-55	Saccharomyces cerevisiae	hypothetical 269.9 kd protein in fkh1-sth1 intergenic region.
CONTIG5256	24323425_c2_5	927	15030	1308	436	P40462	151	2.2(10)-7	Saccharomyces cerevisiae	hypothetical zinc aminopeptidase yll137c (ec 3.4.11.-).
CONTIG5256	15103811_c3_6	928	15031	1785	595	P40462	540	2.2(10)-51	Saccharomyces cerevisiae	hypothetical zinc aminopeptidase yll137c (ec 3.4.11.-).

CONTIG3159	970662_f3_3	929	15032	1017	339	P40460	308	1.1(10)-26	Saccharomyces cerevisiae	hypothetical 80.5 kd protein in shl1-rad25 intergenic region.
CONTIG5785	24413387_f1_3	930	15033	696	232	P40452	243	1.1(10)-20	Saccharomyces cerevisiae	hypothetical 22.0 kd protein in fox3-ubp7 intergenic region.
CONTIG803	16829663_c1_3	931	15034	738	246	P53039	423	8.9(10)-40	Saccharomyces cerevisiae	yip1 protein.
CONTIG2662	4688407_c2_4	932	15035	954	318	P40562	376	2.3(10)-55	Saccharomyces cerevisiae	putative atp-dependent ma helicase yir002c.
CONTIG5659	22301552_f2_9	933	15036	792	264	P40562	467	2.1(10)-43	Saccharomyces cerevisiae	putative atp-dependent ma helicase yir002c.
CONTIG2153	21756938_f3_2	934	15037	822	274	P40563	144	1.8(10)-7	Saccharomyces cerevisiae	hypothetical 74.8 kd protein in bet1-pan1 intergenic region.
CONTIG5798	11760077_c3_42	935	15038	2454	818	P40566	786	9.3(10)-147	Saccharomyces cerevisiae	hypothetical 87.0 kd protein in pan1-prl1 intergenic region.
CONTIG3976	12522826_f1_3	936	15039	1359	453	P35184	803	4.7(10)-80	Saccharomyces cerevisiae	hypothetical trp-asg repeats containing protein in dbf8-mei28 intergenic region.
CONTIG4281	892267_f3_3	937	15040	465	155	P40571	164	2.5(10)-12	Saccharomyces cerevisiae	hypothetical 16.3 kd protein in dbf8-mei28 intergenic region.
CONTIG1326	823751_c3_2	938	15041	723	241	P40582	270	1.5(10)-23	Saccharomyces cerevisiae	hypothetical 26.8 kd protein in hyr1-3'region.
CONTIG2294	33625186_f1_1	939	15042	762	254	P40582	297	2.0(10)-26	Saccharomyces cerevisiae	hypothetical 26.8 kd protein in hyr1-3'region.
CONTIG2427	22532250_c2_4	940	15043	771	257	P40582	396	6.5(10)-37	Saccharomyces cerevisiae	hypothetical 26.8 kd protein in hyr1-3'region.
CONTIG5612	15785801_c1_8	941	15044	777	259	P40582	389	3.6(10)-36	Saccharomyces cerevisiae	hypothetical 26.8 kd protein in hyr1-3'region.
b3x16023.y	35807758_f1_1	942	15045	270	90	P40586	195	1.3(10)-15	Saccharomyces cerevisiae	hypothetical 27.4 kd protein in hyr1-3'region.
CONTIG5502	14878178_f3_5	943	15046	879	293	P47104	347	3.7(10)-33	Saccharomyces cerevisiae	hypothetical 154.9 kd protein in cpr7-pet191 intergenic region.
CONTIG5502	34273500_f2_2	944	15047	2853	951	P47104	791	1.3(10)-92	Saccharomyces cerevisiae	hypothetical 154.9 kd protein in cpr7-pet191 intergenic region.

CONTIG3806	29458057_c2_8	945	15048	1143	381	P47108	327	2.8(10)-28	Saccharomyces cerevisiae	hypothetical 135.1 kd protein in get1-nup85 intergenic region.
CONTIG5258	6628_c2_10	946	15049	1464	488	P47108	202	1.3(10)-12	Saccharomyces cerevisiae	hypothetical 135.1 kd protein in get1-nup85 intergenic region.
CONTIG5635	4804660_c1_15	947	15050	447	149	P47111	215	9.8(10)-18	Saccharomyces cerevisiae	hypothetical 15.7 kd protein in nup85-ssc1 intergenic region.
CONTIG2005	12553817_c1_3	948	15051	762	254	P47112	107	0.003	Saccharomyces cerevisiae	hypothetical 68.4 kd protein in ssc1-hyp1 intergenic region.
CONTIG3937	24485963_c1_4	949	15052	870	290	P47114	307	4.2(10)-27	Saccharomyces cerevisiae	hypothetical 57.5 kd protein in rad7-hit1 intergenic region.
CONTIG3045	21520312_f2_2	950	15053	741	247	P47115	116	4.2(10)-5	Saccharomyces cerevisiae	hypothetical 27.4 kd protein in hit1-cdc8 intergenic region.
CONTIG2275	198518_c1_3	951	15054	831	277	P40355	388	5.5(10)-35	Saccharomyces cerevisiae	hypothetical 108.4 kd protein in cbf1-nat1 intergenic region.
CONTIG4870	34096925_f3_2	952	15055	2463	821	P40355	278	1.3(10)-20	Saccharomyces cerevisiae	hypothetical 108.4 kd protein in cbf1-nat1 intergenic region.
CONTIG5230	24713967_c2_16	953	15056	645	215	P47120	615	4.0(10)-60	Saccharomyces cerevisiae	hypothetical 36.2 kd protein in ham1-pem2 intergenic region.
CONTIG4684	6673562_f2_2	954	15057	1377	459	P47122	1246	5.5(10)-127	Saccharomyces cerevisiae	hypothetical 43.2 kd protein in ham1-pem2 intergenic region.
CONTIG1615	5897793_f3_1	955	15058	870	290	P47127	115	0.00031	Saccharomyces cerevisiae	hypothetical 44.4 kd protein in mir1-ste18 intergenic region.
CONTIG5777	33393927_f2_5	956	15059	549	183	P47131	324	2.7(10)-29	Saccharomyces cerevisiae	hypothetical 11.3 kd protein in mir1-ste18 intergenic region.
CONTIG5324	34175012_c2_13	957	15060	1197	399	P47133	177	2.1(10)-11	Saccharomyces cerevisiae	hypothetical 33.9 kd protein in ste18-grt1 intergenic region.
CONTIG3904	9878143_c1_4	958	15061	1053	351	P47140	688	7.4(10)-68	Saccharomyces cerevisiae	hypothetical 37.5 kd protein in yuh1-ura8 intergenic region.
CONTIG5491	13944376_c2_12	959	15062	822	274	P47141	378	5.2(10)-35	Saccharomyces cerevisiae	hypothetical 30.2 kd protein in yuh1-ura8 intergenic region.
CONTIG5324	10605055_f3_6	960	15063	489	163	P47142	172	3.5(10)-13	Saccharomyces cerevisiae	hypothetical 23.6 kd protein in yuh1-ura8 intergenic region.
CONTIG5244	23865930_c3_17	961	15064	1398	466	P47147	406	1.3(10)-50	Saccharomyces cerevisiae	hypothetical 80.2 kd protein in cpa2-atp2 intergenic region.

b2x15213.y	16287662_f2_1	962	15065	525	175	P47147	229	3.6(10)-18	Saccharomyces cerevisiae	hypothetical 80.2 kd protein in cpa2-atp2 intergenic region.
CONTIG2502	6750802_f3_3	963	15066	396	132	P47148	144	8.5(10)-10	Saccharomyces cerevisiae	hypothetical 32.2 kd protein in cpa2-atp2 intergenic region.
CONTIG2644	11822557_f1_1	964	15067	1158	386	P47148	180	1.3(10)-27	Saccharomyces cerevisiae	hypothetical 32.2 kd protein in cpa2-atp2 intergenic region.
CONTIG2905	4397576_f3_6	965	15068	960	320	P47153	352	3.0(10)-32	Saccharomyces cerevisiae	hypothetical 32.0 kd protein in cpa2-atp2 intergenic region.
CONTIG5728	5128430_c2_21	966	15069	516	172	P47155	247	4.0(10)-21	Saccharomyces cerevisiae	hypothetical 23.6 kd protein in cpa2-atp2 intergenic region.
CONTIG3871	1875_c3_10	967	15070	1308	436	P47160	512	3.2(10)-49	Saccharomyces cerevisiae	hypothetical 45.1 kd protein in rps5-zns1 intergenic region.
CONTIG5774	13688382_c3_30	968	15071	984	328	P47163	382	2.0(10)-35	Saccharomyces cerevisiae	hypothetical 39.0 kd protein in zns1-mns1 intergenic region.
CONTIG5160	9939067_c3_13	969	15072	696	232	P47170	656	3.7(10)-63	Saccharomyces cerevisiae	hypothetical 182.0 kd protein in nmd5-hom6 intergenic region.
CONTIG5160	29039197_c1_9	970	15073	666	222	P47170	356	3.7(10)-31	Saccharomyces cerevisiae	hypothetical 182.0 kd protein in nmd5-hom6 intergenic region.
CONTIG5160	782937_c3_12	971	15074	2508	836	P47170	855	6.4(10)-138	Saccharomyces cerevisiae	hypothetical 182.0 kd protein in nmd5-hom6 intergenic region.
CONTIG5343	22070288_c1_10	972	15075	447	149	P47081	267	3.0(10)-23	Saccharomyces cerevisiae	hypothetical 14.1 kd protein in cyf1-osl1 intergenic region.
CONTIG4229	19537502_f3_4	973	15076	990	330	P47077	531	3.2(10)-51	Saccharomyces cerevisiae	hypothetical 77.7 kd protein in cc3-cc8 intergenic region.
CONTIG4972	4410650_f2_3	974	15077	324	108	P47077	159	1.1(10)-10	Saccharomyces cerevisiae	hypothetical 77.7 kd protein in cc3-cc8 intergenic region.
CONTIG5602	22835965_c1_11	975	15078	654	218	P47076	164	1.8(10)-20	Saccharomyces cerevisiae	hypothetical 18.6 kd protein in cc3-cc8 intergenic region.
CONTIG4122	35360913_f3_4	976	15079	1710	570	P47075	1761	1.5(10)-181	Saccharomyces cerevisiae	hypothetical 75.5 kd protein in cc3-cc8 intergenic region.
CONTIG2474	22381261_f3_1	977	15080	942	314	P47067	252	1.2(10)-21	Saccharomyces cerevisiae	hypothetical 41.2 kd protein in pet130-cc3 intergenic region.
CONTIG4611	14268930_f3_4	978	15081	1605	535	P47057	310	8.4(10)-28	Saccharomyces cerevisiae	hypothetical 49.0 kd protein in nsp1-kar2 intergenic region.

CONTIG2830	30710011_f3_2	979	15082	1176	392	P47054	688	1.7(10)-66	Saccharomyces cerevisiae	hypothetical 191.5 kd protein in nsp1-kar2 intergenic region.
CONTIG3008	33361262_c1_3	980	15083	1131	377	P47054	219	1.2(10)-14	Saccharomyces cerevisiae	hypothetical 191.5 kd protein in nsp1-kar2 intergenic region.
CONTIG5766	1032278_c1_25	981	15084	1062	354	P47054	243	1.0(10)-17	Saccharomyces cerevisiae	hypothetical 191.5 kd protein in nsp1-kar2 intergenic region.
CONTIG5656	21691067_f2_5	982	15085	711	227	P48990	608	2.2(10)-59	Candida albicans	hypothetical protein in dfr1 3'region (fragment).
CONTIG5656	24785138_f1_2	983	15086	663	221	P47045	405	7.2(10)-38	Saccharomyces cerevisiae	hypothetical 54.2 kd protein in nup82-pep8 intergenic region.
CONTIG5643	971886_c2_27	984	15087	699	233	P47044	600	1.6(10)-58	Saccharomyces cerevisiae	hypothetical 26.9 kd protein in nup82-pep8 intergenic region.
CONTIG4633	22445135_f1_1	985	15088	666	222	P47040	390	2.7(10)-36	Saccharomyces cerevisiae	hypothetical 46.4 kd protein in nup82-pep8 intergenic region.
CONTIG3670	16197575_c2_5	986	15089	2040	680	P40367	730	2.2(10)-86	Saccharomyces cerevisiae	hypothetical 94.9 kd protein in mrp18-nup82 intergenic region.
CONTIG386	35634680_c3_2	987	15090	453	151	P40367	260	2.3(10)-21	Saccharomyces cerevisiae	hypothetical 94.9 kd protein in mrp18-nup82 intergenic region.
CONTIG5635	10975930_c2_16	988	15091	975	325	P40364	106	0.0015	Saccharomyces cerevisiae	hypothetical 28.5 kd protein in scp160-mrp18 intergenic region.
CONTIG2126	12533432_f3_2	989	15092	279	93	P40359	218	4.7(10)-18	Saccharomyces cerevisiae	hypothetical 25.1 kd protein in scp160-mrp18 intergenic region.
CONTIG651	10051317_f3_2	990	15093	204	68	P47033	154	5.7(10)-10	Saccharomyces cerevisiae	hypothetical 89.2 kd protein in scp160-mrp18 intergenic region.
CONTIG3566	32304537_c3_10	991	15094	420	140	P47032	339	7.0(10)-31	Saccharomyces cerevisiae	hypothetical 30.6 kd protein in scp160-mrp18 intergenic region precursor.
CONTIG4531	21681887_c2_10	992	15095	879	293	P47032	404	9.1(10)-38	Saccharomyces cerevisiae	hypothetical 30.6 kd protein in scp160-mrp18 intergenic region precursor.
CONTIG5762	34173578_f2_7	993	15096	990	330	P47032	377	6.7(10)-35	Saccharomyces cerevisiae	hypothetical 30.6 kd protein in scp160-mrp18 intergenic region precursor.

CONTIG5762	2921882_f1_5	994	15097	1131	377	P47032	373	1.8(10)-34	Saccharomyces cerevisiae	hypothetical 30.6 kd protein in scp160-mrp18 intergenic region precursor.
CONTIG5104	25567787_c1_6	995	15098	1668	556	P47031	668	9.6(10)-66	Saccharomyces cerevisiae	hypothetical 82.5 kd protein in trl1-ac3 intergenic region.
CONTIG5193	25437785_c3_9	996	15099	882	294	P47031	315	2.2(10)-27	Saccharomyces cerevisiae	hypothetical 82.5 kd protein in trl1-ac3 intergenic region.
CONTIG5629	24004557_c1_11	997	15100	3030	1010	P47029	763	8.3(10)-76	Saccharomyces cerevisiae	hypothetical 117.2 kd protein in trl1-ac3 intergenic region.
CONTIG5797	4406628_c2_22	998	15101	1467	489	P47026	911	1.7(10)-91	Saccharomyces cerevisiae	hypothetical 56.4 kd protein in srs2-sip4 intergenic region.
CONTIG2654	4687627_c2_3	999	15102	465	155	P40857	153	3.6(10)-11	Saccharomyces cerevisiae	hypothetical 24.5 kd protein in sap185-bck1 intergenic region.
CONTIG4790	9875300_f1_1	1000	15103	384	128	P40857	104	1.3(10)-5	Saccharomyces cerevisiae	hypothetical 24.5 kd protein in sap185-bck1 intergenic region.
CONTIG2400	188500_f1_1	1001	15104	936	312	P42951	285	2.5(10)-24	Saccharomyces cerevisiae	hypothetical 70.2 kd protein in gsh1-chs6 intergenic region.
CONTIG3866	6070325_f2_1	1002	15105	525	175	P42951	164	9.5(10)-15	Saccharomyces cerevisiae	hypothetical 70.2 kd protein in gsh1-chs6 intergenic region.
CONTIG5653	12500376_f3_13	1003	15106	384	128	P42949	217	6.0(10)-18	Saccharomyces cerevisiae	hypothetical 16.2 kd protein in sme1-mef2 intergenic region.
CONTIG4846	21532762_c2_10	1004	15107	2166	722	P42945	917	6.2(10)-91	Saccharomyces cerevisiae	hypothetical 200.0 kd protein in gzf3-sme1 intergenic region.
CONTIG5750	4410932_f1_7	1005	15108	603	201	P42945	428	9.4(10)-39	Saccharomyces cerevisiae	hypothetical 200.0 kd protein in gzf3-sme1 intergenic region.
CONTIG5750	35595218_f3_13	1006	15109	2268	756	P42945	239	1.0(10)-32	Saccharomyces cerevisiae	hypothetical 200.0 kd protein in gzf3-sme1 intergenic region.
CONTIG4913	13676013_f3_3	1007	15110	465	155	P47019	136	2.2(10)-9	Saccharomyces cerevisiae	hypothetical 19.3 kd protein in gcd14-pos18 intergenic region.
CONTIG414	22442756_c2_2	1008	15111	573	191	P47018	113	3.3(10)-9	Saccharomyces cerevisiae	hypothetical 53.5 kd protein in gcd14-pos18 intergenic region.
CONTIG5022	35332012_f1_1	1009	15112	504	168	P47018	92	2.8(10)-10	Saccharomyces cerevisiae	hypothetical 53.5 kd protein in gcd14-pos18 intergenic region.

CONTIG3363	23940910_c2_11	1010	15113	1317	439	P47015	137	1.0(10)-6	Saccharomyces cerevisiae	hypothetical 41.5 kd protein in mrs3-ura2 intergenic region.
CONTIG5461	34020907_c1_10	1011	15114	1512	504	P47013	655	5.5(10)-69	Saccharomyces cerevisiae	hypothetical 47.4 kd protein in rps25b-mrs3 intergenic region.
CONTIG1478	17080158_f2_1	1012	15115	1029	343	P47008	496	1.6(10)-47	Saccharomyces cerevisiae	hypothetical 34.4 kd protein in ids2-mpi2 intergenic region.
CONTIG5678	22297032_c1_10	1013	15116	675	225	P47006	214	1.3(10)-17	Saccharomyces cerevisiae	hypothetical 26.9 kd protein in ino1-ids2 intergenic region.
CONTIG5133	24508415_f3_3	1014	15117	834	278	P47005	96	0.07399	Saccharomyces cerevisiae	hypothetical 77.4 kd protein in ino1-ids2 intergenic region.
CONTIG5760	1350630_f2_10	1015	15118	1062	354	P47002	163	4.2(10)-9	Saccharomyces cerevisiae	hypothetical 76.2 kd protein in far1-fbp26 intergenic region.
CONTIG5760	162640_f2_11	1016	15119	1506	502	P47002	298	1.8(10)-50	Saccharomyces cerevisiae	hypothetical 76.2 kd protein in far1-fbp26 intergenic region.
CONTIG143	1063186_f3_2	1017	15120	387	129	P47001	357	8.8(10)-33	Saccharomyces cerevisiae	hypothetical 23.2 kd protein in tpk1-far1 intergenic region precursor.
CONTIG1284	564055_c3_5	1018	15121	852	284	P47001	181	3.8(10)-14	Saccharomyces cerevisiae	hypothetical 23.2 kd protein in tpk1-far1 intergenic region precursor.
CONTIG4099	10959692_c2_10	1019	15122	288	96	P47001	121	1.7(10)-7	Saccharomyces cerevisiae	hypothetical 23.2 kd protein in tpk1-far1 intergenic region precursor.
CONTIG3684	564055_f3_4	1020	15123	855	285	P47001	181	3.8(10)-14	Saccharomyces cerevisiae	hypothetical 23.2 kd protein in tpk1-far1 intergenic region precursor.
CONTIG4863	24641526_f1_1	1021	15124	762	254	P47001	161	5.2(10)-12	Saccharomyces cerevisiae	hypothetical 23.2 kd protein in tpk1-far1 intergenic region precursor.
CONTIG5065	3156525_c1_7	1022	15125	1044	348	P47001	166	2.1(10)-12	Saccharomyces cerevisiae	hypothetical 23.2 kd protein in tpk1-far1 intergenic region precursor.
CONTIG2862	4867317_f3_2	1023	15126	573	191	P46996	170	5.5(10)-12	Saccharomyces cerevisiae	hypothetical 61.5 kd protein in tpk1-far1 intergenic region.

CONTIG4188	24740692_c3_6	1024	15127	687	229	P46995	144	5.2(10)-9	Saccharomyces cerevisiae	hypothetical 84.5 kd protein in cps1-fbp1 intergenic region.
CONTIG4555	10972186_c1_1	1025	15128	1626	542	P46995	932	1.8(10)-104	Saccharomyces cerevisiae	hypothetical 84.5 kd protein in cps1-fbp1 intergenic region.
CONTIG5767	36136432_c3_48	1026	15129	1413	471	P46992	936	3.8(10)-94	Saccharomyces cerevisiae	hypothetical 43.0 kd protein in cps1-fbp1 intergenic region.
CONTIG3300	4484575_c2_9	1027	15130	795	265	P46989	154	2.7(10)-18	Saccharomyces cerevisiae	hypothetical 21.6 kd protein in ap12-sw13 intergenic region.
CONTIG2091	2166663_f1_1	1028	15131	822	274	P46985	427	3.3(10)-40	Saccharomyces cerevisiae	hypothetical 47.8 kd protein in swel-atp12 intergenic region.
CONTIG445	4806325_f2_1	1029	15132	375	125	P46984	157	1.3(10)-11	Saccharomyces cerevisiae	hypothetical 13.6 kd protein in swel-atp12 intergenic region.
CONTIG1444	187800_f3_1	1030	15133	783	261	P32525	269	1.3(10)-22	Saccharomyces cerevisiae	hypothetical 68.5 kd protein in prp21-ubp12 intergenic region.
b3x16402.x	32936_f3_1	1031	15134	300	100	P39531	125	4.9(10)-7	Saccharomyces cerevisiae	hypothetical 97.5 kd protein in nucl-prp21 intergenic region.
CONTIG2207	21884425_f3_2	1032	15135	1257	419	P39526	292	3.2(10)-24	Saccharomyces cerevisiae	hypothetical 229.9 kd protein in nucl-prp21 intergenic region.
CONTIG2479	25604687_c3_4	1033	15136	1113	371	P39526	170	3.0(10)-9	Saccharomyces cerevisiae	hypothetical 229.9 kd protein in nucl-prp21 intergenic region.
CONTIG2801	26775050_c2_11	1034	15137	792	264	P47083	597	3.2(10)-58	Saccharomyces cerevisiae	hypothetical 67.0 kd protein in pre3-sag1 intergenic region.
CONTIG2801	6767163_c2_10	1035	15138	195	65	P47083	149	1.1(10)-9	Saccharomyces cerevisiae	hypothetical 67.0 kd protein in pre3-sag1 intergenic region.
CONTIG5512	1364550_c3_12	1036	15139	462	154	P47084	120	1.3(10)-6	Saccharomyces cerevisiae	hypothetical 62.2 kd protein in pre3-sag1 intergenic region.
CONTIG4077	17000700_c3_8	1037	15140	1026	342	P47085	509	6.9(10)-49	Saccharomyces cerevisiae	hypothetical 38.5 kd protein in sul2-tdh2 intergenic region.
CONTIG2986	12_f2_2	1038	15141	1278	426	P47088	564	1.0(10)-54	Saccharomyces cerevisiae	hypothetical 35.6 kd protein in spe1-iv3 intergenic region.
b1x14739.y	10548463_f1_1	1039	15142	567	189	P47089	178	8.1(10)-14	Saccharomyces cerevisiae	hypothetical 22.5 kd protein in spe1-iv3 intergenic region.
CONTIG5594	21890751_f3_9	1040	15143	855	285	P47095	504	2.2(10)-48	Saccharomyces cerevisiae	hypothetical 27.4 kd protein in mer2-cpr7 intergenic region.

CONTIG3052	30159715_f2_2	1041	15144	621	207	P36119	212	1.5(10)-20	Saccharomyces cerevisiae	hypothetical 60.8 kd protein in ypi52-gcn3 intergenic region.
CONTIG4950	25803180_f1_2	1042	15145	864	288	P36121	222	1.8(10)-18	Saccharomyces cerevisiae	hypothetical 32.1 kd protein in ypi52-gcn3 intergenic region.
b2x13889 y	3132657_f3_1	1043	15146	603	201	P36124	189	8.3(10)-14	Saccharomyces cerevisiae	hypothetical 85.5 kd protein in sap190-spo14 intergenic region.
CONTIG3829	12116252_c1_4	1044	15147	315	105	P36132	284	5.2(10)-25	Saccharomyces cerevisiae	hypothetical 46.6 kd protein in da180-gap1 intergenic region.
CONTIG2386	19954535_f3_2	1045	15148	1218	406	P36142	578	3.3(10)-56	Saccharomyces cerevisiae	hypothetical 48.8 kd protein in trk2-mrs4 intergenic region.
CONTIG1668	24301557_c1_1	1046	15149	690	230	P36144	238	3.6(10)-20	Saccharomyces cerevisiae	hypothetical 31.6 kd protein in ttf1-kr2 intergenic region.
CONTIG3207	2734562_c2_2	1047	15150	522	174	P36147	172	3.5(10)-13	Saccharomyces cerevisiae	hypothetical 22.0 kd protein in las1-ccp1 intergenic region.
b9x10747.x	11222153_f3_2	1048	15151	198	66	P36147	219	3.7(10)-18	Saccharomyces cerevisiae	hypothetical 22.0 kd protein in las1-ccp1 intergenic region.
CONTIG5077	3163377_c2_7	1049	15152	1203	401	P36151	819	9.6(10)-82	Saccharomyces cerevisiae	hypothetical 39.4 kd protein in ccp1-sis2 intergenic region.
CONTIG5097	5906912_c2_5	1050	15153	978	326	P36151	365	1.2(10)-33	Saccharomyces cerevisiae	hypothetical 39.4 kd protein in ccp1-sis2 intergenic region.
b9x13e10.x	22461562_f1_1	1051	15154	522	174	P36152	110	7.7(10)-6	Saccharomyces cerevisiae	hypothetical 38.5 kd protein in ccp1-sis2 intergenic region.
CONTIG258	24416462_c3_1	1052	15155	204	68	P36154	200	3.7(10)-16	Saccharomyces cerevisiae	hypothetical 18.4 kd protein in sis2-mtd1 intergenic region.
CONTIG5720	285875_f3_10	1053	15156	2760	920	P36159	704	1.8(10)-121	Saccharomyces cerevisiae	hypothetical 96.8 kd protein in sis2-mtd1 intergenic region.
CONTIG1054	6057812_f3_3	1054	15157	210	70	P36160	160	2.5(10)-11	Saccharomyces cerevisiae	hypothetical 39.6 kd protein in mtd1-nup133 intergenic region.
CONTIG2222	1210187_f2_2	1055	15158	573	191	P36160	558	4.4(10)-54	Saccharomyces cerevisiae	hypothetical 39.6 kd protein in mtd1-nup133 intergenic region.
CONTIG2223	16583325_f2_1	1056	15159	423	141	P36162	122	7.0(10)-8	Saccharomyces cerevisiae	hypothetical 15.1 kd protein in nup133-hbs1 intergenic region.
CONTIG5330	24017193_c3_15	1057	15160	810	270	P36163	348	7.9(10)-32	Saccharomyces cerevisiae	hypothetical 35.8 kd protein in prp16-srp40 intergenic region.

CONTIG2650	1289750_c3_6	1058	15161	1092	364	P36164	330	6.4(10)-30	Saccharomyces cerevisiae	hypothetical 38.3 kd protein in prp1-6-srp40 intergenic region.
CONTIG4779	36140675_f2_2	1059	15162	1803	601	P36165	510	3.5(10)-48	Saccharomyces cerevisiae	hypothetical 102.7 kd protein in prp1-6-srp40 intergenic region.
CONTIG5720	34410955_c1_21	1060	15163	879	293	P36165	531	1.8(10)-50	Saccharomyces cerevisiae	hypothetical 102.7 kd protein in prp1-6-srp40 intergenic region.
CONTIG5763	859626_c3_22	1061	15164	3180	1060	P36166	356	3.5(10)-32	Saccharomyces cerevisiae	hypothetical 79.4 kd protein in prp1-6-srp40 intergenic region.
b2x18881.x	35805418_f3_2	1062	15165	237	79	P36108	140	8.6(10)-10	Saccharomyces cerevisiae	hypothetical 16.7 kd protein mrp17-mel14 intergenic region.
CONTIG1834	32476432_c3_3	1063	15166	1116	372	P34241	241	7.4(10)-19	Saccharomyces cerevisiae	hypothetical 203.3 kd protein in put3-ecel intergenic region.
CONTIG2893	14964012_f2_2	1064	15167	1191	397	P34241	154	1.3(10)-7	Saccharomyces cerevisiae	hypothetical 203.3 kd protein in put3-ecel intergenic region.
b2x16714.x	24806465_f3_2	1065	15168	831	277	P34241	271	4.7(10)-22	Saccharomyces cerevisiae	hypothetical 203.3 kd protein in put3-ecel intergenic region.
CONTIG4548	2116050_c2_6	1066	15169	1353	451	P34243	91	0.42999	Saccharomyces cerevisiae	hypothetical 78.3 kd protein in ram2-arp7 intergenic region.
CONTIG5762	4956500_f3_14	1067	15170	1281	427	P34243	849	6.4(10)-85	Saccharomyces cerevisiae	hypothetical 78.3 kd protein in ram2-arp7 intergenic region.
b9x12h43.y	35439526_f1_1	1068	15171	675	225	P36104	271	1.1(10)-23	Saccharomyces cerevisiae	hypothetical 37.1 kd protein in ram2-arp7 intergenic region.
CONTIG3125	4728250_c1_5	1069	15172	1206	402	P36097	99	0.11	Saccharomyces cerevisiae	hypothetical 118.9 kd protein in pitn1-ixr1 intergenic region.
CONTIG3125	5208261_c3_8	1070	15173	714	238	P36097	102	0.02	Saccharomyces cerevisiae	hypothetical 118.9 kd protein in pitn1-ixr1 intergenic region.
b9x13h22.y	34414092_f1_1	1071	15174	408	136	P36097	170	1.3(10)-11	Saccharomyces cerevisiae	hypothetical 118.9 kd protein in pitn1-ixr1 intergenic region.
CONTIG3440	24414088_c3_11	1072	15175	1428	476	P36096	395	5.5(10)-36	Saccharomyces cerevisiae	hypothetical 87.9 kd protein precursor in pitn1-ixr1 intergenic region.
CONTIG4145	4883452_c1_7	1073	15176	624	208	P36095	215	9.8(10)-18	Saccharomyces cerevisiae	hypothetical 26.2 kd protein in phd1-pitn1 intergenic region.

CONTIG4611	25510756_f1_1	1074	15177	381	127	P36091	224	4.7(10)-18	Saccharomyces cerevisiae	hypothetical 49.6 kd protein precursor in c1ml1-pri2 intergenic region.
CONTIG5715	4100882_c3_24	1075	15178	948	316	P35735	258	2.0(10)-52	Saccharomyces cerevisiae	hypothetical 40.5 kd protein in nup120-cse4 intergenic region.
CONTIG5091	23516881_f2_6	1076	15179	645	215	P35728	328	1.0(10)-29	Saccharomyces cerevisiae	hypothetical 49.6 kd protein in tba1-toa2 intergenic region.
CONTIG5091	7054563_f1_3	1077	15180	852	284	P35728	185	8.5(10)-14	Saccharomyces cerevisiae	hypothetical 49.6 kd protein in tba1-toa2 intergenic region.
CONTIG5791	22460167_c1_22	1078	15181	555	185	P36088	570	2.3(10)-55	Saccharomyces cerevisiae	hypothetical 19.7 kd protein in tba1-nup100 intergenic region.
CONTIG2635	2625307_f2_1	1079	15182	1182	394	P36081	523	2.2(10)-50	Saccharomyces cerevisiae	hypothetical 46.0 kd protein in smy1-mud2 intergenic region.
CONTIG4893	24236438_c2_9	1080	15183	1353	451	P36080	309	7.5(10)-51	Saccharomyces cerevisiae	hypothetical 50.5 kd protein in mdh1-vma5 intergenic region.
CONTIG2957	21991556_c3_7	1081	15184	456	152	P36078	295	3.2(10)-26	Saccharomyces cerevisiae	hypothetical 13.6 kd protein in mdh1-vma5 intergenic region.
CONTIG3598	4878207_f1_1	1082	15185	408	136	P36077	342	3.3(10)-31	Saccharomyces cerevisiae	hypothetical 13.9 kd protein in cyf2-mdh1 intergenic region.
CONTIG4216	14722812_f1_1	1083	15186	1539	513	P36075	197	7.5(10)-13	Saccharomyces cerevisiae	hypothetical 50.9 kd protein in bud2-mif2 intergenic region.
CONTIG3420	13790927_f1_1	1084	15187	918	306	P28321	588	2.8(10)-57	Saccharomyces cerevisiae	hypothetical 35.5 kd protein in cwp1-mbr1 intergenic region.
CONTIG3596	4484400_c1_5	1085	15188	1104	368	P34246	93	0.12	Saccharomyces cerevisiae	hypothetical 39.8 kd protein in apc1/lap4-cwp1 intergenic region.
CONTIG3052	6679662_c3_7	1086	15189	1113	371	P34252	170	3.7(10)-10	Saccharomyces cerevisiae	hypothetical 52.3 kd protein in hap4-aat1 intergenic region.
CONTIG4253	241703_f3_2	1087	15190	306	102	P32343	106	4.5(10)-5	Saccharomyces cerevisiae	hypothetical 65.1 kd protein in rrm3-srp21 intergenic region.
CONTIG3601	23938412_f1_1	1088	15191	414	138	P36064	117	2.3(10)-7	Saccharomyces cerevisiae	hypothetical 12.0 kd protein in mrp131-apl2 intergenic region.
CONTIG1579	1178132_c2_3	1089	15192	369	123	P36059	137	8.1(10)-9	Saccharomyces cerevisiae	hypothetical 37.4 kd protein in gpm1-mcr1 intergenic region.

CONTIG5757	11726436_c1_12	1090	15193	330	110	P36059	278	2.1(10)-24	Saccharomyces cerevisiae	hypothetical 37.4 kd protein in gpm1-mcr1 intergenic region.
CONTIG1984	986383_c2_8	1091	15194	483	161	P36056	231	1.8(10)-18	Saccharomyces cerevisiae	hypothetical 72.2 kd protein in ape2-gpm1 intergenic region.
CONTIG4699	35831526_f1_1	1092	15195	591	197	P36056	239	2.6(10)-19	Saccharomyces cerevisiae	hypothetical 72.2 kd protein in ape2-gpm1 intergenic region.
CONTIG4522	4879652_c2_6	1093	15196	396	132	P36053	291	8.6(10)-26	Saccharomyces cerevisiae	hypothetical 16.2 kd protein in pit3-ape2 intergenic region.
CONTIG4442	16831551_f2_1	1094	15197	1287	429	P36049	755	5.9(10)-75	Saccharomyces cerevisiae	hypothetical 49.7 kd protein in gin2-site3 intergenic region.
CONTIG2541	21988325_c2_2	1095	15198	1068	356	P34240	118	2.5(10)-6	Saccharomyces cerevisiae	hypothetical 55.4 kd protein in ste3-gin10 intergenic region.
CONTIG3303	17135_f2_4	1096	15199	1587	529	P28817	733	1.3(10)-72	Saccharomyces cerevisiae	hypothetical protein in krs1 5'region (fragment).
CONTIG3824	3917163_f3_3	1097	15200	654	218	P34234	94	0.027	Saccharomyces cerevisiae	hypothetical 34.3 kd protein in ord1-fast intergenic region.
CONTIG3546	25596875_c1_6	1098	15201	273	91	P32464	142	3.2(10)-9	Saccharomyces cerevisiae	hypothetical 45.9 kd protein in cnb1-pat1 intergenic region.
CONTIG3546	16115628_c3_9	1099	15202	378	126	P32464	183	1.1(10)-13	Saccharomyces cerevisiae	hypothetical 45.9 kd protein in cnb1-pat1 intergenic region.
CONTIG5218	16620275_f1_1	1100	15203	261	87	P36046	201	1.3(10)-15	Saccharomyces cerevisiae	hypothetical 47.4 kd protein in pas1-mst1 intergenic region.
CONTIG1962	24416425_f2_2	1101	15204	234	78	P36043	123	6.0(10)-7	Saccharomyces cerevisiae	64.6 kd protein in tor2-pas1 intergenic region.
CONTIG5056	10744037_c2_12	1102	15205	552	184	P36040	185	1.5(10)-14	Saccharomyces cerevisiae	hypothetical 30.7 kd protein in ste6-lost intergenic region.
CONTIG4684	31679687_f1_1	1103	15206	600	200	P36039	307	1.7(10)-27	Saccharomyces cerevisiae	hypothetical 29.4 kd protein in ste6-lost intergenic region.
CONTIG5781	6853455_c2_23	1104	15207	1089	363	Q02202	98	0.025	Saccharomyces cerevisiae	hypothetical 34.5 kd protein in pap1-mrp113 intergenic region.
CONTIG3152	22001582_c1_5	1105	15208	348	116	P36112	230	1.7(10)-18	Saccharomyces cerevisiae	yp152-gen3 intergenic region.
CONTIG4982	7303180_c2_16	1106	15209	1059	353	P36112	95	0.07299	Saccharomyces cerevisiae	yp152-gen3 intergenic region.

CONTIG5653	39680_c3_20	1107	15210	696	232	P36113	217	4.5(10)-17	Saccharomyces cerevisiae	hypothetical 63.6 kd protein in ypi52-gen3 intergenic region.
CONTIG5778	6048377_c2_28	1108	15211	1971	657	P36115	232	4.5(10)-26	Saccharomyces cerevisiae	hypothetical 68.9 kd protein in ypi52-gen3 intergenic region.
CONTIG5245	4380280_c2_20	1109	15212	660	220	P53769	381	2.5(10)-35	Saccharomyces cerevisiae	hypothetical 29.7 kd protein in rec102-sfh1 intergenic region.
CONTIG4474	33832788_f1_1	1110	15213	966	322	P34424	92	0.14999	Caenorhabditis elegans	hypothetical 61.8 kd protein f44b9.3 in chromosome iii.
b9x10u41.y	34114005_f2_1	1111	15214	456	152	P34431	222	7.7(10)-17	Caenorhabditis elegans	hypothetical protein f44e2.1 in chromosome iii (fragment).
CONTIG4985	30257200_c2_8	1112	15215	1371	457	P54007	274	2.0(10)-23	Saccharomyces cerevisiae	hypothetical 41.1 kd protein on cdc91-pau4 intergenic region.
CONTIG4826	15115952_f2_5	1113	15216	2058	686	P40308	609	5.0(10)-98	Saccharomyces cerevisiae	hypothetical 73.6 kd protein in glc8-pre5 intergenic region.
CONTIG3511	14304562_f3_1	1114	15217	1386	462	P54730	125	5.4(10)-5	Saccharomyces cerevisiae	hypothetical 47.0 kd protein in aep1-hms1 intergenic region.
CONTIG3734	25806892_f1_1	1115	15218	1428	476	P49955	1232	1.7(10)-125	Saccharomyces cerevisiae	hypothetical 110.0 kd protein ym8021.14.
CONTIG3470	1953500_f3_5	1116	15219	756	252	P23797	140	1.0(10)-16	Saccharomyces cerevisiae	hypothetical 35.4 kd protein in cat8-ap13 intergenic region (urf2).
CONTIG3854	4859630_c1_7	1117	15220	1563	521	P40210	365	3.2(10)-45	Saccharomyces cerevisiae	hypothetical 55.9 kd protein in mds1-swp1 intergenic region.
CONTIG5211	1979050_f1_2	1118	15221	882	294	P49957	625	2.2(10)-76	Saccharomyces cerevisiae	hypothetical 32.4 kd protein in ppz1-spi5 intergenic region.
CONTIG5820	283501_f1_11	1119	15222	315	105	P03879	281	1.0(10)-24	Saccharomyces cerevisiae	hypothetical cob intron 4 protein.
CONTIG2977	32219067_c1_4	1120	15223	207	69	P54003	145	8.0(10)-10	Saccharomyces cerevisiae	hypothetical 33.8 kd protein in cyb2-gal80 intergenic region.
CONTIG766	10831327_c3_4	1121	15224	618	206	P54003	245	6.5(10)-21	Saccharomyces cerevisiae	hypothetical 33.8 kd protein in cyb2-gal80 intergenic region.
CONTIG3292	5906576_c2_5	1122	15225	321	107	P53759	158	6.7(10)-11	Saccharomyces cerevisiae	hypothetical 48.1 kd protein in tub1-cpi3 intergenic region.

CONTIG4228	3912512_f1_1	1123	15226	432	144	P53759	371	2.8(10)-34	Saccharomyces cerevisiae	hypothetical 48.1 kd protein in tub1-cp3 intergenic region.
CONTIG5781	22397762_f1_1	1124	15227	795	265	P53843	174	9.9(10)-26	Saccharomyces cerevisiae	hypothetical 34.5 kd protein in pik1-pol2 intergenic region.
CONTIG3385	38892_c1_3	1125	15228	1665	555	P53840	263	3.0(10)-19	Saccharomyces cerevisiae	hypothetical 141.1 kd protein in me2-sec2 intergenic region.
CONTIG5684	11051261_f1_5	1126	15229	1755	585	P53840	720	2.3(10)-70	Saccharomyces cerevisiae	hypothetical 141.1 kd protein in me2-sec2 intergenic region.
CONTIG5352	33301007_c3_12	1127	15230	1713	571	P53838	1225	9.1(10)-125	Saccharomyces cerevisiae	hypothetical 65.0 kd protein in me2-sec2 intergenic region.
CONTIG5714	1210900_c1_13	1128	15231	2067	689	P53836	242	5.5(10)-36	Saccharomyces cerevisiae	hypothetical 118.3 kd protein in erg24-me2 intergenic region.
CONTIG3733	2736252_f2_1	1129	15232	1557	519	P53835	198	2.1(10)-26	Saccharomyces cerevisiae	hypothetical 73.4 kd protein in erg24-me2 intergenic region.
CONTIG5707	23478461_f2_7	1130	15233	447	149	P53834	257	3.5(10)-22	Saccharomyces cerevisiae	hypothetical 17.2 kd protein in mrp110-erg24 intergenic region.
CONTIG2342	22445186_c3_3	1131	15234	726	242	P53829	660	6.9(10)-65	Saccharomyces cerevisiae	hypothetical 41.2 kd protein in plcl1-sec21 intergenic region.
CONTIG5357	24485937_c1_15	1132	15235	1248	416	P48567	805	3.0(10)-80	Saccharomyces cerevisiae	hypothetical 45.3 kd protein in claf4-mid1 intergenic region.
CONTIG3763	14647262_f3_2	1133	15236	1056	352	P48566	502	3.7(10)-48	Saccharomyces cerevisiae	hypothetical 73.0 kd protein in claf4-mid1 intergenic region.
CONTIG2393	29853427_f1_1	1134	15237	1020	340	P48565	221	1.6(10)-17	Saccharomyces cerevisiae	hypothetical 61.5 kd protein in claf4-mid1 intergenic region.
CONTIG3204	33756536_c1_4	1135	15238	1557	519	P48563	437	9.1(10)-40	Saccharomyces cerevisiae	hypothetical 186.8 kd protein in claf4-mid1 intergenic region.
CONTIG5709	6292916_f3_9	1136	15239	2976	992	P48563	740	3.0(10)-82	Saccharomyces cerevisiae	hypothetical 186.8 kd protein in claf4-mid1 intergenic region.
CONTIG5496	10339012_c3_20	1137	15240	675	225	P42847	394	1.1(10)-36	Saccharomyces cerevisiae	hypothetical 24.6 kd protein in mck1-mps5b intergenic region.
CONTIG3348	956317_c2_7	1138	15241	1818	606	P42842	1633	5.4(10)-168	Saccharomyces cerevisiae	hypothetical 102.3 kd protein in dal82-rfa2 intergenic region.
CONTIG5051	24414058_f3_6	1139	15242	852	284	P42842	188	1.3(10)-13	Saccharomyces cerevisiae	hypothetical 102.3 kd protein in dal82-rfa2 intergenic region.

CONTIG4412	4023262_f2_1	1140	15243	900	300	P42841	694	1.7(10)-68	Saccharomyces cerevisiae	hypothetical trp-asp repeats containing protein in hxt14-pha2 intergenic region.
CONTIG4733	626953_c2_8	1141	15244	828	276	P42840	623	5.7(10)-61	Saccharomyces cerevisiae	hypothetical 32.3 kd protein in kre1-hxt14 intergenic region.
CONTIG5471	10048888_c3_27	1142	15245	2172	724	P42839	1054	1.6(10)-162	Saccharomyces cerevisiae	hypothetical 102.5 kd protein in kre1-hxt14 intergenic region.
CONTIG978	4884842_c1_4	1143	15246	705	235	P42839	139	8.4(10)-7	Saccharomyces cerevisiae	hypothetical 102.5 kd protein in kre1-hxt14 intergenic region.
CONTIG5583	2149086_f1_5	1144	15247	1041	347	P42838	457	2.2(10)-43	Saccharomyces cerevisiae	hypothetical 47.4 kd protein in egl2-kre1 intergenic region.
CONTIG5428	4062625_c2_15	1145	15248	1170	390	P42836	452	2.1(10)-55	Saccharomyces cerevisiae	hypothetical 39.2 kd protein in egl2-kre1 intergenic region.
CONTIG1533	191436_f3_1	1146	15249	447	149	P42834	278	2.1(10)-24	Saccharomyces cerevisiae	hypothetical 16.5 kd protein in pas8-egl2 intergenic region.
CONTIG5128	4491257_c1_8	1147	15250	2106	702	P40345	1457	2.3(10)-149	Saccharomyces cerevisiae	hypothetical 75.4 kd protein in vps27-cse2 intergenic region.
CONTIG5440	1260937_c3_16	1148	15251	1338	446	P53720	729	3.2(10)-72	Saccharomyces cerevisiae	hypothetical 42.8 kd protein in urk1-fas3 intergenic region.
CONTIG465	21757680_c1_3	1149	15252	591	197	P53721	329	8.1(10)-30	Saccharomyces cerevisiae	hypothetical 25.3 kd protein in tim23-are2 intergenic region.
CONTIG594	27000305_c2_2	1150	15253	633	211	P53721	310	8.4(10)-28	Saccharomyces cerevisiae	hypothetical 25.3 kd protein in tim23-are2 intergenic region.
CONTIG4615	9804686_c3_10	1151	15254	792	264	P53722	688	7.4(10)-68	Saccharomyces cerevisiae	hypothetical 32.2 kd protein in are2-swp73 intergenic region.
CONTIG4775	3337567_f2_3	1152	15255	990	330	P53723	158	3.1(10)-9	Saccharomyces cerevisiae	hypothetical 47.1 kd protein in are2-swp73 intergenic region.
CONTIG4786	22464062_c1_5	1153	15256	921	307	P53727	530	4.0(10)-51	Saccharomyces cerevisiae	hypothetical 35.4 kd protein in sec12-ssk2 intergenic region.
CONTIG3533	26070926_f1_1	1154	15257	1047	349	P53729	744	8.5(10)-74	Saccharomyces cerevisiae	hypothetical 48.1 kd protein in sec12-ssk2 intergenic region.
CONTIG3533	1445337_c3_11	1155	15258	798	266	P53730	219	2.2(10)-26	Saccharomyces cerevisiae	hypothetical 62.7 kd protein in sec12-ssk2 intergenic region.

CONTIG3533	206877_c1_4	1156	15259	489	163	P53730	287	1.1(10)-24	Saccharomyces cerevisiae	hypothetical 62.7 kd protein in sec12-ssk2 intergenic region.
CONTIG878	24642811_c1_3	1157	15260	639	213	P53730	109	0.00025	Saccharomyces cerevisiae	hypothetical 62.7 kd protein in sec12-ssk2 intergenic region.
CONTIG1854	33672643_c2_3	1158	15261	186	62	P53731	133	2.2(10)-8	Saccharomyces cerevisiae	hypothetical 39.6 kd protein in sol1-coq2 intergenic region.
CONTIG4234	10581436_f2_2	1159	15262	378	126	P53731	178	2.5(10)-13	Saccharomyces cerevisiae	hypothetical 39.6 kd protein in sol1-coq2 intergenic region.
CONTIG3548	9774157_f1_1	1160	15263	1281	427	P53734	604	5.9(10)-59	Saccharomyces cerevisiae	putative alp-dependent ma helicase ynf038w.
CONTIG5748	4766925_c1_17	1161	15264	2070	690	P53735	338	2.7(10)-39	Saccharomyces cerevisiae	hypothetical 67.5 kd protein in sol1-coq2 intergenic region.
CONTIG4829	9844140_c1_8	1162	15265	537	179	P53738	441	1.1(10)-41	Saccharomyces cerevisiae	hypothetical 15.1 kd protein in pet494-msol1 intergenic region.
CONTIG4892	12109750_c2_7	1163	15266	1899	633	P53741	157	4.0(10)-20	Saccharomyces cerevisiae	hypothetical 57.7 kd protein in lys9-pop2 intergenic region.
CONTIG3748	22464212_f1_1	1164	15267	1032	344	P53742	1043	1.8(10)-105	Saccharomyces cerevisiae	hypothetical gip-binding protein in pop2-hol1 intergenic region.
CONTIG5585	35807757_c3_22	1165	15268	396	132	P53742	231	1.0(10)-18	Saccharomyces cerevisiae	hypothetical gip-binding protein in pop2-hol1 intergenic region.
CONTIG1293	22445130_c1_3	1166	15269	222	74	P53743	90	0.001	Saccharomyces cerevisiae	hypothetical 36.4 kd protein in pop2-hol1 intergenic region.
CONTIG3486	6067576_c2_6	1167	15270	915	305	P53743	421	1.5(10)-39	Saccharomyces cerevisiae	hypothetical 36.4 kd protein in pop2-hol1 intergenic region.
CONTIG4659	20081903_f1_2	1168	15271	1065	355	P53753	161	1.3(10)-10	Saccharomyces cerevisiae	hypothetical 121.1 kd protein in bio3-hxt17 intergenic region precursor.
CONTIG4659	3143811_f2_4	1169	15272	426	142	P53753	151	1.6(10)-9	Saccharomyces cerevisiae	hypothetical 121.1 kd protein in bio3-hxt17 intergenic region precursor.
CONTIG5454	24489188_c2_9	1170	15273	2985	995	P53753	1907	4.9(10)-197	Saccharomyces cerevisiae	hypothetical 121.1 kd protein in bio3-hxt17 intergenic region precursor.

CONTIG37355	9875932_f1_1	1171	15274	282	94	P41318	261	1.3(10)-22	Saccharomyces cerevisiae	hypothetical trp-asp repeats containing protein in sisl-imp12 intergenic region.
CONTIG3666	21882817_c2_5	1172	15275	498	166	P41318	681	4.0(10)-67	Saccharomyces cerevisiae	hypothetical trp-asp repeats containing protein in sisl-imp12 intergenic region.
CONTIG970	14540932_c3_4	1173	15276	585	195	P53981	489	9.0(10)-47	Saccharomyces cerevisiae	hypothetical 27.5 kd protein in spo1-sisl intergenic region.
CONTIG1883	4947952_f3_1	1174	15277	819	273	P53980	330	6.4(10)-30	Saccharomyces cerevisiae	hypothetical 49.9 kd protein in spo1-sisl intergenic region.
CONTIG2980	4589591_c1_4	1175	15278	1410	470	P53973	442	7.0(10)-52	Saccharomyces cerevisiae	hypothetical 80.1 kd protein in ume3-pub1 intergenic region.
CONTIG1632	16229149_c1_1	1176	15279	1158	386	P53973	1007	1.2(10)-101	Saccharomyces cerevisiae	hypothetical 80.1 kd protein in ume3-pub1 intergenic region.
CONTIG4709	3761_f2_6	1177	15280	1065	355	P53972	569	3.0(10)-55	Saccharomyces cerevisiae	hypothetical 56.2 kd protein in ume3-pub1 intergenic region.
CONTIG4709	5104026_f3_10	1178	15281	213	71	P53972	111	1.0(10)-5	Saccharomyces cerevisiae	hypothetical 56.2 kd protein in ume3-pub1 intergenic region.
CONTIG5396	3954062_f2_3	1179	15282	846	282	P53971	434	6.9(10)-40	Saccharomyces cerevisiae	hypothetical 108.5 kd protein in ume3-pub1 intergenic region.
CONTIG5396	21729527_f2_4	1180	15283	1725	575	P53971	774	5.7(10)-77	Saccharomyces cerevisiae	hypothetical 108.5 kd protein in ume3-pub1 intergenic region.
CONTIG4331	1067693_f1_1	1181	15284	708	236	P53969	316	3.2(10)-28	Saccharomyces cerevisiae	hypothetical 54.4 kd protein in hhr2-ume3 intergenic region.
CONTIG5534	4485688_f2_3	1182	15285	1134	378	P53965	591	1.3(10)-57	Saccharomyces cerevisiae	hypothetical 32.8 kd protein in nce3-hhr2 intergenic region.
CONTIG3366	5266910_f2_1	1183	15286	1092	364	P53962	661	5.4(10)-65	Saccharomyces cerevisiae	hypothetical 43.8 kd protein in nce3-hhr2 intergenic region.
CONTIG5549	959712_c1_4	1184	15287	1206	402	P53960	490	7.0(10)-47	Saccharomyces cerevisiae	hypothetical 51.0 kd protein in yip3-ttc5 intergenic region.
CONTIG5326	1957251_f1_3	1185	15288	2358	786	P53959	441	1.7(10)-50	Saccharomyces cerevisiae	hypothetical 97.0 kd protein in yip3-ttc5 intergenic region.
CONTIG436	10751711_f3_3	1186	15289	660	220	P53958	135	1.8(10)-8	Saccharomyces cerevisiae	hypothetical 43.7 kd protein in yip3-ttc5 intergenic region.

CONTIG914	22304536_f2_2	1187	15290	597	199	P53958	103	0.0033	Saccharomyces cerevisiae	hypothetical 43.7 kd protein in yip3-tfc5 intergenic region.
CONTIG4265	25507687_f2_1	1188	15291	282	94	P53953	198	1.1(10)-14	Saccharomyces cerevisiae	hypothetical 98.9 kd protein in cox5a-yip3 intergenic region.
CONTIG5386	33240886_f1_2	1189	15292	348	116	P53952	114	1.7(10)-6	Saccharomyces cerevisiae	hypothetical 31.4 kd protein in cox5a-yip3 intergenic region.
CONTIG22	22147827_c1_2	1190	15293	474	158	P53951	245	1.3(10)-20	Saccharomyces cerevisiae	hypothetical 45.6 kd protein in cox5a-yip3 intergenic region.
CONTIG4265	34375337_c1_3	1191	15294	1137	379	P53951	288	1.8(10)-25	Saccharomyces cerevisiae	hypothetical 45.6 kd protein in cox5a-yip3 intergenic region.
CONTIG4061	23629662_c1_6	1192	15295	2094	698	P53950	177	6.4(10)-10	Saccharomyces cerevisiae	hypothetical 128.1 kd protein in omp2-msg5 intergenic region.
CONTIG5770	22767181_c2_30	1193	15296	783	261	P53949	210	6.2(10)-31	Saccharomyces cerevisiae	hypothetical 22.5 kd protein in nop2-omp2 intergenic region.
CONTIG3682	23847625_f2_3	1194	15297	345	115	P53944	259	2.1(10)-22	Saccharomyces cerevisiae	hypothetical 35.9 kd protein in mas5-gcd10 intergenic region.
CONTIG4208	24431686_c2_6	1195	15298	744	248	P53941	820	7.5(10)-82	Saccharomyces cerevisiae	hypothetical 33.5 kd protein in mks1-msk1 intergenic region.
CONTIG4734	20391382_f1_1	1196	15299	1428	476	P53938	251	9.3(10)-39	Saccharomyces cerevisiae	hypothetical 41.7 kd protein in pms1-tpm1 intergenic region.
CONTIG3292	4303311_f2_1	1197	15300	534	178	P48233	151	5.2(10)-10	Saccharomyces cerevisiae	putative mitochondrial carrier ynl083w.
CONTIG3292	1226412_f3_3	1198	15301	987	329	P48233	385	7.0(10)-63	Saccharomyces cerevisiae	putative mitochondrial carrier ynl083w.
blx16339.x	14658431_c3_3	1199	15302	567	189	P48231	286	7.0(10)-24	Saccharomyces cerevisiae	hypothetical 132.5 kd protein in top2-mkt1 intergenic region.
CONTIG5614	14652161_f3_16	1200	15303	1185	395	P53934	484	3.1(10)-46	Saccharomyces cerevisiae	hypothetical 45.5 kd protein in ypi53-rho2 intergenic region.
CONTIG4999	13907792_c1_7	1201	15304	573	191	P53932	369	2.0(10)-33	Saccharomyces cerevisiae	hypothetical 71.2 kd protein in ras2-yip53 intergenic region.
CONTIG2241	480207_f2_1	1202	15305	792	264	P50947	262	1.0(10)-22	Saccharomyces cerevisiae	hypothetical 37.0 kd protein in ras2-yip53 intergenic region.
CONTIG377	4803150_f1_1	1203	15306	657	219	P50947	144	3.2(10)-22	Saccharomyces cerevisiae	hypothetical 37.0 kd protein in ras2-yip53 intergenic region.

CONTIG3056	24391087_f2_3	1204	15307	198	66	P50946	123	1.2(10)-7	Saccharomyces cerevisiae	hypothetical 27.2 kd protein in pol1-ras2 intergenic region.
b2x13866.x	10833318_f1_1	1205	15308	600	200	P50946	372	2.2(10)-34	Saccharomyces cerevisiae	hypothetical 27.2 kd protein in pol1-ras2 intergenic region.
CONTIG5369	5275330_c1_7	1206	15309	564	188	P53929	253	9.1(10)-22	Saccharomyces cerevisiae	hypothetical 30.7 kd protein in cyb5-leu4 intergenic region.
CONTIG1997	23991322_c3_9	1207	15310	252	84	P53925	156	2.2(10)-10	Saccharomyces cerevisiae	hypothetical 74.0 kd protein in mls1-rpc19 intergenic region.
b2x12719.x	20709391_c2_4	1208	15311	837	279	P53925	324	1.7(10)-28	Saccharomyces cerevisiae	hypothetical 74.0 kd protein in mls1-rpc19 intergenic region.
CONTIG1997	5100062_c1_7	1209	15312	1140	380	P53924	646	2.1(10)-63	Saccharomyces cerevisiae	hypothetical 57.6 kd protein in mls1-rpc19 intergenic region.
CONTIG3152	24414067_c1_6	1210	15313	561	187	P53923	175	1.3(10)-12	Saccharomyces cerevisiae	hypothetical 56.5 kd protein in tom70-psu1 intergenic region.
CONTIG5813	25673831_f1_1	1211	15314	327	109	P53923	115	3.8(10)-6	Saccharomyces cerevisiae	hypothetical 56.5 kd protein in tom70-psu1 intergenic region.
CONTIG3997	406311_c3_9	1212	15315	321	107	P53921	103	7.2(10)-6	Saccharomyces cerevisiae	hypothetical 13.2 kd protein in spe98-tom70 intergenic region.
CONTIG1346	25416578_f3_2	1213	15316	801	267	P53920	586	2.8(10)-56	Saccharomyces cerevisiae	hypothetical 110.9 kd protein in spe98-tom70 intergenic region.
CONTIG3997	2244792_f3_3	1214	15317	639	213	P53920	395	1.1(10)-35	Saccharomyces cerevisiae	hypothetical 110.9 kd protein in spe98-tom70 intergenic region.
b9x13c42.x	11142039_c2_4	1215	15318	846	282	P53920	886	7.7(10)-89	Saccharomyces cerevisiae	hypothetical 110.9 kd protein in spe98-tom70 intergenic region.
CONTIG3662	16603325_f1_1	1216	15319	1857	619	P53919	293	5.4(10)-24	Saccharomyces cerevisiae	hypothetical 54.9 kd protein in spe98-tom70 intergenic region.
CONTIG3543	29336061_c2_1	1217	15320	2040	680	P53917	220	1.3(10)-30	Saccharomyces cerevisiae	hypothetical 109.8 kd protein in cpl1-spe98 intergenic region.
b1x18806.y	25673905_f2_1	1218	15321	459	153	P53917	199	1.0(10)-14	Saccharomyces cerevisiae	hypothetical 109.8 kd protein in cpl1-spe98 intergenic region.
CONTIG5590	100757_f1_2	1219	15322	804	268	P53915	396	6.5(10)-37	Saccharomyces cerevisiae	hypothetical 27.7 kd protein in cpl1-spe98 intergenic region.
CONTIG5590	863500_c3_21	1220	15323	1263	421	P53914	1232	1.7(10)-125	Saccharomyces cerevisiae	hypothetical 119.3 kd protein in fpl1-tom22 intergenic region.

CONTIG5590	23728402_c3_20	1221	15324	1869	623	P53914	2387	6.7(10)-248	Saccharomyces cerevisiae	hypothetical 119.3 kd protein in fpr1-tom22 intergenic region.
CONTIG680	973563_c3_2	1222	15325	396	132	P53914	349	1.1(10)-30	Saccharomyces cerevisiae	hypothetical 119.3 kd protein in fpr1-tom22 intergenic region.
CONTIG1460	12156511_c3_3	1223	15326	621	207	P53912	286	2.8(10)-25	Saccharomyces cerevisiae	hypothetical 41.2 kd protein in fpr1-tom22 intergenic region.
CONTIG2525	20392877_f1_1	1224	15327	1161	387	P53912	396	6.5(10)-37	Saccharomyces cerevisiae	hypothetical 41.2 kd protein in fpr1-tom22 intergenic region.
CONTIG4017	12156511_c1_6	1225	15328	1128	376	P53912	455	3.6(10)-43	Saccharomyces cerevisiae	hypothetical 41.2 kd protein in fpr1-tom22 intergenic region.
CONTIG5493	4891938_f1_2	1226	15329	1005	335	P53912	429	2.1(10)-40	Saccharomyces cerevisiae	hypothetical 41.2 kd protein in fpr1-tom22 intergenic region.
CONTIG2675	1181250_c2_2	1227	15330	1110	370	P53907	102	7.5(10)-6	Saccharomyces cerevisiae	hypothetical 84.2 kd protein in mfa2-mep2 intergenic region.
CONTIG387	1181250_c3_6	1228	15331	606	202	P53907	103	0.0047	Saccharomyces cerevisiae	hypothetical 84.2 kd protein in mfa2-mep2 intergenic region.
CONTIG5721	10820938_f3_16	1229	15332	231	77	P53905	196	1.0(10)-15	Saccharomyces cerevisiae	hypothetical 12.1 kd protein in rpe8-mfa2 intergenic region.
CONTIG3225	9771875_c3_3	1230	15333	873	291	P53901	202	9.5(10)-16	Saccharomyces cerevisiae	hypothetical 46.2 kd protein in yek2-rpe8 intergenic region.
CONTIG5745	23913250_c1_12	1231	15334	423	141	P53900	269	1.8(10)-23	Saccharomyces cerevisiae	hypothetical 15.2 kd protein in yek2-rpe8 intergenic region.
CONTIG4959	14573311_f1_1	1232	15335	963	321	P53899	197	4.4(10)-32	Saccharomyces cerevisiae	hypothetical 31.5 kd protein in yep1-yek2 intergenic region.
CONTIG4351	3912512_c1_3	1233	15336	1023	341	P53898	106	9.0(10)-6	Saccharomyces cerevisiae	hypothetical 33.7 kd protein in yep1-yek2 intergenic region.
CONTIG5490	6929636_f3_6	1234	15337	411	137	P53897	171	4.5(10)-13	Saccharomyces cerevisiae	hypothetical 18.1 kd protein in yep1-yek2 intergenic region.
CONTIG4149	3926537_c1_3	1235	15338	1110	370	P53890	112	0.00075	Saccharomyces cerevisiae	hypothetical 49.7 kd protein in sko1-rpl44a intergenic region.
CONTIG5109	23634682_f2_5	1236	15339	879	293	P53881	460	1.1(10)-43	Saccharomyces cerevisiae	hypothetical 34.9 kd protein in rps3-psd1 intergenic region.
CONTIG5681	34189038_c3_17	1237	15340	1512	504	P53878	878	5.4(10)-88	Saccharomyces cerevisiae	hypothetical 46.5 kd protein in npr1-rps3 intergenic region.

CONTIG5681	3164067_fl_2	1238	15341	1698	566	P53877	385	3.2(10)-42	Saccharomyces cerevisiae	hypothetical 61.8 kd protein in npr1-rps3 intergenic region.
CONTIG624	23488576_c1_3	1239	15342	351	117	P53872	149	9.6(10)-11	Saccharomyces cerevisiae	hypothetical 22.0 kd protein in chs1-srp1 intergenic region.
b2x18227.x	36425626_fl_1	1240	15343	537	179	P53871	504	2.2(10)-48	Saccharomyces cerevisiae	hypothetical 40.2 kd protein in chs1-srp1 intergenic region.
CONTIG3186	2738942_c3_5	1241	15344	1074	358	P53870	130	1.8(10)-5	Saccharomyces cerevisiae	hypothetical 63.9 kd protein in whi3-chs1 intergenic region.
CONTIG5496	134512_c1_13	1242	15345	600	200	P53870	124	8.0(10)-6	Saccharomyces cerevisiae	hypothetical 63.9 kd protein in whi3-chs1 intergenic region.
CONTIG1744	286441_fl_1	1243	15346	471	157	P40165	216	7.7(10)-18	Saccharomyces cerevisiae	hypothetical 27.5 kd protein in spx19-gcr2 intergenic region.
CONTIG5321	32245432_c1_23	1244	15347	1347	449	P40160	1235	8.0(10)-126	Saccharomyces cerevisiae	hypothetical 49.1 kd protein in ssb2-spx18 intergenic region.
CONTIG2114	7083431_fl_1	1245	15348	525	175	P40157	348	7.4(10)-31	Saccharomyces cerevisiae	hypothetical 88.8 kd protein in rap1-mer1 intergenic region.
CONTIG2947	24273962_c1_8	1246	15349	1269	423	P40157	424	4.2(10)-39	Saccharomyces cerevisiae	hypothetical 88.8 kd protein in rap1-mer1 intergenic region.
CONTIG5440	4882000_c3_19	1247	15350	498	166	P40156	151	5.9(10)-11	Saccharomyces cerevisiae	hypothetical 25.3 kd protein in rap1-mer1 intergenic region.
CONTIG227	25656687_c3_4	1248	15351	834	278	P40154	148	4.4(10)-10	Saccharomyces cerevisiae	hypothetical 36.2 kd protein in rap1-mer1 intergenic region.
CONTIG3868	22297055_c3_7	1249	15352	1002	334	P40154	161	1.6(10)-11	Saccharomyces cerevisiae	hypothetical 36.2 kd protein in rap1-mer1 intergenic region.
CONTIG5666	21603427_fl_4	1250	15353	2040	680	P40151	996	1.7(10)-100	Saccharomyces cerevisiae	hypothetical 66.5 kd protein in ade12-rap1 intergenic region.
CONTIG4979	14176300_f3_8	1251	15354	735	245	P53867	214	8.0(10)-17	Saccharomyces cerevisiae	hypothetical 56.6 kd protein in ure2-ssu72 intergenic region.
CONTIG4979	20119176_fl_3	1252	15355	696	232	P53867	285	1.3(10)-24	Saccharomyces cerevisiae	hypothetical 56.6 kd protein in ure2-ssu72 intergenic region.
CONTIG3425	26230450_f2_1	1253	15356	1353	451	P53866	195	1.6(10)-23	Saccharomyces cerevisiae	hypothetical 86.9 kd protein in ure2-ssu72 intergenic region.
CONTIG5475	9932211_c2_13	1254	15357	1008	336	P53859	387	5.7(10)-36	Saccharomyces cerevisiae	hypothetical 31.6 kd protein in sin4-ure2 intergenic region.

CONTIG5329	480202_c3_10	1255	15358	2961	987	P53858	119	0.00169	Saccharomyces cerevisiae	hypothetical 100.6 kd protein in sin4-ure2 intergenic region.
CONTIG5475	12600775_c3_14	1256	15359	630	210	P53858	254	1.2(10)-20	Saccharomyces cerevisiae	hypothetical 100.6 kd protein in sin4-ure2 intergenic region.
CONTIG4247	5276580_c1_3	1257	15360	849	283	P53857	291	8.6(10)-26	Saccharomyces cerevisiae	hypothetical 47.8 kd protein in sin4-ure2 intergenic region.
CONTIG2129	21516953_f2_1	1258	15361	1791	597	P23503	392	2.8(10)-60	Saccharomyces cerevisiae	hypothetical 54.2 kd protein in zwf1-b1h1/lap3 intergenic region.
CONTIG3387	16492692_c2_2	1259	15362	1167	389	P53855	588	7.0(10)-56	Saccharomyces cerevisiae	hypothetical 178.4 kd protein in sla2-zwf1 intergenic region.
CONTIG3704	21578452_c2_5	1260	15363	684	228	P53855	114	0.00079	Saccharomyces cerevisiae	hypothetical 178.4 kd protein in sla2-zwf1 intergenic region.
CONTIG4992	25470067_f3_5	1261	15364	2769	923	P53855	109	4.7(10)-5	Saccharomyces cerevisiae	hypothetical 178.4 kd protein in sla2-zwf1 intergenic region.
CONTIG3027	16829055_c3_5	1262	15365	471	157	P53854	135	2.8(10)-9	Saccharomyces cerevisiae	hypothetical 20.4 kd protein in rpa49-sui1 intergenic region.
CONTIG2965	26265885_f3_2	1263	15366	501	167	P53853	161	7.0(10)-12	Saccharomyces cerevisiae	hypothetical 30.6 kd protein in rpa49-sui1 intergenic region.
CONTIG5793	4820262_c3_25	1264	15367	1197	399	P53850	144	9.4(10)-9	Saccharomyces cerevisiae	hypothetical 46.2 kd protein in sip3-mnp130 intergenic region.
CONTIG763	19725013_f1_1	1265	15368	666	222	P53847	108	0.00239	Saccharomyces cerevisiae	hypothetical 88.1 kd protein in atx1-sip3 intergenic region.
CONTIG1975	20319632_c1_4	1266	15369	726	242	P34624	130	5.7(10)-6	Caenorhabditis elegans	hypothetical 63.5 kd protein zks353.1 in chromosome iii.
CONTIG5479	2833500_f2_4	1267	15370	1035	345	P17778	111	0.00119	Yersinia pestis	outer membrane protein yopm.
CONTIG833	19666391_f1_1	1268	15371	1200	400	P30638	145	4.2(10)-7	Caenorhabditis elegans	hypothetical 59.1 kd protein zks637.1 in chromosome iii.
CONTIG4986	194813_f3_6	1269	15372	183	61	P29953	100	1.5(10)-5	Sinorhizobium meliloti	hypothetical 18.2 kd protein in pmi5'region (orf1).
CONTIG4923	882807_c2_8	1270	15373	747	249	P43132	212	2.2(10)-28	Saccharomyces cerevisiae	hypothetical protein in ppr1 5'region (orf3) (fragment).
CONTIG1991	10828561_f1_1	1271	15374	912	304	Q09625	101	0.0061	Caenorhabditis elegans	hypothetical 84.3 kd protein zks945.10 in chromosome ii.

CONTIG3059	25399051_c1_7	1272	15375	933	311	Q09625	91	0.28	Caenorhabditis elegans	hypothetical 84.3 kd protein zK945.10 in chromosome ii.
CONTIG2909	134687_f3_3	1273	15376	192	64	P38374	140	8.6(10)-10	Saccharomyces cerevisiae	ysy6 protein.
CONTIG5399	26597138_f3_10	1274	15377	576	192	P38428	176	1.3(10)-13	Saccharomyces cerevisiae	hypothetical 17.4 kd protein in tps3 5'region (orf1).
CONTIG4596	36611686_c3_11	1275	15378	1380	460	Q11157	238	2.0(10)-21	Mycobacterium tuberculosis	hypothetical 57.3 kd protein gmc-type oxidoreductase cy20g9.18c.
CONTIG5510	4956886_f3_12	1276	15379	696	232	Q10532	227	2.8(10)-18	Mycobacterium tuberculosis	probable monooxygenase mtey31.20 (ec 1.14.13.-).
CONTIG3344	11961463_f2_1	1277	15380	1929	643	P47732	150	1.7(10)-8	Chilo iridescent virus	zinc finger protein.
CONTIG5374	79715_c3_11	1278	15381	204	68	Q07844	105	9.3(10)-5	Saccharomyces cerevisiae	hypothetical 93.1 kd protein yll034c.
CONTIG1736	3907762_f2_1	1279	15382	399	133	Q04749	149	6.5(10)-10	Saccharomyces cerevisiae	hypothetical 47.1 kd protein in ncal-hms1 intergenic region.
CONTIG1840	1229032_c2_2	1280	15383	1302	434	Q04749	211	1.1(10)-14	Saccharomyces cerevisiae	hypothetical 47.1 kd protein in ncal-hms1 intergenic region.
CONTIG5308	19573286_f3_8	1281	15384	939	313	Q00314	1088	3.0(10)-110	Candida albicans	vanadate resistance protein.
CONTIG3859	4954510_f2_2	1282	15385	552	184	Q00614	733	1.3(10)-72	Candida tropicalis	carnitine o-acetyltransferase precursor (ec 2.3.1.7) (carnitine acetylase).
CONTIG3859	40117002_f1_1	1283	15386	933	311	Q00614	1371	3.1(10)-140	Candida tropicalis	carnitine o-acetyltransferase precursor (ec 2.3.1.7) (carnitine acetylase).
CONTIG4306	10625285_f3_3	1284	15387	243	81	Q00614	403	2.7(10)-37	Candida tropicalis	carnitine o-acetyltransferase precursor (ec 2.3.1.7) (carnitine acetylase).
CONTIG3855	24235927_f3_3	1285	15388	708	236	Q17391	279	2.0(10)-23	Caenorhabditis elegans	cul-3 protein.
CONTIG5274	7040968_f3_8	1286	15389	729	243	Q03529	482	5.0(10)-46	Saccharomyces cerevisiae	hypothetical 44.9 kd protein in ura10-nrc1 intergenic region.

CONTIG5274	5970340_f1_1	1287	15390	429	143	Q03529	435	4.7(10)-41	Saccharomyces cerevisiae	hypothetical 44.9 kd protein in ura1-0-nrc1 intergenic region.
CONTIG3166	6828532_c1_7	1288	15391	1527	509	Q62871	158	3.6(10)-8	Rattus norvegicus	dynein intermediate chain 2, cytosolic (dh ic-2).
CONTIG5734	4037755_c3_21	1289	15392	261	87	Q24117	278	2.1(10)-24	Drosophila melanogaster	dynein light chain 1, cytoplasmic.
CONTIG2780	9900317_f1_1	1290	15393	939	313	Q00310	1487	1.6(10)-152	Candida albicans	glycolipid 2-alpha-mannosyltransferase (ec 2.4.1.131) (alpha-1,2- mannosyltransferase).
CONTIG5223	23453407_f1_3	1291	15394	2538	846	Q04660	1512	2.8(10)-242	Saccharomyces cerevisiae	hypothetical trp-asp repeats containing protein in nup116-far3 intergenic region.
CONTIG5208	15021941_f2_5	1292	15395	1584	528	Q04225	1537	8.0(10)-158	Saccharomyces cerevisiae	hypothetical trp-asp repeats containing protein in pom152-rec114 intergenic region.
CONTIG2071	23985937_f2_1	1293	15396	864	288	Q10010	101	0.0032	Caenorhabditis elegans	hypothetical 26.6 kd protein t19c3.4 in chromosome iii.
CONTIG5431	22443787_c1_10	1294	15397	1584	528	Q03103	537	7.4(10)-52	Saccharomyces cerevisiae	hypothetical 65.0 kd protein in cox14 5'region precursor.
CONTIG3692	23444692_f3_4	1295	15398	669	223	Q03104	256	2.2(10)-21	Saccharomyces cerevisiae	hypothetical 59.6 kd protein in cox14-hmgs intergenic region.
b3x11010.x	29407627_c2_2	1296	15399	636	212	Q03104	180	4.0(10)-13	Saccharomyces cerevisiae	hypothetical 59.6 kd protein in cox14-hmgs intergenic region.
CONTIG5790	23625900_c2_24	1297	15400	1944	648	Q03124	198	4.7(10)-28	Saccharomyces cerevisiae	hypothetical 65.2 kd protein in cox14-hmgs intergenic region.
CONTIG5785	26266876_f3_19	1298	15401	1104	368	Q03210	100	0.029	Saccharomyces cerevisiae	hypothetical 57.7 kd protein in ndi1-ar1 intergenic region.
CONTIG4158	25492881_f2_3	1299	15402	1539	513	Q03735	387	1.1(10)-34	Saccharomyces cerevisiae	hypothetical 126.1 kd protein in ndi1-ar1 intergenic region.
CONTIG5322	78512_f1_3	1300	15403	1245	415	Q03750	128	2.2(10)-5	Saccharomyces cerevisiae	hypothetical 58.0 kd protein in van1-dat1 intergenic region.
CONTIG5790	1985062_c2_25	1301	15404	276	92	Q04493	166	1.5(10)-12	Saccharomyces cerevisiae	hypothetical 18.4 kd protein in rad10-prs4 intergenic region.

CONTIG3067	33632692_c3_9	1302	15405	1746	582	Q04500	605	1.2(10)-104	Saccharomyces cerevisiae	hypothetical 103.0 kd protein in rad10-prs4 intergenic region.
CONTIG5172	34103430_fl_2	1303	15406	1434	478	Q04511	200	8.3(10)-13	Saccharomyces cerevisiae	hypothetical 76.9 kd protein in rpm2-tub1 intergenic region.
CONTIG3610	21484517_c2_8	1304	15407	546	182	Q03630	152	4.7(10)-11	Saccharomyces cerevisiae	hypothetical 18.4 kd protein in cpr3-hmg1 intergenic region.
CONTIG3604	35180258_c1_7	1305	15408	744	248	Q03640	615	8.5(10)-59	Saccharomyces cerevisiae	hypothetical 17.1 kd protein in y16a-dak1 intergenic region.
CONTIG3938	24236061_c2_3	1306	15409	1512	504	Q04632	143	1.0(10)-6	Saccharomyces cerevisiae	hypothetical 69.8 kd protein in y16a-dak1 intergenic region.
CONTIG5538	1957043_c3_20	1307	15410	1521	507	Q04638	396	6.5(10)-37	Saccharomyces cerevisiae	hypothetical 54.1 kd protein in dak1-orc1 intergenic region.
CONTIG4112	21526632_c2_3	1308	15411	285	95	Q04651	140	4.2(10)-9	Saccharomyces cerevisiae	hypothetical 40.7 kd protein in dak1-orc1 intergenic region.
CONTIG5538	14730276_fl_5	1309	15412	594	198	Q04651	269	1.8(10)-23	Saccharomyces cerevisiae	hypothetical 40.7 kd protein in dak1-orc1 intergenic region.
CONTIG5804	4866442_f2_13	1310	15413	927	309	Q04658	166	4.5(10)-10	Saccharomyces cerevisiae	hypothetical 40.9 kd protein in dak1-orc1 intergenic region.
CONTIG1190	1190880_c3_2	1311	15414	603	201	Q04693	164	8.5(10)-11	Saccharomyces cerevisiae	hypothetical 153.8 kd protein in gal80-prp39 intergenic region.
CONTIG2411	20426300_c1_4	1312	15415	495	165	Q03697	149	7.0(10)-10	Saccharomyces cerevisiae	hypothetical 49.6 kd protein in cat2-and1 intergenic region.
CONTIG3113	24322033_c2_3	1313	15416	726	242	Q03705	179	6.4(10)-14	Saccharomyces cerevisiae	hypothetical 20.7 kd protein in cat2-and1 intergenic region.
CONTIG1146	23548550_c3_2	1314	15417	402	134	Q03707	247	3.7(10)-20	Saccharomyces cerevisiae	hypothetical 74.2 kd protein in and1-rad52 intergenic region.
blx19622.x	34160942_f3_2	1315	15418	429	143	Q03707	105	6.9(10)-5	Saccharomyces cerevisiae	hypothetical 74.2 kd protein in and1-rad52 intergenic region.
CONTIG3459	954431_c1_3	1316	15419	282	94	Q03712	167	1.2(10)-12	Saccharomyces cerevisiae	hypothetical 17.7 kd protein in and1-rad52 intergenic region.
CONTIG2638	409661_c2_6	1317	15420	447	149	Q03713	284	4.7(10)-25	Saccharomyces cerevisiae	hypothetical 18.5 kd protein in ndc1-tsai intergenic region.
CONTIG4246	20197175_c3_6	1318	15421	801	267	Q03722	123	3.2(10)-10	Saccharomyces cerevisiae	hypothetical 76.1 kd protein in ung1-psp2 intergenic region.

CONTIG4843	48637_f1_1	1319	15422	804	268	Q03722	417	1.6(10)-53	Saccharomyces cerevisiae	hypothetical 76.1 kd protein in ungl1-psp2 intergenic region.
CONTIG1350	32634401_f2_2	1320	15423	375	125	Q03723	108	1.2(10)-5	Saccharomyces cerevisiae	hypothetical 37.9 kd protein in ungl1-psp2 intergenic region.
CONTIG5667	270161_c3_23	1321	15424	1278	426	Q03730	561	2.1(10)-54	Saccharomyces cerevisiae	hypothetical 43.7 kd protein in ungl1-psp2 intergenic region.
CONTIG5626	9978387_c1_8	1322	15425	1779	593	Q04228	176	5.0(10)-12	Saccharomyces cerevisiae	hypothetical 66.8 kd protein in ppz1-sps5 intergenic region.
CONTIG2720	34610936_c2_3	1323	15426	1146	382	Q04235	557	5.5(10)-54	Saccharomyces cerevisiae	hypothetical 52.7 kd protein in pdf4-glo1 intergenic region.
CONTIG4496	14881563_f1_1	1324	15427	264	88	Q04257	132	2.0(10)-8	Saccharomyces cerevisiae	hypothetical 34.0 kd protein in glo1-yp17 intergenic region.
CONTIG4496	6020342_f2_3	1325	15428	1890	630	Q04263	371	2.0(10)-31	Saccharomyces cerevisiae	hypothetical 84.6 kd protein in glo1-yp17 intergenic region.
CONTIG304	878427_c1_1	1326	15429	504	168	Q03667	183	2.3(10)-14	Saccharomyces cerevisiae	hypothetical 16.7 kd protein in cdc5-mvp1 intergenic region.
CONTIG4412	7070337_c3_6	1327	15430	543	181	Q03677	473	4.5(10)-45	Saccharomyces cerevisiae	hypothetical 20.9 kd protein in plb1-hx12 intergenic region.
CONTIG2648	24816442_c2_3	1328	15431	291	97	Q03687	90	0.0015	Saccharomyces cerevisiae	hypothetical 46.9 kd protein in plb1-hx12 intergenic region.
CONTIG1044	10438137_f2_1	1329	15432	969	323	Q03690	178	2.3(10)-19	Saccharomyces cerevisiae	hypothetical 145.2 kd protein in hxl2-sec59 intergenic region.
CONTIG4741	34453912_f2_3	1330	15433	972	324	Q04347	124	1.2(10)-14	Saccharomyces cerevisiae	hypothetical 60.1 kd protein in sec59-erg5 intergenic region.
CONTIG4060	11932275_c2_4	1331	15434	1329	443	Q04371	854	1.8(10)-85	Saccharomyces cerevisiae	hypothetical 54.1 kd protein in mrp13-tap42 intergenic region.
CONTIG5334	23988281_c2_10	1332	15435	1779	593	Q05040	149	2.3(10)-7	Saccharomyces cerevisiae	hypothetical 59.3 kd protein in tap42-imp2 intergenic region.
CONTIG4931	10974010_f3_9	1333	15436	1242	414	Q05131	1170	6.2(10)-119	Saccharomyces cerevisiae	hypothetical 48.4 kd protein in tap42-imp2 intergenic region.
CONTIG5673	178188_f3_16	1334	15437	243	81	Q04212	192	6.0(10)-15	Saccharomyces cerevisiae	hypothetical 38.2 kd protein in sub1-argr1 intergenic region.
CONTIG2721	23925000_c2_8	1335	15438	867	289	Q04213	114	4.7(10)-5	Saccharomyces cerevisiae	hypothetical 55.4 kd protein in mcm1-nup116 intergenic region.

CONTIG3004	781630_f2_1	1336	15439	1434	478	Q04213	114	0.00048	Saccharomyces cerevisiae	hypothetical 55.4 kd protein in mcm1-nup116 intergenic region.
b9x10v23.x	20394062_f1_1	1337	15440	525	175	Q04213	112	2.2(10) ⁻¹⁴	Saccharomyces cerevisiae	hypothetical 55.4 kd protein in mcm1-nup116 intergenic region.
CONTIG3141	4100318_f1_1	1338	15441	921	307	Q04639	151	5.5(10) ⁻⁹	Saccharomyces cerevisiae	hypothetical 36.4 kd protein in nup116-far3 intergenic region.
CONTIG5130	15651077_c3_14	1339	15442	522	174	Q04767	424	7.0(10) ⁻⁴⁰	Saccharomyces cerevisiae	hypothetical 18.7 kd protein in hms1-abf2 intergenic region.
CONTIG5016	4065682_f2_2	1340	15443	1110	370	Q04779	233	2.7(10) ⁻²⁹	Saccharomyces cerevisiae	hypothetical 78.8 kd protein in abf2-chl12 intergenic region.
CONTIG5742	210838_c2_25	1341	15444	711	237	Q04264	324	6.9(10) ⁻²⁸	Saccharomyces cerevisiae	hypothetical 147.0 kd protein in abf2-chl12 intergenic region.
CONTIG5742	22351410_c1_20	1342	15445	2239	753	Q04264	812	2.7(10) ⁻⁸⁰	Saccharomyces cerevisiae	hypothetical 147.0 kd protein in abf2-chl12 intergenic region.
CONTIG5742	5136561_c2_24	1343	15446	798	266	Q04264	415	1.3(10) ⁻³⁷	Saccharomyces cerevisiae	hypothetical 147.0 kd protein in abf2-chl12 intergenic region.
CONTIG1154	34158377_c3_1	1344	15447	579	193	Q04305	516	1.2(10) ⁻⁴⁹	Saccharomyces cerevisiae	hypothetical 57.7 kd protein in aip1-ctf13 intergenic region.
CONTIG2587	4064188_f3_4	1345	15448	240	80	Q04305	161	4.5(10) ⁻¹¹	Saccharomyces cerevisiae	hypothetical 57.7 kd protein in aip1-ctf13 intergenic region.
CONTIG2587	4776637_f2_2	1346	15449	555	185	Q04305	227	3.2(10) ⁻¹⁸	Saccharomyces cerevisiae	hypothetical 57.7 kd protein in aip1-ctf13 intergenic region.
CONTIG4456	781250_f3_6	1347	15450	1237	419	Q03151	580	2.1(10) ⁻⁵⁶	Saccharomyces cerevisiae	hypothetical 42.1 kd protein in ctf13-ypk2 intergenic region.
CONTIG1690	6892876_f1_1	1348	15451	873	291	Q03153	202	2.3(10) ⁻¹⁵	Saccharomyces cerevisiae	hypothetical 70.4 kd protein in ctf13-ypk2 intergenic region.
CONTIG5282	2145292_c3_12	1349	15452	915	305	Q03161	909	2.7(10) ⁻⁹¹	Saccharomyces cerevisiae	hypothetical 34.0 kd protein in ctf13-ypk2 intergenic region.
CONTIG5465	13863177_f2_2	1350	15453	1989	663	Q03162	413	2.2(10) ⁻⁵²	Saccharomyces cerevisiae	hypothetical 72.2 kd protein in ctf13-ypk2 intergenic region.
CONTIG1456	35979055_c1_4	1351	15454	582	194	Q99278	112	8.0(10) ⁻⁷	Saccharomyces cerevisiae	hypothetical 15.2 kd protein in itv2-ade17 intergenic region.
CONTIG5205	4065662_f3_2	1352	15455	1674	558	Q04472	412	1.0(10) ⁻⁵¹	Saccharomyces cerevisiae	hypothetical 58.0 kd protein in itv2-ade17 intergenic region.

CONTIG4176	14221890_f3_3	1353	15456	1041	347	Q04223	323	3.5(10)-29	Saccharomyces cerevisiae	hypothetical 35.3 kd protein in pom152-rec114 intergenic region.
CONTIG4201	25788432_f2_1	1354	15457	1743	581	Q03795	352	1.6(10)-57	Saccharomyces cerevisiae	hypothetical 60.0 kd protein in impl-hlj1 intergenic region.
CONTIG4237	2938801_c2_8	1355	15458	663	221	Q03795	127	4.2(10)-6	Saccharomyces cerevisiae	hypothetical 60.0 kd protein in impl-hlj1 intergenic region.
CONTIG4477	13750157_c2_14	1356	15459	894	298	Q03798	131	1.8(10)-6	Saccharomyces cerevisiae	hypothetical 29.1 kd protein in impl-hlj1 intergenic region.
CONTIG4477	20354682_f2_4	1357	15460	183	61	Q03799	96	4.0(10)-5	Saccharomyces cerevisiae	hypothetical 17.5 kd protein in impl-hlj1 intergenic region.
CONTIG4477	33476001_f1_2	1358	15461	372	124	Q03799	263	8.0(10)-23	Saccharomyces cerevisiae	hypothetical 17.5 kd protein in impl-hlj1 intergenic region.
CONTIG5731	22457807_f3_12	1359	15462	1608	536	Q03212	597	3.2(10)-58	Saccharomyces cerevisiae	hypothetical 62.5 kd protein in ald5-ddf48 intergenic region.
CONTIG5790	3145661_f3_17	1360	15463	1221	407	Q03214	215	6.4(10)-22	Saccharomyces cerevisiae	hypothetical 162.7 kd protein in sip18-spt21 intergenic region.
CONTIG2867	33203900_f2_2	1361	15464	939	313	Q03218	289	5.0(10)-25	Saccharomyces cerevisiae	hypothetical 56.2 kd protein in sip18-spt21 intergenic region.
CONTIG2412	29332563_f2_4	1362	15465	606	202	Q03219	207	6.9(10)-17	Saccharomyces cerevisiae	hypothetical 31.1 kd protein in sip18-spt21 intergenic region.
CONTIG2417	45585506_c2_3	1363	15466	366	122	Q03219	122	2.2(10)-7	Saccharomyces cerevisiae	hypothetical 31.1 kd protein in sip18-spt21 intergenic region.
CONTIG5818	214453_f3_26	1364	15467	2700	900	Q12751	574	7.5(10)-89	Saccharomyces cerevisiae	hypothetical 113.2 kd protein in ss02-hsc82 intergenic region.
CONTIG5344	4803260_f3_9	1365	15468	2337	779	Q04336	1823	3.2(10)-254	Saccharomyces cerevisiae	hypothetical 126.6 kd protein in rp139-cik1 intergenic region.
CONTIG5344	24651577_f1_2	1366	15469	963	321	Q04336	586	4.2(10)-56	Saccharomyces cerevisiae	hypothetical 126.6 kd protein in rp139-cik1 intergenic region.
CONTIG5723	2750511_c2_24	1367	15470	633	211	Q03691	398	4.0(10)-37	Saccharomyces cerevisiae	hypothetical 28.9 kd protein in cln1-rad14 intergenic region.
CONTIG699	24320282_c3_5	1368	15471	1017	339	Q03694	122	5.2(10)-5	Saccharomyces cerevisiae	hypothetical 47.3 kd protein in tom40-pfk2 intergenic region.
CONTIG3934	182156_c2_6	1369	15472	624	208	Q03648	256	1.5(10)-21	Saccharomyces cerevisiae	hypothetical 52.2 kd protein in rar1-scl1 intergenic region.

CONTIG5497	2907513_f2_3	1370	15473	1716	572	Q03652	183	1.6(10)-18	Saccharomyces cerevisiae	hypothetical 55.3 kd protein in rar1-sci1 intergenic region.
CONTIG1993	2112625_f2_1	1371	15474	1185	395	Q03653	115	0.00169	Saccharomyces cerevisiae	hypothetical 89.2 kd protein in rar1-sci1 intergenic region.
CONTIG5315	2906375_c3_15	1372	15475	261	87	Q03653	106	6.7(10)-5	Saccharomyces cerevisiae	hypothetical 89.2 kd protein in rar1-sci1 intergenic region.
CONTIG5134	4376436_f2_1	1373	15476	3180	1060	Q03660	174	2.8(10)-28	Saccharomyces cerevisiae	hypothetical 128.1 kd protein in gual-erg8 intergenic region.
CONTIG1641	25673931_f2_2	1374	15477	729	243	Q04991	568	3.7(10)-55	Saccharomyces cerevisiae	hypothetical 56.2 kd protein in erg8-mre11 intergenic region.
CONTIG2874	414026_c3_7	1375	15478	1059	353	Q04991	568	3.7(10)-55	Saccharomyces cerevisiae	hypothetical 56.2 kd protein in erg8-mre11 intergenic region.
b9x10437.x	10676260_f3_2	1376	15479	537	179	Q04991	389	3.6(10)-36	Saccharomyces cerevisiae	hypothetical 56.2 kd protein in erg8-mre11 intergenic region.
CONTIG4948	23867062_f2_5	1377	15480	507	169	Q05024	200	3.7(10)-16	Saccharomyces cerevisiae	hypothetical 26.5 kd protein in fus2-rml1 intergenic region.
CONTIG4452	1300025_c1_7	1378	15481	1509	503	Q05031	1260	1.8(10)-128	Saccharomyces cerevisiae	hypothetical 50.5 kd protein in mal1-rml1 intergenic region.
CONTIG5397	23525262_c2_19	1379	15482	909	303	Q04013	1128	1.8(10)-114	Saccharomyces cerevisiae	hypothetical 34.2 kd protein in cus1-rpl18a1 intergenic region.
CONTIG2938	25582885_c3_7	1380	15483	1455	485	Q04781	657	2.8(10)-63	Saccharomyces cerevisiae	hypothetical 180.2 kd protein in faa4-cox7 intergenic region.
CONTIG5180	21525077_f3_7	1381	15484	372	124	Q04781	148	5.0(10)-9	Saccharomyces cerevisiae	hypothetical 180.2 kd protein in faa4-cox7 intergenic region.
CONTIG5180	3298211_f1_3	1382	15485	1089	363	Q04781	188	1.3(10)-11	Saccharomyces cerevisiae	hypothetical 180.2 kd protein in faa4-cox7 intergenic region.
CONTIG2039	36589425_c2_4	1383	15486	1197	399	Q04847	215	6.0(10)-15	Saccharomyces cerevisiae	hypothetical 64.4 kd protein in pel11-tif11 intergenic region.
CONTIG5689	4397680_c3_28	1384	15487	2568	856	Q03496	249	5.5(10)-25	Saccharomyces cerevisiae	hypothetical 163.6 kd protein in pel11-tif11 intergenic region.
CONTIG5214	29304817_c3_22	1385	15488	234	78	Q03516	153	8.1(10)-10	Saccharomyces cerevisiae	hypothetical 107.7 kd protein in tsp3-ipp2 intergenic region.
CONTIG5214	23851512_c1_14	1386	15489	2226	742	Q03516	1462	7.0(10)-150	Saccharomyces cerevisiae	hypothetical 107.7 kd protein in tsp3-ipp2 intergenic region.

CONTIG5739	54715_c2_23	1387	15490	594	198	Q03525	97	0.00033	Saccharomyces cerevisiae	hypothetical 16.2 kd protein in prp24-rm9 intergenic region.
CONTIG2885	30896938_c2_5	1388	15491	705	235	Q03254	166	2.2(10)-11	Saccharomyces cerevisiae	hypothetical 83.4 kd protein in dsk2-ca8 intergenic region.
CONTIG595	4473518_fl_1	1389	15492	1101	367	Q03254	753	2.6(10)-79	Saccharomyces cerevisiae	hypothetical 83.4 kd protein in dsk2-ca8 intergenic region.
CONTIG4612	4073541_c3_5	1390	15493	960	320	Q03266	273	7.0(10)-24	Saccharomyces cerevisiae	hypothetical 42.6 kd protein in msu1-jim1 intergenic region.
CONTIG2973	195205_c3_5	1391	15494	396	132	Q03559	213	1.6(10)-17	Saccharomyces cerevisiae	hypothetical 22.2 kd protein in jim1-lcb1 intergenic region.
CONTIG2973	266050_c3_4	1392	15495	342	114	Q03559	125	3.3(10)-8	Saccharomyces cerevisiae	hypothetical 22.2 kd protein in jim1-lcb1 intergenic region.
CONTIG5511	19804537_c2_17	1393	15496	1230	410	Q04951	953	6.0(10)-96	Saccharomyces cerevisiae	hypothetical 40.5 kd protein in adh2-gas1 intergenic region precursor.
CONTIG5723	14328401_c1_16	1394	15497	1128	376	Q04867	343	2.7(10)-31	Saccharomyces cerevisiae	hypothetical 35.9 kd protein in nlp1-gl8 intergenic region.
CONTIG4422	582785_c1_6	1395	15498	1131	377	Q04869	829	8.5(10)-83	Saccharomyces cerevisiae	hypothetical 38.2 kd protein in pre5-fet4 intergenic region.
CONTIG5353	906325_c1_11	1396	15499	1146	382	Q03829	876	8.9(10)-88	Saccharomyces cerevisiae	putative mitochondrial carrier ymr166c.
CONTIG3577	11907193_c1_7	1397	15500	1197	399	Q16739	131	9.3(10)-20	Homo sapiens	ceramide glucosyltransferase (cc 2.4.1.80) (fragment).
CONTIG3577	25397768_c1_6	1398	15501	504	168	Q16739	122	4.7(10)-7	Homo sapiens	ceramide glucosyltransferase (cc 2.4.1.80) (fragment).
CONTIG5166	7112750_c1_7	1399	15502	2352	784	Q12387	238	2.1(10)-16	Saccharomyces cerevisiae	dec1 protein (mdm20 protein).
CONTIG5345	4385790_c3_22	1400	15503	1233	411	Q92206	2055	1.0(10)-212	Candida albicans	squalene monooxygenase (cc 1.14.99.7) (squalene epoxidase) (se).
CONTIG2584	2392002_c2_8	1401	15504	444	148	Q12328	426	4.2(10)-40	Saccharomyces cerevisiae	mitochondrial import inner membrane translocase subunit tim22.

CONTIG2455	5281950_c3_9	1402	15505	735	245	Q12446	92	0.12	Saccharomyces cerevisiae	proline-rich protein las17.
CONTIG477	4188518_c2_3	1403	15506	270	90	Q12446	108	3.1(10)-5	Saccharomyces cerevisiae	proline-rich protein las17.
CONTIG5033	30720953_c1_7	1404	15507	1998	666	Q12446	583	9.9(10)-57	Saccharomyces cerevisiae	proline-rich protein las17.
CONTIG5540	23985180_f3_12	1405	15508	1410	470	Q09329	294	2.6(10)-52	Schizosaccharomyces pombe	mlo2 protein.
CONTIG1987	26798466_f3_4	1406	15509	1023	341	Q00312	579	2.1(10)-73	Candida albicans	transcription factor rbf1.
CONTIG4207	11799055_c2_6	1407	15510	1743	581	Q00312	103	0.019	Candida albicans	transcription factor rbf1.
CONTIG73	26756682_c2_5	1408	15511	537	179	Q00312	509	6.9(10)-49	Candida albicans	transcription factor rbf1.
CONTIG4868	2531286_f3_5	1409	15512	1209	403	Q12600	555	6.5(10)-87	Candida tropicalis	sis2 protein (thalotolerance protein hal3).
CONTIG3844	38175_f3_1	1410	15513	1536	512	Q92331	326	3.7(10)-27	Saccharomyces cerevisiae	vacuolar protein sorting-associated protein vps5.
CONTIG4023	1962563_f3_3	1411	15514	486	162	Q16718	161	5.2(10)-12	Homo sapiens	nadh-ubiquinone oxidoreductase 13 kd-b subunit (ec 1.6.5.3) (ec 1.6.99.3) (complex i-13kd-b) (ci-13kd-b) (b13).
CONTIG4798	390925_f1_2	1412	15515	1230	410	Q92213	1818	1.3(10)-187	Candida albicans	phosphatidylinositol 3-kinase vps34 (ec 2.7.1.137) (pi3-kinase) (pidins-3-kinase) (pi3k) (vacuolar sorting protein 34).
CONTIG4798	7781_f1_3	1413	15516	213	71	Q92213	311	1.2(10)-26	Candida albicans	phosphatidylinositol 3-kinase vps34 (ec 2.7.1.137) (pi3-kinase) (pidins-3-kinase) (pi3k) (vacuolar sorting protein 34).
CONTIG4798	781567_f1_4	1414	15517	1602	534	Q92213	2540	4.0(10)-264	Candida albicans	phosphatidylinositol 3-kinase vps34 (ec 2.7.1.137) (pi3-kinase) (pidins-3-kinase) (pi3k) (vacuolar sorting protein 34).

CONTIG3437	21522677_c2_9	1415	15518	1059	353	Q92212	723	1.1(10)-70	Candida albicans	serine/threonine-protein kinase cst20 (ec 2.7.1.-).
CONTIG3437	29472503_c1_7	1416	15519	1074	358	Q92212	1097	3.3(10)-111	Candida albicans	serine/threonine-protein kinase cst20 (ec 2.7.1.-).
CONTIG2686	23995392_c1_8	1417	15520	642	214	Q12196	394	1.1(10)-36	Saccharomyces cerevisiae	rii1 protein.
CONTIG3377	4865656_c3_8	1418	15521	1035	345	Q03532	1457	2.3(10)-149	Saccharomyces cerevisiae	putative atp-dependent mra helicase ymr290c.
CONTIG3814	23600407_f3_21	1419	15522	3813	1271	Q04217	1924	1.1(10)-295	Saccharomyces cerevisiae	putative atp-dependent mra helicase ymr128w.
CONTIG5735	26370160_f1_1	1420	15523	2232	744	Q08162	2124	5.0(10)-220	Saccharomyces cerevisiae	dis3 protein.
CONTIG5735	24629511_f2_5	1421	15524	915	305	Q08162	1129	1.3(10)-114	Saccharomyces cerevisiae	dis3 protein.
CONTIG5808	1990656_c3_38	1422	15525	1578	526	Q03649	554	1.2(10)-53	Saccharomyces cerevisiae	hypothetical 51.4 kd protein in rar1-sci1 intergenic region.
CONTIG2215	19814763_f2_1	1423	15526	468	156	Q04958	485	7.4(10)-45	Saccharomyces cerevisiae	hypothetical 187.1 kd protein in ogg1-cna2 intergenic region.
b3x17744.y	954688_c1_2	1424	15527	444	148	Q17308	109	5.0(10)-5	Caenorhabditis briggsae	sex-determining transformer protein 1.
CONTIG5820	10158568_f2_30	1425	15528	321	107	S15157	382	2.0(10)-35	Saccharomyces sp.	ubiquinol--cytochrome-c reductase (ec 1.10.2.2) cytochrome b- yeast (saccharomyces sp.) mitochondrion (strain 4707-22d)(sgc2)
CONTIG5232	34380_c3_15	1426	15529	693	231	A27331	794	4.2(10)-79	Candida tropicalis	acyl-coa oxidase (ec 1.3.3.6) pxp2, peroxisomal - yeast(candida tropicalis) this enzyme, located in peroxisomes, catalyzes the oxygen-specific oxidation of long-chain (8 and up) acyl-coa to trans-2, 3- dehydroacyl-coa with oxygen being converted to hydrog

b2x16736,y	23517882_c2_2	1427	15530	561	187	A25123	691	3,6(10)-68	Candida tropicalis	acyl-coa oxidase (ec 1.3.3.6) pox4, peroxisomal - yeast(candida tropicalis) this enzyme, located in peroxisomes, catalyzes the oxygen-specific oxidation of long-chain (8 and up) acyl-coa to trans-2, 3-dehydroacyl-coa with oxygen being converted to hydrog
CONTIG5453	10970285_f3_16	1428	15531	1998	666	B25123	2996	0	Candida tropicalis	acyl-coa oxidase (ec 1.3.3.6) pox5, peroxisomal - yeast(candida tropicalis) this enzyme, located in peroxisomes, catalyzes the oxygen-specific oxidation of long-chain (8 and up) acyl-coa to trans-2, 3-dehydroacyl-coa with oxygen being converted to hydrog
CONTIG5656	21489635_c3_30	1429	15532	237	79	A35427	111	1,2(10)-5	Oryctolagus cuniculus	dimethyl/laniline monooxygenase (n-oxide-forming) (ec1.14.13.8), hepatic 1 - rabbit this enzyme is involved in the metabolism of many drugs, pesticides, and other foreign compounds, including xenobiotics, by catalyzing the nadph-dependent oxidation of vari
CONTIG781	24641317_c1_4	1430	15533	918	306	S43743	1276	3,6(10)-130	Candida albicans	probable dual specificity phosphatase (ec 3.1.3.-) - yeast(candida albicans) this enzyme interferes with the s.cerevisiae pheromone response pathway.
CONTIG5585	26361557_f3_9	1431	15534	912	304	A03324	509	1,5(10)-47	Drosophila melanogaster	retrovirus-related polypotein - fruit fly (drosophilamelanogaster) transposon copia

CONTIG2913	24110931_f1_3	1432	15535	1014	338	A26896	93	0.22	Human parainfluenza virus 3	polymerase-associated nucleocapsid phosphoprotein (version 2)- parainfluenza virus type 3 the na sequence was obtained from genbank, release 52.0. this protein may be a component of the active polymerase.
CONTIG5766	20517561_c1_24	1433	15536	462	154	B40576	694	1.7(10)-68	Candida maltosa	cytochrome p450 alk3-a - yeast (candida maltosa)
CONTIG5766	503885_c2_30	1434	15537	1647	549	A40576	2161	6.0(10)-224	Candida maltosa	cytochrome p450 alk2-a - yeast (candida maltosa)
CONTIG5783	7265957_c2_37	1435	15538	672	224	JS0726	914	8.3(10)-92	Candida maltosa	cytochrome p450 alk8, alkane- inducible - yeast (candidamaltosa)
CONTIG5783	2925050_c1_28	1436	15539	948	316	JS0726	1058	4.5(10)-107	Candida maltosa	cytochrome p450 alk8, alkane- inducible - yeast (candidamaltosa)
CONTIG5695	37577_f2_3	1437	15540	1524	508	JS0724	1563	1.3(10)-160	Candida maltosa	cytochrome p450 alk6-a, alkane- inducible - yeast (candidamaltosa)
CONTIG5471	34098453_f1_1	1438	15541	1710	570	A45249	2900	2.8(10)-302	Candida albicans	alpha-glucosidase (ec 3.2.1.20) mal62 - yeast (candidaalbicans)
CONTIG5820	134635_c3_89	1439	15542	270	90	S44135	235	7.5(10)-20	Candida parapsilosis	h+-transporting atp synthase (ec 3.6.1.34) protein 9 - yeast(candida parapsilosis) mitochondrion (sgc3)
CONTIG3842	10660005_c3_15	1440	15543	348	116	S61168	344	2.1(10)-31	Saccharomyces cerevisiae	hypothetical protein ydi373w - yeast (saccharomycescerevisiae)
CONTIG3996	21953160_f1_1	1441	15544	915	305	S61979	673	2.8(10)-66	Saccharomyces cerevisiae	probable membrane protein yp1087w - yeast (saccharomycescerevisiae)
CONTIG4146	34665932_c1_6	1442	15545	471	157	S30284	104	0.0008	Streptococcus pyogenes	m protein precursor - streptococcus pyogenes (serotype m52)
CONTIG5460	35189205_f1_7	1443	15546	894	298	S21347	167	6.5(10)-10	Rattus norvegicus	hypothetical protein 3 - rat

CONTIG5712	33610776_c1_18	1444	15547	2715	905	S21347	447	2.1(10)-41	Rattus norvegicus	hypothetical protein 3 - rat
CONTIG142	1298937_f3_2	1445	15548	462	154	S12588	178	4.0(10)-13	Mink cell focus-forming virus	pol polyprotein - mink cell focus-forming virus (fragment)
CONTIG5820	1459800_f3_48	1446	15549	411	137	S23209	181	3.2(10)-13	Saccharomyces sp.	mna maturase b13 - yeast (saccharomyces sp.) mitochondrion(strain 4707-22d) (sgc2)
CONTIG1281	35823958_f3_1	1447	15550	636	212	S42250	90	0.031	Fowlpox virus	hypothetical protein 4 - fowlpox virus
CONTIG3723	16501550_f2_2	1448	15551	903	301	A56976	95	0.12	Staphylococcus aureus	transfer complex protein trsi - staphylococcus aureus
CONTIG5469	34187550_f3_6	1449	15552	1143	381	JC6009	116	0.0019	Mycoplasma hominis	surface-located membrane protein Imp3 - mycoplasma hominis(sgc3)
CONTIG4741	24094125_f2_2	1450	15553	570	190	S31142	90	0.078	Mycoplasma pulmonis	probable transposase (insertion sequence is1138) - mycoplasmapulmonis (sgc3)
CONTIG3041	10680381_c2_6	1451	15554	198	66	S54738	95	7.7(10)-5	Desulfurococcus mobilis	hypothetical protein c179 - desulfurococcus mobilis
CONTIG5254	24303151_f3_9	1452	15555	552	184	S54738	224	1.1(10)-18	Desulfurococcus mobilis	hypothetical protein c179 - desulfurococcus mobilis
CONTIG5539	10680381_c2_14	1453	15556	198	66	S54738	95	7.7(10)-5	Desulfurococcus mobilis	hypothetical protein c179 - desulfurococcus mobilis
CONTIG4740	16878533_f2_3	1454	15557	630	210	S04714	124	4.2(10)-8	Sulfolobus acidocaldarius	hypothetical protein end - sulfolobus acidocaldarius(fragment)
CONTIG5204	29423756_f1_1	1455	15558	336	112	S59860	151	3.2(10)-10	Sulfolobus shibatae	hypothetical protein - sulfolobus shibatae
CONTIG5351	4876557_f2_4	1456	15559	1011	337	S42651	284	4.7(10)-25	Brassica napus	hypothetical protein - rape
CONTIG5543	14978380_c2_15	1457	15560	1596	532	S20500	109	0.0025	Oryza sativa	hydroxyproline-rich glycoprotein - rice
CONTIG5341	22831438_f3_13	1458	15561	801	267	S52645	123	2.7(10)-5	Zea mays	probable 1-acyl-glycerol-3-phosphate acyltransferase - maize

CONTIG5270	4725035_c2_11	1459	15562	753	251	S28720	94	0.027	Dietyostelium discoidium	gene d-4 protein - slime mold (dictyostelium discoidium)plasmid ddp1
CONTIG4720	156505_c1_7	1460	15563	468	156	S55723	217	6.0(10)-18	Schizosaccharo myces pombe	pac2 protein - fission yeast (schizosaccharomyces pombe)
CONTIG5619	22032952_f3_13	1461	15564	987	329	S52837	92	0.17	Schizosaccharo myces pombe	sll1 protein - fission yeast (schizosaccharomyces pombe)
CONTIG5263	14489063_c1_11	1462	15565	762	254	S63669	757	4.5(10)-74	Schizosaccharo myces pombe	udp-glucose--glycoprotein glucosylphosphotransferase (ec2.7.8.19) - fission yeast (schizosaccharomyces pombe)
CONTIG5545	29329557_c1_13	1463	15566	2550	850	S30356	3985	0	Candida albicans	cdc25 protein homolog - yeast (candida albicans)
CONTIG670	35198453_f2_1	1464	15567	1206	402	S30356	1855	1.6(10)-191	Candida albicans	cdc25 protein homolog - yeast (candida albicans)
CONTIG2208	3953436_f1_2	1465	15568	747	249	S43279	1075	7.2(10)-109	Candida albicans	cell division control protein cdc3 - yeast (candida albicans)
CONTIG5334	25485782_c2_8	1466	15569	363	121	A47259	650	7.9(10)-64	Candida albicans	corticosteroid-binding protein - yeast (candida albicans)
CONTIG5190	3913400_f3_4	1467	15570	1521	507	JC4828	2033	2.2(10)-210	Candida albicans	cyclin b - yeast (candida albicans)
CONTIG4973	4334425_c1_4	1468	15571	1407	469	S51613	2115	4.5(10)-219	Candida albicans	cyclin homolog cln2 - yeast (candida albicans)
CONTIG3138	4025277_f3_6	1469	15572	651	217	A36990	1048	5.2(10)-106	Candida albicans	estrogen-binding protein - yeast (candida albicans)
CONTIG4960	19718792_c2_8	1470	15573	1245	415	A36990	1689	6.2(10)-174	Candida albicans	estrogen-binding protein - yeast (candida albicans)
CONTIG5794	7082041_c1_24	1471	15574	924	308	S27407	808	1.3(10)-80	Candida albicans	finger protein znf1 - yeast (candida albicans)
CONTIG3328	22445176_c2_3	1472	15575	2082	694	S49206	2457	2.6(10)-255	Candida albicans	gl cyclin cln1 - yeast (candida albicans)
CONTIG5727	9932660_f3_16	1473	15576	1305	435	A44384	2054	1.3(10)-212	Candida albicans	gip-binding regulatory protein g alpha chain cag1 - yeast(candida albicans)

CONTIG1662	4884377_c2_4	1474	15577	948	316	S58135	1139	1.2(10)-115	Candida albicans	hypothally regulated protein - yeast (candida albicans)
CONTIG4906	30344703_c3_9	1475	15578	1986	662	S58135	681	4.0(10)-67	Candida albicans	hypothally regulated protein - yeast (candida albicans)
CONTIG4971	22070427_f2_1	1476	15579	2934	978	S58135	646	1.6(10)-73	Candida albicans	hypothally regulated protein - yeast (candida albicans)
CONTIG5290	1208437_c2_13	1477	15580	882	294	S58135	541	1.7(10)-51	Candida albicans	hypothally regulated protein - yeast (candida albicans)
CONTIG2790	32281575_c2_6	1478	15581	294	98	JG6013	299	1.2(10)-26	Candida albicans	hypothetical k protein - yeast (candida albicans)
CONTIG4345	21579430_f2_4	1479	15582	594	198	S43029	97	3.7(10)-5	Candida albicans	hypothetical protein 1 - yeast (candida albicans)
CONTIG5725	35586038_f2_6	1480	15583	393	131	S43029	197	7.9(10)-16	Candida albicans	hypothetical protein 1 - yeast (candida albicans)
CONTIG4283	2787552_c1_4	1481	15584	237	79	S43030	170	5.7(10)-13	Candida albicans	hypothetical protein 2 - yeast (candida albicans)
CONTIG5746	2787552_f3_11	1482	15585	345	115	S43030	241	1.7(10)-20	Candida albicans	hypothetical protein 2 - yeast (candida albicans)
CONTIG4222	5078186_c1_11	1483	15586	1215	405	A55588	2146	2.2(10)-222	Candida albicans	mannosyl-glycoprotein endo-beta-n-acetylglucosaminidase (ec3.2.1.96) precursor - yeast (candida albicans)
CONTIG5500	10976437_c2_14	1484	15587	999	333	A43302	1662	4.5(10)-171	Candida albicans	probable finger protein casucl - yeast (candida albicans)
CONTIG5441	23682638_c1_11	1485	15588	2577	859	S47220	3680	0	Candida albicans	protein kinase c - yeast (candida albicans)
CONTIG104	23719051_c3_2	1486	15589	273	91	JN0320	357	8.8(10)-33	Candida albicans	rapamycin-binding protein - yeast (candida albicans) this protein possesses peptidyl-prolyl cis-trans isomerase activity which is inhibited by the binding of rapamycin.

CONTIG1295	10975877_c3_5	1487	15590	381	127	JN0320	578	3.3(10)-56	Candida albicans	rapamycin-binding protein - yeast (candida albicans) this protein possesses peptidyl-prolyl cis-trans isomerase activity which is inhibited by the binding of rapamycin.
CONTIG5203	13703132_f1_1	1488	15591	1401	467	S37606	2146	2.2(10)-222	Candida albicans	sec18 protein - yeast (candida albicans)
CONTIG1225	478207_f3_3	1489	15592	1041	347	S60154	956	3.0(10)-96	Candida albicans	serine/threonine-specific kinase (ec 2.7.1.-) isoform hst7-q- yeast (candida albicans)
CONTIG5448	23492064_c1_11	1490	15593	459	153	B48329	133	4.7(10)-9	Candida maltosa	hypothetical protein (c-his5 3 region) - yeast (candidamaltosa) (fragment)
CONTIG4988	10975882_f2_2	1491	15594	390	130	JS0155	566	6.2(10)-55	Candida tropicalis	poxi8 protein - yeast (candida tropicalis) this protein is one of the oleate-inducible peroxisomal proteins. peroxisomes purified from oleate-grown cells contain approx. 20 proteins. this protein is the smallest among them.
CONTIG5820	390933_f2_24	1492	15595	486	162	SI7996	358	1.7(10)-32	Kluyveromyces lactis	gene cox1 intron 2 protein - yeast (kluyveromyces marxianusvar. lactis) mitochondrion (sgc2)
CONTIG5820	894800_f1_12	1493	15596	186	62	SI7998	120	2.1(10)-6	Kluyveromyces lactis	gene cox1 intron 4 protein - yeast (kluyveromyces marxianusvar. lactis) mitochondrion (sgc2)
CONTIG3252	1412528_f2_2	1494	15597	846	282	S67800	513	2.6(10)-49	Saccharomyces cerevisiae	4-nitrophenylphosphatase (ec 3.1.3.41) - yeast (saccharomycescerevisiae) the activity of this enzyme is enhanced by mg2+ ion but inhibited by ca2+, zn2+ and be2+ ions.

CONTIG4732	4023307_f3_8	1495	15598	567	189	S59317	500	4.9(10)-47	Saccharomyces cerevisiae	dip2 protein - yeast (Saccharomyces cerevisiae)
CONTIG4732	10743813_f1_4	1496	15599	1464	488	S59317	951	1.0(10)-95	Saccharomyces cerevisiae	dip2 protein - yeast (Saccharomyces cerevisiae)
CONTIG1025	2535306_f2_1	1497	15600	705	235	S31848	279	1.6(10)-24	Saccharomyces cerevisiae	heat shock protein hsp30 - yeast (Saccharomyces cerevisiae)
CONTIG5756	1354707_f1_5	1498	15601	1263	421	S49776	108	0.0037	Saccharomyces cerevisiae	hypothetical protein (sdh4 3 region) - yeast (Saccharomyces cerevisiae) (fragment)
CONTIG5756	24619052_f3_12	1499	15602	546	182	S61367	291	8.6(10)-26	Saccharomyces cerevisiae	hypothetical protein yd8142a.01 - yeast (Saccharomyces cerevisiae) (fragment)
CONTIG5756	32069076_f1_7	1500	15603	492	164	S61367	425	5.5(10)-40	Saccharomyces cerevisiae	hypothetical protein yd8142a.01 - yeast (Saccharomyces cerevisiae) (fragment)
CONTIG2258	15891442_f2_1	1501	15604	1107	369	S67592	163	1.3(10)-9	Saccharomyces cerevisiae	hypothetical protein yd1057w - yeast (Saccharomyces cerevisiae)
CONTIG5271	23962782_f2_1	1502	15605	2529	843	S67595	955	1.7(10)-143	Saccharomyces cerevisiae	hypothetical protein yd1060w - yeast (Saccharomyces cerevisiae)
CONTIG3376	26567127_c3_5	1503	15606	690	230	S67612	163	6.2(10)-11	Saccharomyces cerevisiae	hypothetical protein yd1076c - yeast (Saccharomyces cerevisiae)
CONTIG3267	24240803_f1_1	1504	15607	384	128	S67622	429	2.1(10)-40	Saccharomyces cerevisiae	hypothetical protein yd1086w - yeast (Saccharomyces cerevisiae)
CONTIG1281	13675000_f3_3	1505	15608	456	152	S67623	281	1.0(10)-24	Saccharomyces cerevisiae	hypothetical protein yd1087c - yeast (Saccharomyces cerevisiae)
CONTIG541	4885325_c2_2	1506	15609	504	168	S67639	484	3.1(10)-46	Saccharomyces cerevisiae	hypothetical protein yd1097c - yeast (Saccharomyces cerevisiae)
CONTIG3360	26069452_f2_3	1507	15610	732	244	S67640	117	1.0(10)-5	Saccharomyces cerevisiae	hypothetical protein yd1098c - yeast (Saccharomyces cerevisiae)
CONTIG4511	828403_f1_2	1508	15611	1251	417	S67658	111	4.2(10)-11	Saccharomyces cerevisiae	hypothetical protein yd1115c - yeast (Saccharomyces cerevisiae)
CONTIG3814	11047182_f2_2	1509	15612	2301	767	S67660	653	1.8(10)-70	Saccharomyces cerevisiae	hypothetical protein yd1117w - yeast (Saccharomyces cerevisiae)

CONTIG1335	2822180_c1_3	1510	15613	861	287	S67662	257	1.8(10)-36	Saccharomyces cerevisiae	hypothetical protein ydl119c - yeast (saccharomycescerevisiae)
CONTIG2522	23548786_f1_1	1511	15614	582	194	S67663	227	5.2(10)-19	Saccharomyces cerevisiae	hypothetical protein ydl120w - yeast (saccharomycescerevisiae)
CONTIG5132	23626552_f3_7	1512	15615	1992	664	S67685	106	0.00419	Saccharomyces cerevisiae	hypothetical protein ydl139c - yeast (saccharomycescerevisiae)
CONTIG5798	23914693_f1_8	1513	15616	1590	530	S67695	844	2.2(10)-84	Saccharomyces cerevisiae	hypothetical protein ydl147w - yeast (saccharomycescerevisiae)
CONTIG3001	24402261_c2_6	1514	15617	210	70	S67704	117	2.6(10)-6	Saccharomyces cerevisiae	hypothetical protein ydl156w - yeast (saccharomycescerevisiae)
CONTIG366	650760_f1_1	1515	15618	528	176	S67704	244	4.7(10)-20	Saccharomyces cerevisiae	hypothetical protein ydl156w - yeast (saccharomycescerevisiae)
CONTIG2209	972507_f3_2	1516	15619	321	107	S61056	116	3.0(10)-7	Saccharomyces cerevisiae	hypothetical protein ydl157c - yeast (saccharomycescerevisiae)
CONTIG5437	15678552_f2_5	1517	15620	282	94	S61047	97	6.0(10)-5	Saccharomyces cerevisiae	hypothetical protein ydl166c - yeast (saccharomycescerevisiae)
CONTIG5437	10347000_f3_9	1518	15621	660	220	S61047	377	6.7(10)-35	Saccharomyces cerevisiae	hypothetical protein ydl166c - yeast (saccharomycescerevisiae)
CONTIG4210	2115886_c2_9	1519	15622	426	142	S61039	122	2.7(10)-7	Saccharomyces cerevisiae	hypothetical protein ydl173w - yeast (saccharomycescerevisiae)
CONTIG5130	12705287_c1_9	1520	15623	615	205	S61037	404	9.1(10)-38	Saccharomyces cerevisiae	hypothetical protein ydl175c - yeast (saccharomycescerevisiae)
CONTIG4319	4812568_c3_10	1521	15624	1242	414	S67744	115	5.4(10)-5	Saccharomyces cerevisiae	hypothetical protein ydl189w - yeast (saccharomycescerevisiae)
CONTIG5163	24413505_f3_3	1522	15625	1113	371	S67760	768	2.5(10)-76	Saccharomyces cerevisiae	hypothetical protein ydl201w - yeast (saccharomycescerevisiae)
CONTIG5681	22069692_f1_3	1523	15626	804	268	S67772	225	8.5(10)-19	Saccharomyces cerevisiae	hypothetical protein ydl213c - yeast (saccharomycescerevisiae)
CONTIG1456	26343811_f3_2	1524	15627	231	77	S50994	262	1.0(10)-22	Saccharomyces cerevisiae	hypothetical protein ydl013w - yeast (saccharomycescerevisiae)
CONTIG5565	24266882_f2_11	1525	15628	525	175	S54639	140	8.6(10)-10	Saccharomyces cerevisiae	hypothetical protein ydl016c - yeast (saccharomycescerevisiae)
CONTIG5040	19703382_f3_7	1526	15629	345	115	S67845	180	5.0(10)-14	Saccharomyces cerevisiae	hypothetical protein ydl031w - yeast (saccharomycescerevisiae)

CONTIG1950	5329400_c3_2	1527	15630	525	175	S54036	301	7.5(10)-27	Saccharomyces cerevisiae	hypothetical protein ydr051c - yeast (saccharomycescerevisiae)
CONTIG3403	4800788_c1_5	1528	15631	798	266	S58837	152	2.1(10)-8	Saccharomyces cerevisiae	hypothetical protein ydr057w - yeast (saccharomycescerevisiae)
CONTIG5806	29960017_f2_13	1529	15632	372	124	S54047	143	4.2(10)-10	Saccharomyces cerevisiae	hypothetical protein ydr063w - yeast (saccharomycescerevisiae)
CONTIG5118	14254175_f3_4	1530	15633	612	204	S49826	274	5.5(10)-24	Saccharomyces cerevisiae	hypothetical protein ydr071c - yeast (saccharomycescerevisiae)
CONTIG113	11757800_f3_1	1531	15634	570	190	S52682	101	0.00044	Saccharomyces cerevisiae	hypothetical protein ydr117c - yeast (saccharomycescerevisiae)
CONTIG1796	11754562_c1_5	1532	15635	486	162	S52682	232	1.2(10)-18	Saccharomyces cerevisiae	hypothetical protein ydr117c - yeast (saccharomycescerevisiae)
CONTIG3998	46051031_f2_2	1533	15636	900	300	S52682	254	8.1(10)-34	Saccharomyces cerevisiae	hypothetical protein ydr117c - yeast (saccharomycescerevisiae)
CONTIG5814	4798188_f3_19	1534	15637	330	110	S52686	222	1.8(10)-18	Saccharomyces cerevisiae	hypothetical protein ydr121w - yeast (saccharomycescerevisiae)
CONTIG5787	23726576_c2_30	1535	15638	1341	447	S52689	207	8.6(10)-15	Saccharomyces cerevisiae	hypothetical protein ydr124w - yeast (saccharomycescerevisiae)
CONTIG5778	785932_c1_22	1536	15639	453	151	S52690	155	1.6(10)-10	Saccharomyces cerevisiae	hypothetical protein ydr125c - yeast (saccharomycescerevisiae)
CONTIG5778	4037512_c3_30	1537	15640	1176	392	S52690	206	5.0(10)-14	Saccharomyces cerevisiae	hypothetical protein ydr125c - yeast (saccharomycescerevisiae)
CONTIG2385	30504689_c2_4	1538	15641	444	148	S52690	141	5.2(10)-9	Saccharomyces cerevisiae	hypothetical protein ydr125c - yeast (saccharomycescerevisiae)
CONTIG3719	35196911_f2_2	1539	15642	2679	893	S51855	397	2.1(10)-62	Saccharomyces cerevisiae	hypothetical protein ydr128w - yeast (saccharomycescerevisiae)
CONTIG5784	1038187_c3_21	1540	15643	1131	377	S51855	148	2.5(10)-15	Saccharomyces cerevisiae	hypothetical protein ydr128w - yeast (saccharomycescerevisiae)
CONTIG1982	199155_f2_1	1541	15644	1359	453	S51859	359	5.2(10)-37	Saccharomyces cerevisiae	hypothetical protein ydr132c - yeast (saccharomycescerevisiae)
CONTIG4661	287_c3_5	1542	15645	723	241	S51868	599	2.0(10)-58	Saccharomyces cerevisiae	hypothetical protein ydr140w - yeast (saccharomycescerevisiae)
CONTIG3367	267067_f2_4	1543	15646	588	196	S57978	198	6.2(10)-16	Saccharomyces cerevisiae	hypothetical protein ydr152w - yeast (saccharomycescerevisiae)

CONTIG2706	173135_c1_3	1544	15647	330	110	S57987	103	7.5(10)-6	Saccharomyces cerevisiae	hypothetical protein ydr163w - yeast (saccharomycescerevisiae)
CONTIG4745	5195930_f3_4	1545	15648	942	314	S49771	440	1.3(10)-41	Saccharomyces cerevisiae	hypothetical protein ydr175c - yeast (saccharomycescerevisiae)
CONTIG5676	15663382_f1_5	1546	15649	690	230	S49778	142	4.2(10)-8	Saccharomyces cerevisiae	hypothetical protein ydr181c - yeast (saccharomycescerevisiae)
CONTIG829	961017_c2_4	1547	15650	420	140	S49781	98	0.00012	Saccharomyces cerevisiae	hypothetical protein ydr184c - yeast (saccharomycescerevisiae)
CONTIG5794	22712807_f1_6	1548	15651	918	306	S52698	1331	5.4(10)-136	Saccharomyces cerevisiae	hypothetical protein ydr190c - yeast (saccharomycescerevisiae)
CONTIG5794	1182807_f2_10	1549	15652	531	177	S52698	509	6.9(10)-49	Saccharomyces cerevisiae	hypothetical protein ydr190c - yeast (saccharomycescerevisiae)
CONTIG5476	29346963_f1_1	1550	15653	1164	388	S52708	295	3.2(10)-26	Saccharomyces cerevisiae	hypothetical protein ydr202c - yeast (saccharomycescerevisiae)
CONTIG5458	16442162_f1_2	1551	15654	1053	351	S61581	618	1.8(10)-60	Saccharomyces cerevisiae	hypothetical protein ydr214w - yeast (saccharomycescerevisiae)
CONTIG5400	13848962_c1_8	1552	15655	1215	405	S54531	391	2.2(10)-36	Saccharomyces cerevisiae	hypothetical protein ydr235w - yeast (saccharomycescerevisiae)
CONTIG5146	14540957_f1_4	1553	15656	882	294	S70126	492	4.4(10)-47	Saccharomyces cerevisiae	hypothetical protein ydr266c - yeast (saccharomycescerevisiae)
CONTIG1324	26803465_c1_4	1554	15657	669	223	S70127	338	9.0(10)-31	Saccharomyces cerevisiae	hypothetical protein ydr267c - yeast (saccharomycescerevisiae)
CONTIG5232	12538182_f2_5	1555	15658	219	73	S70224	154	2.8(10)-11	Saccharomyces cerevisiae	hypothetical protein ydr276c - yeast (saccharomycescerevisiae)
CONTIG3858	12500061_c1_4	1556	15659	681	227	S70138	447	2.6(10)-42	Saccharomyces cerevisiae	hypothetical protein ydr282c - yeast (saccharomycescerevisiae)
CONTIG2423	3022217_c2_5	1557	15660	732	244	S70114	458	1.7(10)-43	Saccharomyces cerevisiae	hypothetical protein ydr284c - yeast (saccharomycescerevisiae)
CONTIG3184	4500007_c2_7	1558	15661	891	297	S70114	397	5.0(10)-37	Saccharomyces cerevisiae	hypothetical protein ydr284c - yeast (saccharomycescerevisiae)
CONTIG5351	21671882_c2_10	1559	15662	387	129	S70116	175	1.7(10)-13	Saccharomyces cerevisiae	hypothetical protein ydr286c - yeast (saccharomycescerevisiae)
CONTIG4041	24485875_f3_3	1560	15663	1137	379	S70118	108	0.00169	Saccharomyces cerevisiae	hypothetical protein ydr288w - yeast (saccharomycescerevisiae)

CONTIG5343	23602342_c2_17	1561	15664	1086	362	S70119	257	6.2(10)-22	Saccharomyces cerevisiae	hypothetical protein ydr289c - yeast (saccharomycescerevisiae)
CONTIG3679	26260462_f1_1	1562	15665	480	160	S70120	359	9.5(10)-32	Saccharomyces cerevisiae	hypothetical protein ydr291w - yeast (saccharomycescerevisiae)
CONTIG1487	3942512_c1_6	1563	15666	534	178	S61181	104	9.0(10)-5	Saccharomyces cerevisiae	hypothetical protein ydr295c - yeast (saccharomycescerevisiae)
CONTIG4990	24015882_c2_11	1564	15667	564	188	S61182	382	2.0(10)-35	Saccharomyces cerevisiae	hypothetical protein ydr296w - yeast (saccharomycescerevisiae)
CONTIG1445	24507042_c1_3	1565	15668	840	280	S61185	331	7.4(10)-52	Saccharomyces cerevisiae	hypothetical protein ydr299w - yeast (saccharomycescerevisiae)
CONTIG1212	5112843_c1_3	1566	15669	678	226	S61185	204	4.5(10)-22	Saccharomyces cerevisiae	hypothetical protein ydr299w - yeast (saccharomycescerevisiae)
CONTIG5732	391961_c1_27	1567	15670	1389	463	S61192	735	4.2(10)-79	Saccharomyces cerevisiae	hypothetical protein ydr306c - yeast (saccharomycescerevisiae)
CONTIG4909	16664627_c3_9	1568	15671	807	269	S61199	173	4.2(10)-13	Saccharomyces cerevisiae	hypothetical protein ydr313c - yeast (saccharomycescerevisiae)
b9x13e01.x	25595263_c3_2	1569	15672	678	226	S59784	99	0.0051	Saccharomyces cerevisiae	hypothetical protein ydr318w - yeast (saccharomycescerevisiae)
CONTIG5614	273552_c2_20	1570	15673	1470	490	S59786	121	0.00027	Saccharomyces cerevisiae	hypothetical protein ydr320c - yeast (saccharomycescerevisiae)
CONTIG5215	29486627_c2_11	1571	15674	957	319	S59788	414	8.0(10)-39	Saccharomyces cerevisiae	hypothetical protein ydr322w - yeast (saccharomycescerevisiae)
CONTIG2732	12933333_f1_1	1572	15675	615	205	S59790	201	4.5(10)-15	Saccharomyces cerevisiae	hypothetical protein ydr324c - yeast (saccharomycescerevisiae)
CONTIG3381	157691_c2_3	1573	15676	612	204	S59790	478	5.0(10)-45	Saccharomyces cerevisiae	hypothetical protein ydr324c - yeast (saccharomycescerevisiae)
b3x1231.y	477291_f3_1	1574	15677	558	186	S59790	508	2.2(10)-48	Saccharomyces cerevisiae	hypothetical protein ydr324c - yeast (saccharomycescerevisiae)
CONTIG4570	14534653_c2_8	1575	15678	366	122	S59795	149	8.6(10)-10	Saccharomyces cerevisiae	hypothetical protein ydr330w - yeast (saccharomycescerevisiae)
CONTIG4570	22067152_c3_10	1576	15679	990	330	S59795	488	1.2(10)-46	Saccharomyces cerevisiae	hypothetical protein ydr330w - yeast (saccharomycescerevisiae)
CONTIG1423	24300265_c3_2	1577	15680	789	263	S59797	446	8.1(10)-42	Saccharomyces cerevisiae	hypothetical protein ydr332w - yeast (saccharomycescerevisiae)

CONTIG4737	22445262_c2_4	1578	15681	1059	353	SS9797	470	1.3(10)-44	Saccharomyces cerevisiae	hypothetical protein ydr332w - yeast (saccharomycescerevisiae)
CONTIG4853	14565637_c3_9	1579	15682	1839	613	S70098	728	4.2(10)-72	Saccharomyces cerevisiae	hypothetical protein ydr333c - yeast (saccharomycescerevisiae)
b3x16841.y	4881536_c2_3	1580	15683	276	92	S70104	231	2.0(10)-19	Saccharomyces cerevisiae	hypothetical protein ydr339c - yeast (saccharomycescerevisiae)
CONTIG1948	12676532_f2_3	1581	15684	282	94	S70111	197	5.0(10)-15	Saccharomyces cerevisiae	hypothetical protein ydr346c - yeast (saccharomycescerevisiae)
CONTIG5756	1259657_c1_14	1582	15685	480	160	S61153	121	9.0(10)-8	Saccharomyces cerevisiae	hypothetical protein ydr357c - yeast (saccharomycescerevisiae)
CONTIG2562	16178317_c2_6	1583	15686	765	255	S61155	176	2.8(10)-12	Saccharomyces cerevisiae	hypothetical protein ydr359c - yeast (saccharomycescerevisiae)
CONTIG837	35338180_f3_1	1584	15687	639	213	S61156	154	6.2(10)-11	Saccharomyces cerevisiae	hypothetical protein ydr361c - yeast (saccharomycescerevisiae)
CONTIG2049	21492958_f3_2	1585	15688	582	194	S61160	213	1.6(10)-16	Saccharomyces cerevisiae	hypothetical protein ydr365c - yeast (saccharomycescerevisiae)
CONTIG4064	19956686_f3_2	1586	15689	1419	473	S61160	606	3.3(10)-69	Saccharomyces cerevisiae	hypothetical protein ydr367w - yeast (saccharomycescerevisiae)
CONTIG4064	13725781_f3_1	1587	15690	603	201	S70234	139	1.1(10)-9	Saccharomyces cerevisiae	hypothetical protein ydr372c - yeast (saccharomycescerevisiae)
CONTIG3376	10664175_c3_17	1588	15691	1038	346	S61167	969	1.2(10)-97	Saccharomyces cerevisiae	hypothetical protein ydr374c - yeast (saccharomycescerevisiae)
CONTIG2269	632640_f1_1	1589	15692	414	138	S61169	281	1.0(10)-24	Saccharomyces cerevisiae	hypothetical protein ydr386w - yeast (saccharomycescerevisiae)
CONTIG5467	14230276_c1_14	1590	15693	1860	620	S69670	569	3.2(10)-83	Saccharomyces cerevisiae	hypothetical protein ydr398w - yeast (saccharomycescerevisiae)
CONTIG5310	22516308_f2_3	1591	15694	2046	682	S69681	322	7.0(10)-55	Saccharomyces cerevisiae	hypothetical protein ydr399w - yeast (saccharomycescerevisiae)
CONTIG5108	29333377_c1_6	1592	15695	657	219	S69682	655	2.2(10)-64	Saccharomyces cerevisiae	hypothetical protein ydr407c - yeast (saccharomycescerevisiae)
CONTIG3928	31331900_f1_1	1593	15696	1764	588	S69689	310	4.0(10)-26	Saccharomyces cerevisiae	hypothetical protein ydr407c - yeast (saccharomycescerevisiae)
CONTIG4662	26806510_c2_8	1594	15697	597	199	S69689	284	1.3(10)-23	Saccharomyces cerevisiae	hypothetical protein ydr407c - yeast (saccharomycescerevisiae)

CONTIG5447	14158186_f1_4	1595	15698	1173	391	S69696	198	1.5(10)-13	Saccharomyces cerevisiae	hypothetical protein ydr411c - yeast (saccharomycescerevisiae)
CONTIG4744	4376257_f2_3	1596	15699	819	273	S69697	208	3.7(10)-29	Saccharomyces cerevisiae	hypothetical protein ydr412w - yeast (saccharomycescerevisiae)
CONTIG3306	9772762_c3_5	1597	15700	1014	338	S69702	614	5.0(10)-60	Saccharomyces cerevisiae	hypothetical protein ydr419w - yeast (saccharomycescerevisiae)
CONTIG5556	25792887_c3_19	1598	15701	1443	481	S69704	447	4.0(10)-50	Saccharomyces cerevisiae	hypothetical protein ydr421w - yeast (saccharomycescerevisiae)
CONTIG5556	33378176_c2_15	1599	15702	1578	526	S69704	468	2.2(10)-66	Saccharomyces cerevisiae	hypothetical protein ydr421w - yeast (saccharomycescerevisiae)
CONTIG336	16500153_f3_2	1600	15703	558	186	S69707	132	8.1(10)-8	Saccharomyces cerevisiae	hypothetical protein ydr425w - yeast (saccharomycescerevisiae)
CONTIG4761	23457157_f3_5	1601	15704	1269	423	S69708	367	1.1(10)-48	Saccharomyces cerevisiae	hypothetical protein ydr427w - yeast (saccharomycescerevisiae)
CONTIG5754	26604683_f2_11	1602	15705	810	270	S69709	277	2.6(10)-24	Saccharomyces cerevisiae	hypothetical protein ydr428c - yeast (saccharomycescerevisiae)
CONTIG3700	212677_c2_2	1603	15706	2718	906	S69711	912	1.3(10)-91	Saccharomyces cerevisiae	hypothetical protein ydr430c - yeast (saccharomycescerevisiae)
CONTIG5465	10554007_c1_10	1604	15707	459	153	S69711	412	1.7(10)-37	Saccharomyces cerevisiae	hypothetical protein ydr430c - yeast (saccharomycescerevisiae)
CONTIG5211	4798800_f2_6	1605	15708	1143	381	S69715	273	7.0(10)-24	Saccharomyces cerevisiae	hypothetical protein ydr435c - yeast (saccharomycescerevisiae)
CONTIG3209	42212_c2_5	1606	15709	723	241	S69718	112	8.4(10)-5	Saccharomyces cerevisiae	hypothetical protein ydr438w - yeast (saccharomycescerevisiae)
CONTIG3209	20441380_c1_4	1607	15710	612	204	S69718	156	8.3(10)-11	Saccharomyces cerevisiae	hypothetical protein ydr438w - yeast (saccharomycescerevisiae)
CONTIG1109	25580378_c3_2	1608	15711	438	146	S69720	182	3.1(10)-13	Saccharomyces cerevisiae	hypothetical protein ydr440w - yeast (saccharomycescerevisiae)
CONTIG5555	22680286_c3_23	1609	15712	2193	731	S69723	512	5.0(10)-75	Saccharomyces cerevisiae	hypothetical protein ydr444w - yeast (saccharomycescerevisiae)
CONTIG4200	25429703_f2_1	1610	15713	666	222	S69728	441	1.1(10)-41	Saccharomyces cerevisiae	hypothetical protein ydr449c - yeast (saccharomycescerevisiae)
CONTIG4875	33303442_f3_4	1611	15714	1470	490	S69731	622	8.0(10)-93	Saccharomyces cerevisiae	hypothetical protein ydr452w - yeast (saccharomycescerevisiae)

CONTIG1367	979750_c1_5	1612	15715	1206	402	S69625	320	6.2(10)-27	Saccharomyces cerevisiae	hypothetical protein ydr457w - yeast (saccharomycescerevisiae)
CONTIG1275	12144516_f2_1	1613	15716	1344	448	S69625	490	5.5(10)-45	Saccharomyces cerevisiae	hypothetical protein ydr457w - yeast (saccharomycescerevisiae)
CONTIG1949	10646875_c3_4	1614	15717	708	236	S69625	251	1.3(10)-19	Saccharomyces cerevisiae	hypothetical protein ydr457w - yeast (saccharomycescerevisiae)
CONTIG1949	10629567_c3_3	1615	15718	786	262	S69625	516	9.5(10)-48	Saccharomyces cerevisiae	hypothetical protein ydr457w - yeast (saccharomycescerevisiae)
CONTIG2556	23836502_f2_2	1616	15719	972	324	S69625	194	8.9(10)-12	Saccharomyces cerevisiae	hypothetical protein ydr457w - yeast (saccharomycescerevisiae)
CONTIG901	23449043_f3_2	1617	15720	525	175	S69625	730	1.8(10)-70	Saccharomyces cerevisiae	hypothetical protein ydr457w - yeast (saccharomycescerevisiae)
CONTIG5684	4320340_c2_16	1618	15721	1227	409	S69627	197	2.2(10)-13	Saccharomyces cerevisiae	hypothetical protein ydr459c - yeast (saccharomycescerevisiae)
CONTIG3693	12_f3_2	1619	15722	1458	486	S69633	704	1.8(10)-93	Saccharomyces cerevisiae	hypothetical protein ydr465c - yeast (saccharomycescerevisiae)
CONTIG981	175340_c2_4	1620	15723	684	228	S69635	190	4.4(10)-15	Saccharomyces cerevisiae	hypothetical protein ydr468c - yeast (saccharomycescerevisiae)
CONTIG2217	21485000_f1_1	1621	15724	450	150	S69636	156	1.8(10)-11	Saccharomyces cerevisiae	hypothetical protein ydr469w - yeast (saccharomycescerevisiae)
CONTIG2217	9853412_f1_2	1622	15725	240	80	S69637	106	3.7(10)-5	Saccharomyces cerevisiae	hypothetical protein ydr470c - yeast (saccharomycescerevisiae)
CONTIG3070	1067628_f1_1	1623	15726	1698	566	S69641	151	1.3(10)-7	Saccharomyces cerevisiae	hypothetical protein ydr474c - yeast (saccharomycescerevisiae)
CONTIG5095	24098387_f2_2	1624	15727	1878	626	S69646	315	8.3(10)-33	Saccharomyces cerevisiae	hypothetical protein ydr479c - yeast (saccharomycescerevisiae)
CONTIG5707	16978125_c3_23	1625	15728	519	173	S69652	195	2.1(10)-14	Saccharomyces cerevisiae	hypothetical protein ydr485c - yeast (saccharomycescerevisiae)
CONTIG5140	23613385_c2_10	1626	15729	378	126	S69660	191	3.3(10)-15	Saccharomyces cerevisiae	hypothetical protein ydr493w - yeast (saccharomycescerevisiae)
CONTIG3718	4002217_c2_9	1627	15730	924	308	S69557	148	2.0(10)-7	Saccharomyces cerevisiae	hypothetical protein ydr499w - yeast (saccharomycescerevisiae)
CONTIG1874	12901541_c1_3	1628	15731	261	87	S69568	253	9.1(10)-22	Saccharomyces cerevisiae	hypothetical protein ydr511w - yeast (saccharomycescerevisiae)

CONTIG4717	29375312_c2_4	1629	15732	552	184	S69569	147	1.6(10)-10	Saccharomyces cerevisiae	hypothetical protein ydf512c - yeast (saccharomycescerevisiae)
CONTIG5454	24429682_c3_13	1630	15733	879	293	S69574	144	1.7(10)-7	Saccharomyces cerevisiae	hypothetical protein ydf517w - yeast (saccharomycescerevisiae)
CONTIG4648	13673307_f3_3	1631	15734	2742	914	S69580	279	2.6(10)-21	Saccharomyces cerevisiae	hypothetical protein ydf524c - yeast (saccharomycescerevisiae)
CONTIG5684	21882_c2_17	1632	15735	1422	474	S69582	546	8.3(10)-53	Saccharomyces cerevisiae	hypothetical protein ydf527w - yeast (saccharomycescerevisiae)
CONTIG5459	11906503_c3_15	1633	15736	1719	573	S69586	646	1.3(10)-67	Saccharomyces cerevisiae	hypothetical protein ydf531w - yeast (saccharomycescerevisiae)
CONTIG4549	15672152_c3_10	1634	15737	477	159	S69588	480	8.0(10)-46	Saccharomyces cerevisiae	hypothetical protein yer007c-a - yeast (saccharomycescerevisiae)
CONTIG3725	4804007_f3_2	1635	15738	378	126	S53543	405	7.2(10)-38	Saccharomyces cerevisiae	hypothetical protein yer007c-a - yeast (saccharomycescerevisiae)
CONTIG5390	12507212_c2_17	1636	15739	525	175	S53547	191	3.3(10)-15	Saccharomyces cerevisiae	hypothetical protein yer093c-a - yeast (saccharomycescerevisiae)
CONTIG2504	4485253_c2_5	1637	15740	711	237	S46791	723	1.3(10)-71	Saccharomyces cerevisiae	hypothetical protein yhr016c - yeast (saccharomycescerevisiae)
CONTIG5367	25397135_c1_10	1638	15741	1338	446	S64752	739	2.8(10)-73	Saccharomyces cerevisiae	hypothetical protein yll010c - yeast (saccharomycescerevisiae)
CONTIG2282	6672187_c3_3	1639	15742	1305	435	S64755	128	9.0(10)-5	Saccharomyces cerevisiae	hypothetical protein yll013c - yeast (saccharomycescerevisiae)
CONTIG5451	190932_f3_5	1640	15743	2838	946	S64755	842	3.5(10)-84	Saccharomyces cerevisiae	hypothetical protein yll013c - yeast (saccharomycescerevisiae)
CONTIG1958	7242067_f2_1	1641	15744	1122	374	S64780	647	1.6(10)-63	Saccharomyces cerevisiae	hypothetical protein yll029w - yeast (saccharomycescerevisiae)
CONTIG3575	29565882_c1_5	1642	15745	318	106	S64780	186	1.7(10)-13	Saccharomyces cerevisiae	hypothetical protein yll029w - yeast (saccharomycescerevisiae)
CONTIG5645	21523937_f1_1	1643	15746	765	255	S64780	781	1.0(10)-77	Saccharomyces cerevisiae	hypothetical protein yll029w - yeast (saccharomycescerevisiae)
CONTIG4196	34381575_c3_6	1644	15747	1422	474	S64786	259	1.8(10)-19	Saccharomyces cerevisiae	hypothetical protein yll035w - yeast (saccharomycescerevisiae)
CONTIG5683	24662502_c1_15	1645	15748	987	329	S64789	105	0.002	Saccharomyces cerevisiae	hypothetical protein yll038c - yeast (saccharomycescerevisiae)

CONTIG51512	7760_f2_1	1646	15749	768	256	S64824	304	2.7(10)-26	Saccharomyces cerevisiae	hypothetical protein ylr002c - yeast (saccharomycescerevisiae)
CONTIG4372	7064177_f1_1	1647	15750	237	79	S64824	105	6.9(10)-5	Saccharomyces cerevisiae	hypothetical protein ylr002c - yeast (saccharomycescerevisiae)
CONTIG576	12402137_f2_1	1648	15751	657	219	S64824	241	1.7(10)-19	Saccharomyces cerevisiae	hypothetical protein ylr002c - yeast (saccharomycescerevisiae)
b2x14796.y	23650037_c3_3	1649	15752	516	172	S64825	91	0.01299	Saccharomyces cerevisiae	hypothetical protein ylr003c - yeast (saccharomycescerevisiae)
CONTIG5774	34179687_f1_1	1650	15753	1722	574	S64860	243	4.0(10)-33	Saccharomyces cerevisiae	hypothetical protein ylr033w - yeast (saccharomycescerevisiae)
CONTIG5450	4882812_f1_2	1651	15754	669	223	S61625	396	6.5(10)-37	Saccharomyces cerevisiae	hypothetical protein ylr051c - yeast (saccharomycescerevisiae)
CONTIG3527	21878793_c3_7	1652	15755	423	141	S64906	188	7.0(10)-15	Saccharomyces cerevisiae	hypothetical protein ylr074c - yeast (saccharomycescerevisiae)
CONTIG5277	33242325_f2_6	1653	15756	1374	458	S64931	233	2.1(10)-29	Saccharomyces cerevisiae	hypothetical protein ylr097c - yeast (saccharomycescerevisiae)
CONTIG5779	22300817_f2_7	1654	15757	1161	387	S64944	443	6.7(10)-42	Saccharomyces cerevisiae	hypothetical protein ylr107w - yeast (saccharomycescerevisiae)
CONTIG4656	4782200_c1_6	1655	15758	2460	820	S64951	794	4.2(10)-79	Saccharomyces cerevisiae	hypothetical protein ylr114c - yeast (saccharomycescerevisiae)
CONTIG5112	34094688_f1_1	1656	15759	1320	440	S64954	678	8.5(10)-67	Saccharomyces cerevisiae	hypothetical protein ylr117c - yeast (saccharomycescerevisiae)
CONTIG5705	21617625_f3_11	1657	15760	1698	566	S59315	144	2.1(10)-6	Saccharomyces cerevisiae	hypothetical protein ylr127c - yeast (saccharomycescerevisiae)
CONTIG5705	234702_f3_12	1658	15761	783	261	S59315	199	8.5(10)-15	Saccharomyces cerevisiae	hypothetical protein ylr127c - yeast (saccharomycescerevisiae)
CONTIG5705	30588436_c1_18	1659	15762	930	310	S59316	162	1.1(10)-17	Saccharomyces cerevisiae	hypothetical protein ylr128w - yeast (saccharomycescerevisiae)
CONTIG5383	4789063_f3_3	1660	15763	2028	676	S64985	707	9.5(10)-115	Saccharomyces cerevisiae	hypothetical protein ylr143w - yeast (saccharomycescerevisiae)
CONTIG5433	5188430_f2_2	1661	15764	2262	754	S64993	1108	2.2(10)-112	Saccharomyces cerevisiae	hypothetical protein ylr144c - yeast (saccharomycescerevisiae)
CONTIG5638	6814055_f3_12	1662	15765	1728	576	S64998	227	6.2(10)-39	Saccharomyces cerevisiae	hypothetical protein ylr149c - yeast (saccharomycescerevisiae)

CONTIG1155	33751687_f1_1	1663	15766	390	130	S68481	103	2.5(10)-5	Saccharomyces cerevisiae	hypothetical protein ylr165c - yeast (saccharomycescerevisiae)
CONTIG1580	33751687_c1_4	1664	15767	462	154	S68481	136	4.7(10)-9	Saccharomyces cerevisiae	hypothetical protein ylr165c - yeast (saccharomycescerevisiae)
CONTIG3733	13006378_c2_3	1665	15768	261	87	S51438	215	5.7(10)-17	Saccharomyces cerevisiae	hypothetical protein ylr183c - yeast (saccharomycescerevisiae)
CONTIG2333	4687575_f3_1	1666	15769	870	290	S51431	951	1.0(10)-95	Saccharomyces cerevisiae	hypothetical protein ylr186w - yeast (saccharomycescerevisiae)
CONTIG1558	22666275_c3_5	1667	15770	1020	340	S51432	633	2.5(10)-61	Saccharomyces cerevisiae	hypothetical protein ylr187w - yeast (saccharomycescerevisiae)
CONTIG435	34166062_c1_4	1668	15771	819	273	S51434	122	5.0(10)-11	Saccharomyces cerevisiae	hypothetical protein ylr189c - yeast (saccharomycescerevisiae)
CONTIG565	36115631_c3_2	1669	15772	1014	338	S51434	124	0.00012	Saccharomyces cerevisiae	hypothetical protein ylr189c - yeast (saccharomycescerevisiae)
b2x19027.x	480041_f3_1	1670	15773	507	169	S51434	333	6.9(10)-29	Saccharomyces cerevisiae	hypothetical protein ylr189c - yeast (saccharomycescerevisiae)
CONTIG5696	5360762_f3_6	1671	15774	762	254	S48545	287	2.2(10)-25	Saccharomyces cerevisiae	hypothetical protein ylr192c - yeast (saccharomycescerevisiae)
CONTIG4850	36131316_c1_8	1672	15775	627	209	S48546	375	1.1(10)-34	Saccharomyces cerevisiae	hypothetical protein ylr193c - yeast (saccharomycescerevisiae)
CONTIG2729	3164062_c3_2	1673	15776	876	292	S48553	291	8.6(10)-26	Saccharomyces cerevisiae	hypothetical protein ylr201c - yeast (saccharomycescerevisiae)
CONTIG4667	6832926_f2_1	1674	15777	1638	546	S48557	410	4.7(10)-59	Saccharomyces cerevisiae	hypothetical protein ylr206w - yeast (saccharomycescerevisiae)
CONTIG3918	34555217_f3_4	1675	15778	1059	353	S48566	565	8.0(10)-55	Saccharomyces cerevisiae	hypothetical protein ylr215c - yeast (saccharomycescerevisiae)
CONTIG5132	2386286_f3_6	1676	15779	219	73	S48568	237	4.5(10)-20	Saccharomyces cerevisiae	hypothetical protein ylr218c - yeast (saccharomycescerevisiae)
CONTIG4279	24613561_c2_4	1677	15780	693	231	S51444	143	4.2(10)-10	Saccharomyces cerevisiae	hypothetical protein ylr221c - yeast (saccharomycescerevisiae)
CONTIG3494	4882830_f1_2	1678	15781	294	98	S51447	124	2.6(10)-7	Saccharomyces cerevisiae	hypothetical protein ylr224w - yeast (saccharomycescerevisiae)
CONTIG5756	4866312_c2_21	1679	15782	978	326	S51458	414	8.0(10)-39	Saccharomyces cerevisiae	hypothetical protein ylr239c - yeast (saccharomycescerevisiae)

CONTIG5796	13878135_f3_14	1680	15783	999	333	S51406	678	2.2(10)-78	Saccharomyces cerevisiae	hypothetical protein ylr270w - yeast (saccharomycescerevisiae)
CONTIG5788	34179702_f3_11	1681	15784	816	272	S51407	161	4.7(10)-19	Saccharomyces cerevisiae	hypothetical protein ylr271w - yeast (saccharomycescerevisiae)
CONTIG1977	198582_c2_3	1682	15785	1200	400	S51408	478	2.1(10)-44	Saccharomyces cerevisiae	hypothetical protein ylr272c - yeast (saccharomycescerevisiae)
CONTIG3262	12503875_c2_7	1683	15786	261	87	S51408	107	8.4(10)-5	Saccharomyces cerevisiae	hypothetical protein ylr272c - yeast (saccharomycescerevisiae)
CONTIG2680	31593_c1_5	1684	15787	975	325	S50372	110	0.00042	Saccharomyces cerevisiae	hypothetical protein ylr287c - yeast (saccharomycescerevisiae)
CONTIG3348	5273437_c1_13	1685	15788	849	283	S50375	479	1.0(10)-45	Saccharomyces cerevisiae	hypothetical protein ylr290c - yeast (saccharomycescerevisiae)
CONTIG3321	10992128_c1_6	1686	15789	1476	492	S51441	94	0.34	Saccharomyces cerevisiae	hypothetical protein ylr309c - yeast (saccharomycescerevisiae)
CONTIG886	21972809_c2_2	1687	15790	621	207	S51441	100	0.01499	Saccharomyces cerevisiae	hypothetical protein ylr309c - yeast (saccharomycescerevisiae)
CONTIG5416	9859833_c3_13	1688	15791	825	275	S53395	338	9.0(10)-31	Saccharomyces cerevisiae	hypothetical protein ylr316c - yeast (saccharomycescerevisiae)
CONTIG1468	35973266_f1_1	1689	15792	804	268	S53396	134	5.7(10)-6	Saccharomyces cerevisiae	hypothetical protein ylr318w - yeast (saccharomycescerevisiae)
CONTIG3328	10345281_f1_1	1690	15793	561	187	S51388	526	1.1(10)-50	Saccharomyces cerevisiae	hypothetical protein ylr370c - yeast (saccharomycescerevisiae)
CONTIG1673	33672638_f2_1	1691	15794	288	96	S51467	142	3.3(10)-9	Saccharomyces cerevisiae	hypothetical protein ylr380w - yeast (saccharomycescerevisiae)
CONTIG5165	14298557_c2_16	1692	15795	732	244	S51474	243	3.2(10)-20	Saccharomyces cerevisiae	hypothetical protein ylr387c - yeast (saccharomycescerevisiae)
CONTIG5753	35674013_f3_8	1693	15796	798	266	S51474	541	2.7(10)-52	Saccharomyces cerevisiae	hypothetical protein ylr387c - yeast (saccharomycescerevisiae)
CONTIG5337	4183432_f1_1	1694	15797	999	333	S55950	159	5.5(10)-9	Saccharomyces cerevisiae	hypothetical protein ylr394w - yeast (saccharomycescerevisiae)
CONTIG4139	980026_c2_11	1695	15798	1011	337	S59376	532	6.0(10)-56	Saccharomyces cerevisiae	hypothetical protein ylr410w - yeast (saccharomycescerevisiae)
CONTIG2295	10833318_c1_3	1696	15799	1182	394	S59376	811	9.4(10)-81	Saccharomyces cerevisiae	hypothetical protein ylr410w - yeast (saccharomycescerevisiae)

b9x13a89.x	25401392_c3_4	1697	15800	693	231	S59376	630	9.0(10)-61	Saccharomyces cerevisiae	hypothetical protein yll410w - yeast (saccharomycescerevisiae)
CONTIG4001	16836002_f1_2	1698	15801	483	161	S59378	225	8.5(10)-19	Saccharomyces cerevisiae	hypothetical protein yll412w - yeast (saccharomycescerevisiae)
CONTIG3034	35426637_c2_1	1699	15802	1041	347	S59382	183	1.3(10)-11	Saccharomyces cerevisiae	hypothetical protein yll417w - yeast (saccharomycescerevisiae)
CONTIG2903	23475836_c2_6	1700	15803	1095	365	S59384	263	2.6(10)-21	Saccharomyces cerevisiae	hypothetical protein yll419w - yeast (saccharomycescerevisiae)
CONTIG5705	34117217_c2_19	1701	15804	387	129	S59384	282	2.5(10)-23	Saccharomyces cerevisiae	hypothetical protein yll419w - yeast (saccharomycescerevisiae)
b9x11f43.x	24353442_f1_1	1702	15805	729	243	S59384	320	2.2(10)-27	Saccharomyces cerevisiae	hypothetical protein yll419w - yeast (saccharomycescerevisiae)
CONTIG4618	23862537_c2_4	1703	15806	354	118	S69319	186	1.2(10)-14	Saccharomyces cerevisiae	hypothetical protein yll421c - yeast (saccharomycescerevisiae)
CONTIG4085	9798432_f3_4	1704	15807	1863	621	S53411	142	3.0(10)-6	Saccharomyces cerevisiae	hypothetical protein yll424w - yeast (saccharomycescerevisiae)
CONTIG4399	5272561_f1_1	1705	15808	351	117	S59404	366	9.8(10)-34	Saccharomyces cerevisiae	hypothetical protein yll435w - yeast (saccharomycescerevisiae)
b9x13a50.x	89026_f3_2	1706	15809	570	190	S55966	197	4.2(10)-15	Saccharomyces cerevisiae	hypothetical protein yll443w - yeast (saccharomycescerevisiae)
CONTIG5458	16428311_c1_11	1707	15810	339	113	S69858	227	5.2(10)-19	Saccharomyces cerevisiae	hypothetical protein yml244c-a - yeast (saccharomycescerevisiae)
CONTIG4905	4772130_f1_1	1708	15811	1806	602	S66717	744	2.2(10)-73	Saccharomyces cerevisiae	hypothetical protein yll034w - yeast (saccharomycescerevisiae)
CONTIG5635	20890654_c1_13	1709	15812	1446	482	S66717	625	2.6(10)-60	Saccharomyces cerevisiae	hypothetical protein yll034w - yeast (saccharomycescerevisiae)
CONTIG5468	10976588_f1_3	1710	15813	1374	458	S66726	605	2.1(10)-71	Saccharomyces cerevisiae	hypothetical protein yll041c - yeast (saccharomycescerevisiae)
CONTIG5481	10975937_f2_4	1711	15814	2109	703	S66749	1246	1.3(10)-154	Saccharomyces cerevisiae	hypothetical protein yll057w - yeast (saccharomycescerevisiae)
CONTIG5704	567151_c1_12	1712	15815	750	250	S66763	206	5.9(10)-16	Saccharomyces cerevisiae	hypothetical protein yll070c - yeast (saccharomycescerevisiae)
CONTIG3842	1210312_f1_2	1713	15816	474	158	S66764	340	5.5(10)-31	Saccharomyces cerevisiae	hypothetical protein yll071w - yeast (saccharomycescerevisiae)

CONTIG4914	19957626_f2_3	1714	15817	885	295	S66773	563	1.3(10)-54	Saccharomyces cerevisiae	hypothetical protein y0l080c - yeast (saccharomycescerevisiae)
CONTIG3055	23865953_c1_3	1715	15818	861	287	S57382	129	2.7(10)-5	Saccharomyces cerevisiae	hypothetical protein y0l087c - yeast (saccharomycescerevisiae)
CONTIG3580	433340_f2_1	1716	15819	789	263	S57382	201	7.5(10)-15	Saccharomyces cerevisiae	hypothetical protein y0l087c - yeast (saccharomycescerevisiae)
b3x17370.x	212557_f3_2	1717	15820	183	61	S57376	135	9.6(10)-9	Saccharomyces cerevisiae	hypothetical protein y0l093w - yeast (saccharomycescerevisiae)
b9x13a48.y	22632202_c1_3	1718	15821	678	226	S57376	288	1.8(10)-25	Saccharomyces cerevisiae	hypothetical protein y0l093w - yeast (saccharomycescerevisiae)
CONTIG2227	4566306_f1_1	1719	15822	1095	365	S51900	261	5.7(10)-29	Saccharomyces cerevisiae	hypothetical protein y0l098c - yeast (saccharomycescerevisiae)
CONTIG3647	22689087_c3_6	1720	15823	636	212	S51900	432	1.3(10)-39	Saccharomyces cerevisiae	hypothetical protein y0l098c - yeast (saccharomycescerevisiae)
CONTIG659	25582750_f1_1	1721	15824	798	266	S51900	422	1.6(10)-38	Saccharomyces cerevisiae	hypothetical protein y0l098c - yeast (saccharomycescerevisiae)
CONTIG4769	10344655_c3_10	1722	15825	594	198	S51883	256	4.4(10)-22	Saccharomyces cerevisiae	hypothetical protein y0l114c - yeast (saccharomycescerevisiae)
CONTIG5521	7070260_c3_30	1723	15826	1425	475	S63447	1204	1.5(10)-122	Saccharomyces cerevisiae	hypothetical protein y0l124c - yeast (saccharomycescerevisiae)
CONTIG4741	30507200_c3_18	1724	15827	348	116	S63445	107	1.6(10)-10	Saccharomyces cerevisiae	hypothetical protein y0l125w - yeast (saccharomycescerevisiae)
CONTIG4741	2120393_c3_17	1725	15828	936	312	S63445	290	2.7(10)-25	Saccharomyces cerevisiae	hypothetical protein y0l125w - yeast (saccharomycescerevisiae)
CONTIG5142	24301550_f1_1	1726	15829	936	312	S66832	148	6.0(10)-22	Saccharomyces cerevisiae	hypothetical protein y0l135c - yeast (saccharomycescerevisiae)
CONTIG3025	33322155_f2_1	1727	15830	1593	531	S61873	689	5.7(10)-68	Saccharomyces cerevisiae	hypothetical protein y0l141w - yeast (saccharomycescerevisiae)
CONTIG2493	24495442_c3_9	1728	15831	366	122	S61872	177	1.0(10)-13	Saccharomyces cerevisiae	hypothetical protein y0l142w - yeast (saccharomycescerevisiae)
CONTIG4677	4953427_c2_7	1729	15832	1968	656	S61870	205	1.7(10)-30	Saccharomyces cerevisiae	hypothetical protein y0l144w - yeast (saccharomycescerevisiae)
CONTIG5396	20425805_c2_13	1730	15833	828	276	S61987	570	2.3(10)-55	Saccharomyces cerevisiae	hypothetical protein y0r004w - yeast (saccharomycescerevisiae)

CONTIG4975	20900336_f2_3	1731	15834	624	208	S54627	714	1.3(10)-70	Saccharomyces cerevisiae	hypothetical protein yor021c - yeast (saccharomycescerevisiae)
CONTIG4536	22829638_f1_2	1732	15835	714	238	S54628	316	1.7(10)-27	Saccharomyces cerevisiae	hypothetical protein yor022c - yeast (saccharomycescerevisiae)
CONTIG4975	6745177_c1_7	1733	15836	1524	508	S54628	583	9.9(10)-57	Saccharomyces cerevisiae	hypothetical protein yor022c - yeast (saccharomycescerevisiae)
CONTIG5310	13960187_f2_2	1734	15837	912	304	S54629	173	1.3(10)-10	Saccharomyces cerevisiae	hypothetical protein yor023c - yeast (saccharomycescerevisiae)
CONTIG5639	16834680_c3_24	1735	15838	981	327	S66916	177	5.4(10)-13	Saccharomyces cerevisiae	hypothetical protein yor042w - yeast (saccharomycescerevisiae)
CONTIG2032	29563878_c1_3	1736	15839	744	248	S66923	106	0.00012	Saccharomyces cerevisiae	hypothetical protein yor049c - yeast (saccharomycescerevisiae)
CONTIG3741	33804687_c3_5	1737	15840	1056	352	S66923	343	2.7(10)-31	Saccharomyces cerevisiae	hypothetical protein yor049c - yeast (saccharomycescerevisiae)
CONTIG3987	1954063_c3_8	1738	15841	1362	454	S66923	380	3.2(10)-35	Saccharomyces cerevisiae	hypothetical protein yor049c - yeast (saccharomycescerevisiae)
CONTIG4353	4707125_f3_3	1739	15842	1506	502	S66923	373	1.8(10)-34	Saccharomyces cerevisiae	hypothetical protein yor049c - yeast (saccharomycescerevisiae)
CONTIG5819	16834683_f2_13	1740	15843	1272	424	S66925	536	9.5(10)-52	Saccharomyces cerevisiae	hypothetical protein yor051c - yeast (saccharomycescerevisiae)
CONTIG5819	6837757_c2_45	1741	15844	561	187	S66926	190	4.4(10)-15	Saccharomyces cerevisiae	hypothetical protein yor052c - yeast (saccharomycescerevisiae)
CONTIG5778	4970252_c2_27	1742	15845	1413	471	S66939	730	3.8(10)-95	Saccharomyces cerevisiae	hypothetical protein yor056c - yeast (saccharomycescerevisiae)
CONTIG5406	14256667_f1_4	1743	15846	903	301	S66943	95	0.028	Saccharomyces cerevisiae	hypothetical protein yor060c - yeast (saccharomycescerevisiae)
CONTIG5730	3992010_f2_6	1744	15847	1083	361	S66947	156	1.6(10)-19	Saccharomyces cerevisiae	hypothetical protein yor064c - yeast (saccharomycescerevisiae)
CONTIG3290	26597180_c2_2	1745	15848	360	120	S66963	129	2.2(10)-7	Saccharomyces cerevisiae	hypothetical protein yor080w - yeast (saccharomycescerevisiae)
CONTIG3093	33370300_f2_5	1746	15849	702	234	S61651	585	6.0(10)-57	Saccharomyces cerevisiae	hypothetical protein yor091w - yeast (saccharomycescerevisiae)
CONTIG4999	14631876_c3_12	1747	15850	1230	410	S66977	447	2.6(10)-42	Saccharomyces cerevisiae	hypothetical protein yor092w - yeast (saccharomycescerevisiae)

CONTIG2135	26344010_f2_4	1748	15851	645	215	S60992	243	1.3(10)-19	Saccharomyces cerevisiae	hypothetical protein yor112w - yeast (saccharomycescerevisiae)
CONTIG4511	23609655_f1_1	1749	15852	720	240	S61003	297	2.0(10)-26	Saccharomyces cerevisiae	hypothetical protein yor115c - yeast (saccharomycescerevisiae)
CONTIG4911	4900252_f2_2	1750	15853	2697	899	S61698	281	4.7(10)-25	Saccharomyces cerevisiae	hypothetical protein yor144c - yeast (saccharomycescerevisiae)
CONTIG5696	16835187_c2_18	1751	15854	837	279	S67033	886	7.7(10)-89	Saccharomyces cerevisiae	hypothetical protein yor145c - yeast (saccharomycescerevisiae)
CONTIG2288	12500090_f2_1	1752	15855	561	187	S67043	305	3.1(10)-27	Saccharomyces cerevisiae	hypothetical protein yor155c - yeast (saccharomycescerevisiae)
CONTIG383	10625278_f2_3	1753	15856	618	206	S67043	384	1.2(10)-35	Saccharomyces cerevisiae	hypothetical protein yor155c - yeast (saccharomycescerevisiae)
CONTIG2160	35417293_f2_1	1754	15857	495	165	S67051	317	1.5(10)-28	Saccharomyces cerevisiae	hypothetical protein yor163w - yeast (saccharomycescerevisiae)
CONTIG2160	24314575_c2_5	1755	15858	1026	342	S67052	266	3.8(10)-23	Saccharomyces cerevisiae	hypothetical protein yor164c - yeast (saccharomycescerevisiae)
CONTIG5479	21675000_c2_12	1756	15859	1611	537	S67059	633	6.0(10)-101	Saccharomyces cerevisiae	hypothetical protein yor171c - yeast (saccharomycescerevisiae)
CONTIG5788	33320292_c1_18	1757	15860	1008	336	S67062	195	4.0(10)-18	Saccharomyces cerevisiae	hypothetical protein yor174w - yeast (saccharomycescerevisiae)
CONTIG3393	12290927_c2_5	1758	15861	1428	476	S67083	621	2.2(10)-59	Saccharomyces cerevisiae	hypothetical protein yor191w - yeast (saccharomycescerevisiae)
CONTIG5802	24226387_c1_25	1759	15862	1371	457	S67089	978	1.3(10)-98	Saccharomyces cerevisiae	hypothetical protein yor197w - yeast (saccharomycescerevisiae)
CONTIG2957	4725675_c1_4	1760	15863	837	279	S60947	126	6.5(10)-6	Saccharomyces cerevisiae	hypothetical protein yor220w - yeast (saccharomycescerevisiae)
CONTIG1321	11113876_c1_3	1761	15864	321	107	S67131	186	1.8(10)-14	Saccharomyces cerevisiae	hypothetical protein yor238w - yeast (saccharomycescerevisiae)
CONTIG5813	485931_c2_48	1762	15865	810	270	S67155	300	8.0(10)-31	Saccharomyces cerevisiae	hypothetical protein yor258w - yeast (saccharomycescerevisiae)
CONTIG3777	187817_c2_3	1763	15866	378	126	S67183	213	1.6(10)-17	Saccharomyces cerevisiae	hypothetical protein yor281c - yeast (saccharomycescerevisiae)
CONTIG4807	10649055_c3_10	1764	15867	858	286	S67189	372	2.2(10)-34	Saccharomyces cerevisiae	hypothetical protein yor287c - yeast (saccharomycescerevisiae)

CONTIG1842	277317_f1_1	1765	15868	657	219	S67191	253	9.1(10)-22	Saccharomyces cerevisiae	hypothetical protein yor289w - yeast (Saccharomycescerevisiae)
CONTIG4948	9852290_f3_6	1766	15869	633	211	S67198	732	1.6(10)-72	Saccharomyces cerevisiae	hypothetical protein yor294w - yeast (Saccharomycescerevisiae)
CONTIG4691	24647656_f2_2	1767	15870	2433	811	S67200	540	2.0(10)-93	Saccharomyces cerevisiae	hypothetical protein yor296w - yeast (Saccharomycescerevisiae)
CONTIG4948	978125_f1_3	1768	15871	927	309	S67200	139	4.5(10)-9	Saccharomyces cerevisiae	hypothetical protein yor296w - yeast (Saccharomycescerevisiae)
CONTIG5812	4038125_f3_13	1769	15872	744	248	S67209	132	4.7(10)-7	Saccharomyces cerevisiae	hypothetical protein yor305w - yeast (Saccharomycescerevisiae)
CONTIG1727	2385942_f1_1	1770	15873	408	136	S58319	117	3.1(10)-6	Saccharomyces cerevisiae	hypothetical protein yor308c - yeast (Saccharomycescerevisiae)
CONTIG2180	10829192_f1_1	1771	15874	513	171	S58319	117	3.1(10)-6	Saccharomyces cerevisiae	hypothetical protein yor308c - yeast (Saccharomycescerevisiae)
CONTIG4545	11894432_f1_1	1772	15875	1608	536	S58319	130	6.7(10)-10	Saccharomyces cerevisiae	hypothetical protein yor308c - yeast (Saccharomycescerevisiae)
b2x17256.y	46876260_f2_1	1773	15876	507	169	S67247	394	1.1(10)-36	Saccharomyces cerevisiae	hypothetical protein yor338w - yeast (Saccharomycescerevisiae)
CONTIG5698	898457_f1_7	1774	15877	501	167	S67269	292	6.7(10)-26	Saccharomyces cerevisiae	hypothetical protein yor357c - yeast (Saccharomycescerevisiae)
CONTIG3335	14225307_c3_3	1775	15878	1434	478	S67283	198	2.3(10)-12	Saccharomyces cerevisiae	hypothetical protein yor371c - yeast (Saccharomycescerevisiae)
CONTIG5699	24007061_c2_28	1776	15879	1818	606	S52526	207	2.1(10)-13	Saccharomyces cerevisiae	hypothetical protein yp1005w - yeast (Saccharomycescerevisiae)
CONTIG1935	32214077_f3_3	1777	15880	606	202	S52522	473	5.2(10)-44	Saccharomyces cerevisiae	hypothetical protein yp1009c - yeast (Saccharomycescerevisiae)
b2x14507.y	480083_f3_1	1778	15881	546	182	S52522	133	1.2(10)-7	Saccharomyces cerevisiae	hypothetical protein yp1009c - yeast (Saccharomycescerevisiae)
CONTIG3925	4303879_c1_3	1779	15882	1233	411	S52522	691	1.1(10)-67	Saccharomyces cerevisiae	hypothetical protein yp1009c - yeast (Saccharomycescerevisiae)
CONTIG2812	33786557_f1_1	1780	15883	315	105	S52520	181	1.3(10)-13	Saccharomyces cerevisiae	hypothetical protein yp1011c - yeast (Saccharomycescerevisiae)
CONTIG5209	24480301_c1_8	1781	15884	1215	405	S59679	93	0.11	Saccharomyces cerevisiae	hypothetical protein yp1014w - yeast (Saccharomycescerevisiae)

CONTIG3455	2118806_f2_2	1782	15885	348	116	S63462	90	0.00259	Saccharomyces cerevisiae	hypothetical protein ypl020c - yeast (saccharomycescerevisiae)
CONTIG4940	11109702_f3_3	1783	15886	1476	492	S63462	425	7.2(10)-40	Saccharomyces cerevisiae	hypothetical protein ypl020c - yeast (saccharomycescerevisiae)
CONTIG5317	26775253_f3_11	1784	15887	510	170	S63458	95	0.0051	Saccharomyces cerevisiae	hypothetical protein ypl024w - yeast (saccharomycescerevisiae)
CONTIG3310	26261077_f1_1	1785	15888	249	83	S63452	143	4.7(10)-9	Saccharomyces cerevisiae	hypothetical protein ypl030w - yeast (saccharomycescerevisiae)
CONTIG3632	20329457_c2_8	1786	15889	1008	336	S63452	502	1.7(10)-63	Saccharomyces cerevisiae	hypothetical protein ypl030w - yeast (saccharomycescerevisiae)
CONTIG3949	9961006_f2_2	1787	15890	516	172	S60927	294	9.5(10)-26	Saccharomyces cerevisiae	hypothetical protein ypl063w - yeast (saccharomycescerevisiae)
CONTIG4163	16500028_c3_6	1788	15891	558	186	S60925	262	1.0(10)-22	Saccharomyces cerevisiae	hypothetical protein ypl065w - yeast (saccharomycescerevisiae)
CONTIG3302	4772187_f3_2	1789	15892	399	133	S60923	142	5.2(10)-10	Saccharomyces cerevisiae	hypothetical protein ypl067c - yeast (saccharomycescerevisiae)
CONTIG2472	5913918_f1_1	1790	15893	1263	421	S61105	164	2.5(10)-9	Saccharomyces cerevisiae	hypothetical protein ypl083c - yeast (saccharomycescerevisiae)
CONTIG3765	4457682_c1_5	1791	15894	1443	481	S61980	2203	2.1(10)-228	Saccharomyces cerevisiae	hypothetical protein ypl086c - yeast (saccharomycescerevisiae)
CONTIG2177	4879567_f3_2	1792	15895	1008	336	S61973	1346	1.3(10)-137	Saccharomyces cerevisiae	hypothetical protein ypl093w - yeast (saccharomycescerevisiae)
CONTIG4346	194657_c1_2	1793	15896	570	190	S61973	360	2.0(10)-32	Saccharomyces cerevisiae	hypothetical protein ypl093w - yeast (saccharomycescerevisiae)
CONTIG2762	24877343_f1_1	1794	15897	516	172	S61970	215	4.0(10)-22	Saccharomyces cerevisiae	hypothetical protein ypl096w - yeast (saccharomycescerevisiae)
CONTIG5200	174092_f2_4	1795	15898	1491	497	S61997	544	1.2(10)-51	Saccharomyces cerevisiae	hypothetical protein ypl125w - yeast (saccharomycescerevisiae)
b9x1lu37.y	29335425_c2_4	1796	15899	642	214	S61997	396	9.5(10)-36	Saccharomyces cerevisiae	hypothetical protein ypl125w - yeast (saccharomycescerevisiae)
CONTIG5666	24414052_c2_14	1797	15900	1287	429	S69047	306	2.2(10)-27	Saccharomyces cerevisiae	hypothetical protein ypl138c - yeast (saccharomycescerevisiae)
CONTIG4841	35573416_c3_6	1798	15901	1002	334	S65157	239	2.3(10)-38	Saccharomyces cerevisiae	hypothetical protein ypl146c - yeast (saccharomycescerevisiae)

CONTIG2343	5163282_c3_7	1799	15902	1026	342	S65168	314	3.2(10)-28	Saccharomyces cerevisiae	hypothetical protein ypl157w - yeast (saccharomycescerevisiae)
CONTIG5586	3929551_c3_18	1800	15903	1176	392	S65176	450	1.2(10)-42	Saccharomyces cerevisiae	hypothetical protein ypl165c - yeast (saccharomycescerevisiae)
CONTIG3690	10211532_c2_5	1801	15904	735	245	S65180	394	2.0(10)-36	Saccharomyces cerevisiae	hypothetical protein ypl169c - yeast (saccharomycescerevisiae)
CONTIG4361	38155_c2_9	1802	15905	963	321	S65180	450	1.2(10)-42	Saccharomyces cerevisiae	hypothetical protein ypl169c - yeast (saccharomycescerevisiae)
CONTIG4361	13704035_c2_8	1803	15906	513	171	S65181	350	4.9(10)-32	Saccharomyces cerevisiae	hypothetical protein ypl170w - yeast (saccharomycescerevisiae)
CONTIG5292	23694452_c1_10	1804	15907	1440	480	S65193	220	6.4(10)-24	Saccharomyces cerevisiae	hypothetical protein ypl181w - yeast (saccharomycescerevisiae)
CONTIG3555	3906336_c1_4	1805	15908	1482	494	S65210	144	3.7(10)-11	Saccharomyces cerevisiae	hypothetical protein ypl191c - yeast (saccharomycescerevisiae)
CONTIG3550	970187_f2_7	1806	15909	1494	498	S65213	170	1.3(10)-9	Saccharomyces cerevisiae	hypothetical protein ypl194w - yeast (saccharomycescerevisiae)
CONTIG2909	22166562_c3_6	1807	15910	243	81	S65215	140	2.2(10)-9	Saccharomyces cerevisiae	hypothetical protein ypl196w - yeast (saccharomycescerevisiae)
CONTIG3550	23875762_c2_15	1808	15911	1083	361	S65215	297	4.7(10)-42	Saccharomyces cerevisiae	hypothetical protein ypl196w - yeast (saccharomycescerevisiae)
CONTIG1085	23550143_f1_1	1809	15912	603	201	S65218	355	1.3(10)-32	Saccharomyces cerevisiae	hypothetical protein ypl199c - yeast (saccharomycescerevisiae)
CONTIG590	4171931_f3_1	1810	15913	555	185	S65230	789	1.5(10)-78	Saccharomyces cerevisiae	hypothetical protein ypl211w - yeast (saccharomycescerevisiae)
CONTIG4363	239536_f3_5	1811	15914	729	243	S65232	246	5.0(10)-21	Saccharomyces cerevisiae	hypothetical protein ypl213w - yeast (saccharomycescerevisiae)
CONTIG4264	12694693_c2_7	1812	15915	276	92	S65241	116	4.7(10)-6	Saccharomyces cerevisiae	hypothetical protein ypl222w - yeast (saccharomycescerevisiae)
CONTIG5334	24017176_c1_7	1813	15916	468	156	S65244	439	1.8(10)-41	Saccharomyces cerevisiae	hypothetical protein ypl225w - yeast (saccharomycescerevisiae)
CONTIG5624	35312876_f3_8	1814	15917	1584	528	S61706	322	2.1(10)-34	Saccharomyces cerevisiae	hypothetical protein ypl228w - yeast (saccharomycescerevisiae)
CONTIG5661	25439030_c2_10	1815	15918	738	246	S61706	269	1.0(10)-22	Saccharomyces cerevisiae	hypothetical protein ypl228w - yeast (saccharomycescerevisiae)

CONTIG3371	23938802_f2_2	1816	15919	732	244	S61701	212	2.0(10)-17	Saccharomyces cerevisiae	hypothetical protein ypl233w - yeast (saccharomycetaceae)
CONTIG3515	110637_c3_6	1817	15920	1524	508	S61029	1782	8.6(10)-184	Saccharomyces cerevisiae	hypothetical protein ypl235w - yeast (saccharomycetaceae)
CONTIG5539	10719063_c2_12	1818	15921	279	93	S61017	103	2.2(10)-9	Saccharomyces cerevisiae	hypothetical protein ypl247c - yeast (saccharomycetaceae)
CONTIG5578	3907812_f3_5	1819	15922	1509	503	S61017	442	3.1(10)-55	Saccharomyces cerevisiae	hypothetical protein ypl247c - yeast (saccharomycetaceae)
CONTIG5815	14570181_f1_6	1820	15923	1659	553	S61015	827	1.3(10)-82	Saccharomyces cerevisiae	hypothetical protein ypl249c - yeast (saccharomycetaceae)
CONTIG5344	22915955_f3_10	1821	15924	615	205	S61012	343	2.7(10)-31	Saccharomyces cerevisiae	hypothetical protein ypl252c - yeast (saccharomycetaceae)
CONTIG5565	24020003_c1_22	1822	15925	1953	651	S65296	796	2.2(10)-129	Saccharomyces cerevisiae	hypothetical protein ypl263c - yeast (saccharomycetaceae)
CONTIG683	12691692_f1_1	1823	15926	894	298	S65302	139	1.2(10)-6	Saccharomyces cerevisiae	hypothetical protein ypl269w - yeast (saccharomycetaceae)
CONTIG5575	30517575_f3_8	1824	15927	1578	526	S52820	113	0.00309	Saccharomyces cerevisiae	hypothetical protein ypr007c - yeast (saccharomycetaceae)
CONTIG5434	10348402_c2_7	1825	15928	789	263	S57550	1170	6.2(10)-119	Saccharomyces cerevisiae	hypothetical protein ypr016c - yeast (saccharomycetaceae)
b9x11g23.x	23594413_f2_1	1826	15929	243	81	S54497	159	4.7(10)-11	Saccharomyces cerevisiae	hypothetical protein ypr023c - yeast (saccharomycetaceae)
CONTIG5491	23617062_c3_13	1827	15930	1170	390	S61061	578	3.3(10)-56	Saccharomyces cerevisiae	hypothetical protein ypr040w - yeast (saccharomycetaceae)
CONTIG3651	4790902_c2_2	1828	15931	1011	337	S69063	91	8.4(10)-5	Saccharomyces cerevisiae	hypothetical protein ypr075c - yeast (saccharomycetaceae)
CONTIG4087	9975186_c3_4	1829	15932	969	323	S69065	316	1.8(10)-28	Saccharomyces cerevisiae	hypothetical protein ypr079w - yeast (saccharomycetaceae)
CONTIG5154	36362812_f2_4	1830	15933	453	151	S69068	528	6.7(10)-51	Saccharomyces cerevisiae	hypothetical protein ypr082c - yeast (saccharomycetaceae)
CONTIG4864	4490801_c2_10	1831	15934	1017	339	S69070	365	1.2(10)-33	Saccharomyces cerevisiae	hypothetical protein ypr084w - yeast (saccharomycetaceae)
CONTIG3878	7144105_c1_4	1832	15935	1623	541	S69074	257	9.8(10)-38	Saccharomyces cerevisiae	hypothetical protein ypr090w - yeast (saccharomycetaceae)

CONTIG2912	26269501_c3_8	1833	15936	1326	442	S69075	214	9.5(10)-15	Saccharomyces cerevisiae	hypothetical protein ypr091c - yeast (saccharomycescerevisiae)
CONTIG3060	12128176_c2_5	1834	15937	1602	534	S69075	367	3.6(10)-53	Saccharomyces cerevisiae	hypothetical protein ypr091c - yeast (saccharomycescerevisiae)
CONTIG4806	10969030_f1_3	1835	15938	366	122	S69077	326	1.7(10)-29	Saccharomyces cerevisiae	hypothetical protein ypr094w - yeast (saccharomycescerevisiae)
CONTIG3317	2166288_c2_9	1836	15939	780	260	S69079	293	1.1(10)-24	Saccharomyces cerevisiae	hypothetical protein ypr097w - yeast (saccharomycescerevisiae)
CONTIG4173	2131385_c1_5	1837	15940	882	294	S59773	819	9.6(10)-82	Saccharomyces cerevisiae	hypothetical protein ypr108w - yeast (saccharomycescerevisiae)
CONTIG3341	10744077_c1_16	1838	15941	1866	622	S59777	1490	7.5(10)-153	Saccharomyces cerevisiae	hypothetical protein ypr112c - yeast (saccharomycescerevisiae)
CONTIG3341	2110650_c2_17	1839	15942	321	107	S59777	244	1.3(10)-19	Saccharomyces cerevisiae	hypothetical protein ypr112c - yeast (saccharomycescerevisiae)
CONTIG5054	9788202_c1_7	1840	15943	876	292	S69019	407	4.4(10)-38	Saccharomyces cerevisiae	hypothetical protein ypr128c - yeast (saccharomycescerevisiae)
CONTIG5247	3251562_c3_20	1841	15944	249	83	S69019	123	2.7(10)-7	Saccharomyces cerevisiae	hypothetical protein ypr128c - yeast (saccharomycescerevisiae)
CONTIG2405	14172182_c1_3	1842	15945	1263	421	S69026	587	4.2(10)-67	Saccharomyces cerevisiae	hypothetical protein ypr137w - yeast (saccharomycescerevisiae)
CONTIG5223	35949128_f1_2	1843	15946	1035	345	S69028	141	2.1(10)-7	Saccharomyces cerevisiae	hypothetical protein ypr139c - yeast (saccharomycescerevisiae)
CONTIG5789	24306563_c2_27	1844	15947	1341	447	S69029	633	7.0(10)-115	Saccharomyces cerevisiae	hypothetical protein ypr140w - yeast (saccharomycescerevisiae)
CONTIG1570	9852291_f3_3	1845	15948	204	68	S69031	157	1.5(10)-11	Saccharomyces cerevisiae	hypothetical protein ypr143w - yeast (saccharomycescerevisiae)
CONTIG4164	26382812_f2_2	1846	15949	705	235	S69031	355	1.3(10)-32	Saccharomyces cerevisiae	hypothetical protein ypr143w - yeast (saccharomycescerevisiae)
CONTIG2759	35953288_f1_1	1847	15950	975	325	S69032	541	2.7(10)-52	Saccharomyces cerevisiae	hypothetical protein ypr144c - yeast (saccharomycescerevisiae)
CONTIG3152	24800343_c2_8	1848	15951	225	75	S69034	96	0.00021	Saccharomyces cerevisiae	hypothetical protein ypr147c - yeast (saccharomycescerevisiae)
CONTIG3152	12681385_c2_7	1849	15952	765	255	S69034	170	1.5(10)-11	Saccharomyces cerevisiae	hypothetical protein ypr147c - yeast (saccharomycescerevisiae)

CONTIG5244	23630132_c3_16	1850	15953	996	332	S59828	384	1.2(10)-35	Saccharomyces cerevisiae	hypothetical protein ypr169w - yeast (saccharomycescerevisiae)
CONTIG5244	13832575_c1_11	1851	15954	636	212	S59828	327	2.7(10)-29	Saccharomyces cerevisiae	hypothetical protein ypr169w - yeast (saccharomycescerevisiae)
CONTIG2056	19704752_c3_3	1852	15955	1320	440	S59836	144	1.1(10)-25	Saccharomyces cerevisiae	hypothetical protein ypr179c - yeast (saccharomycescerevisiae)
CONTIG66	12600452_c2_2	1853	15956	267	89	S69459	137	1.8(10)-9	Saccharomyces cerevisiae	hypothetical protein ypr197c - yeast (saccharomycescerevisiae)
CONTIG5739	2757307_c2_25	1854	15957	1596	532	S47445	200	2.0(10)-12	Saccharomyces cerevisiae	mdm1 protein - yeast (saccharomyces cerevisiae)
b9x10b37.y	26368813_f2_2	1855	15958	459	153	S57976	109	0.00064	Saccharomyces cerevisiae	nuclear migration protein num1 - yeast (saccharomycescerevisiae)
CONTIG1390	32429582_f2_1	1856	15959	756	252	S62011	188	2.1(10)-13	Saccharomyces cerevisiae	pho85 protein - yeast (saccharomyces cerevisiae)
CONTIG3594	1429625_c1_6	1857	15960	264	88	S62011	113	2.0(10)-5	Saccharomyces cerevisiae	pho85 protein - yeast (saccharomyces cerevisiae)
CONTIG5491	7277062_c1_9	1858	15961	2421	807	S62011	980	2.5(10)-140	Saccharomyces cerevisiae	pho85 protein - yeast (saccharomyces cerevisiae)
CONTIG2454	5867026_c2_4	1859	15962	420	140	S65200	102	1.7(10)-11	Saccharomyces cerevisiae	pos5 protein - yeast (saccharomyces cerevisiae)
CONTIG35	33400325_c3_4	1860	15963	627	209	S59296	120	8.3(10)-7	Saccharomyces cerevisiae	probable finger protein yoi054w - yeast (saccharomycescerevisiae)
CONTIG667	14085885_f1_1	1861	15964	564	188	S50981	109	1.3(10)-5	Saccharomyces cerevisiae	probable membrane protein ydi001w - yeast (saccharomycescerevisiae)
CONTIG988	24611028_c2_2	1862	15965	597	199	S50981	665	2.0(10)-65	Saccharomyces cerevisiae	probable membrane protein ydi001w - yeast (saccharomycescerevisiae)
CONTIG1094	35438932_f2_2	1863	15966	243	81	S52507	115	3.8(10)-7	Saccharomyces cerevisiae	probable membrane protein ydi012c - yeast (saccharomycescerevisiae)
CONTIG1530	13142916_f3_2	1864	15967	894	298	S52504	399	3.1(10)-37	Saccharomyces cerevisiae	probable membrane protein ydi015c - yeast (saccharomycescerevisiae)

CONTIG2203	22713577_c1_4	1865	15968	1320	440	S67568	169	1.8(10)-9	Saccharomyces cerevisiae	probable membrane protein ydl035c - yeast (saccharomycetaceae)
CONTIG5432	4332161_c1_18	1866	15969	1320	440	S67589	329	5.4(10)-46	Saccharomyces cerevisiae	probable membrane protein ydl054c - yeast (saccharomycetaceae)
CONTIG4382	6739075_c3_4	1867	15970	1305	435	S67598	300	6.2(10)-26	Saccharomyces cerevisiae	probable membrane protein ydl063c - yeast (saccharomycetaceae)
CONTIG5027	9796950_f1_1	1868	15971	2094	698	S67610	505	8.0(10)-62	Saccharomyces cerevisiae	probable membrane protein ydl074c - yeast (saccharomycetaceae)
CONTIG531	24305432_f3_1	1869	15972	855	285	S67627	108	0.00068	Saccharomyces cerevisiae	probable membrane protein ydl091c - yeast (saccharomycetaceae)
b9x12p19.x	4017818_c3_2	1870	15973	699	233	S67655	287	7.2(10)-24	Saccharomyces cerevisiae	probable membrane protein ydl112w - yeast (saccharomycetaceae)
CONTIG2633	10442599_c1_4	1871	15974	1485	495	S67655	620	3.2(10)-86	Saccharomyces cerevisiae	probable membrane protein ydl112w - yeast (saccharomycetaceae)
CONTIG1661	25585925_c3_3	1872	15975	762	254	S67679	303	4.5(10)-27	Saccharomyces cerevisiae	probable membrane protein ydl133w - yeast (saccharomycetaceae)
CONTIG3866	10973426_c3_4	1873	15976	1077	359	S67691	469	1.2(10)-44	Saccharomyces cerevisiae	probable membrane protein ydl144c - yeast (saccharomycetaceae)
b2x14977.x	9953207_c2_1	1874	15977	609	203	S67696	173	4.7(10)-12	Saccharomyces cerevisiae	probable membrane protein ydl148c - yeast (saccharomycetaceae)
b9x11904.x	26350250_f3_1	1875	15978	546	182	S67696	239	4.0(10)-19	Saccharomyces cerevisiae	probable membrane protein ydl148c - yeast (saccharomycetaceae)

CONTIG4991	16907808_f2_1	1876	15979	1608	536	S67697	361	1.6(10)-58	Saccharomyces cerevisiae	probable membrane protein ydl149w - yeast (saccharomycescerevisiae)
CONTIG924	13754782_f3_2	1877	15980	735	245	S67697	268	4.5(10)-22	Saccharomyces cerevisiae	probable membrane protein ydl149w - yeast (saccharomycescerevisiae)
CONTIG5563	24786090_c1_18	1878	15981	183	61	S58784	213	4.0(10)-17	Saccharomyces cerevisiae	probable membrane protein ydl193w - yeast (saccharomycescerevisiae)
CONTIG5563	34062507_c3_25	1879	15982	954	318	S58784	327	1.3(10)-29	Saccharomyces cerevisiae	probable membrane protein ydl193w - yeast (saccharomycescerevisiae)
CONTIG4890	15645035_f1_1	1880	15983	1206	402	S67801	282	4.0(10)-39	Saccharomyces cerevisiae	probable membrane protein ydl237w - yeast (saccharomycescerevisiae)
CONTIG4770	167707_f3_4	1881	15984	645	215	S50934	189	1.1(10)-13	Saccharomyces cerevisiae	probable membrane protein ydr027c - yeast (saccharomycescerevisiae)
CONTIG4949	25660878_c3_9	1882	15985	1464	488	S50934	299	4.0(10)-26	Saccharomyces cerevisiae	probable membrane protein ydr027c - yeast (saccharomycescerevisiae)
CONTIG5689	15864033_c2_19	1883	15986	900	300	S54034	241	5.5(10)-39	Saccharomyces cerevisiae	probable membrane protein ydr049w - yeast (saccharomycescerevisiae)
CONTIG1573	33298575_f2_1	1884	15987	651	217	S54044	600	9.9(10)-58	Saccharomyces cerevisiae	probable membrane protein ydr060w - yeast (saccharomycescerevisiae)
CONTIG1574	412817_c2_4	1885	15988	537	179	S54044	110	3.3(10)-5	Saccharomyces cerevisiae	probable membrane protein ydr060w - yeast (saccharomycescerevisiae)
b9x12u01.y	24397507_c3_2	1886	15989	615	205	S54044	659	3.3(10)-64	Saccharomyces cerevisiae	probable membrane protein ydr060w - yeast (saccharomycescerevisiae)

CONTIG4672	21642137_c1_7	1887	15990	771	257	S58090	611	1.1(10)-59	Saccharomyces cerevisiae	probable membrane protein ydr1090c - yeast (saccharomycescerevisiae)
CONTIG5210	25650426_c1_9	1888	15991	489	163	S51251	192	2.7(10)-15	Saccharomyces cerevisiae	probable membrane protein ydr100w - yeast (saccharomycescerevisiae)
CONTIG2110	26854540_c2_3	1889	15992	819	273	S51252	483	3.8(10)-46	Saccharomyces cerevisiae	probable membrane protein ydr101c - yeast (saccharomycescerevisiae)
CONTIG5666	4417200_c3_17	1890	15993	840	280	S51252	500	2.8(10)-76	Saccharomyces cerevisiae	probable membrane protein ydr101c - yeast (saccharomycescerevisiae)
CONTIG5138	11132692_f1_1	1891	15994	2010	670	S51255	409	1.2(10)-62	Saccharomyces cerevisiae	probable membrane protein ydr104c - yeast (saccharomycescerevisiae)
CONTIG1266	35599056_f2_1	1892	15995	1188	396	S51256	867	8.0(10)-87	Saccharomyces cerevisiae	probable membrane protein ydr105c - yeast (saccharomycescerevisiae)
CONTIG1176	29424150_f3_1	1893	15996	831	277	S52675	296	1.7(10)-39	Saccharomyces cerevisiae	probable membrane protein ydr109c - yeast (saccharomycescerevisiae)
CONTIG187	6052217_f3_1	1894	15997	363	121	S52675	157	2.1(10)-10	Saccharomyces cerevisiae	probable membrane protein ydr109c - yeast (saccharomycescerevisiae)
CONTIG720	29344642_f3_3	1895	15998	963	321	S52675	942	9.0(10)-95	Saccharomyces cerevisiae	probable membrane protein ydr109c - yeast (saccharomycescerevisiae)
CONTIG1663	113907_f1_1	1896	15999	717	239	S52691	341	4.4(10)-31	Saccharomyces cerevisiae	probable membrane protein ydr126w - yeast (saccharomycescerevisiae)
CONTIG3848	24875300_f1_1	1897	16000	2064	688	S51869	460	7.2(10)-41	Saccharomyces cerevisiae	probable membrane protein ydr141c - yeast (saccharomycescerevisiae)

CONTIG5191	25571937_c2_10	1898	16001	2112	704	SS1869	401	8.1(10)-62	Saccharomyces cerevisiae	probable membrane protein ydr141c - yeast (saccharomycescerevisiae)
CONTIG2041	25548438_f3_1	1899	16002	1053	351	SS7985	280	1.8(10)-42	Saccharomyces cerevisiae	probable membrane protein ydr161w - yeast (saccharomycescerevisiae)
CONTIG4113	20585202_f3_2	1900	16003	1131	377	SS7989	399	3.1(10)-37	Saccharomyces cerevisiae	probable membrane protein ydr165w - yeast (saccharomycescerevisiae)
CONTIG4689	390637_f2_3	1901	16004	1341	447	SS2705	280	2.1(10)-35	Saccharomyces cerevisiae	probable membrane protein ydr198c - yeast (saccharomycescerevisiae)
CONTIG2356	23948386_f1_1	1902	16005	747	249	SS2706	95	0.02599	Saccharomyces cerevisiae	probable membrane protein ydr200c - yeast (saccharomycescerevisiae)
CONTIG5794	4876438_f2_8	1903	16006	339	113	SS1568	120	2.0(10)-6	Saccharomyces cerevisiae	probable membrane protein ydr205w - yeast (saccharomycescerevisiae)
CONTIG2458	9765686_c1_2	1904	16007	618	206	SS9437	265	4.9(10)-23	Saccharomyces cerevisiae	probable membrane protein ydr231c - yeast (saccharomycescerevisiae)
CONTIG5163	179502_c2_7	1905	16008	1125	375	SS9439	366	9.8(10)-34	Saccharomyces cerevisiae	probable membrane protein ydr233c - yeast (saccharomycescerevisiae)
CONTIG850	30360635_c3_3	1906	16009	381	127	SS4532	245	6.5(10)-21	Saccharomyces cerevisiae	probable membrane protein ydr236c - yeast (saccharomycescerevisiae)
CONTIG4231	26445327_f2_4	1907	16010	564	188	SS1117	119	3.3(10)-6	Saccharomyces cerevisiae	probable membrane protein ydr262w - yeast (saccharomycescerevisiae)
CONTIG3309	5316_c1_9	1908	16011	1413	471	SS1202	663	2.6(10)-75	Saccharomyces cerevisiae	probable membrane protein ydr316w - yeast (saccharomycescerevisiae)

CONTIG3590	30476455_c3_4	1909	16012	1272	424	S59791	278	7.4(10)-36	Saccharomyces cerevisiae	probable membrane protein ydr325w - yeast (saccharomycescerevisiae)
CONTIG4280	32612552_f1_1	1910	16013	2586	862	S59791	525	4.5(10)-59	Saccharomyces cerevisiae	probable membrane protein ydr325w - yeast (saccharomycescerevisiae)
CONTIG5710	14649053_f3_8	1911	16014	2334	778	S59792	402	4.5(10)-37	Saccharomyces cerevisiae	probable membrane protein ydr326c - yeast (saccharomycescerevisiae)
CONTIG4221	29400278_c1_4	1912	16015	741	247	S61149	140	5.7(10)-14	Saccharomyces cerevisiae	probable membrane protein ydr352w - yeast (saccharomycescerevisiae)
CONTIG4267	4084555_c2_4	1913	16016	1584	528	S62018	1586	5.0(10)-163	Saccharomyces cerevisiae	probable membrane protein ydr539w - yeast (saccharomycescerevisiae)
CONTIG4639	1194053_c3_5	1914	16017	2034	678	S64747	429	4.5(10)-38	Saccharomyces cerevisiae	probable membrane protein yll005c - yeast (saccharomycescerevisiae)
CONTIG3769	14879541_f2_2	1915	16018	1218	406	S64749	114	6.2(10)-7	Saccharomyces cerevisiae	probable membrane protein yll007c - yeast (saccharomycescerevisiae)
CONTIG4424	22287825_c3_8	1916	16019	351	117	S64756	184	1.8(10)-14	Saccharomyces cerevisiae	probable membrane protein yll014w - yeast (saccharomycescerevisiae)
CONTIG3955	2134385_c2_6	1917	16020	1125	375	S64782	401	6.5(10)-63	Saccharomyces cerevisiae	probable membrane protein yll031c - yeast (saccharomycescerevisiae)
CONTIG3955	173811_c1_3	1918	16021	378	126	S64782	134	9.4(10)-8	Saccharomyces cerevisiae	probable membrane protein yll031c - yeast (saccharomycescerevisiae)
CONTIG3955	13907813_c3_7	1919	16022	921	307	S64782	516	1.2(10)-48	Saccharomyces cerevisiae	probable membrane protein yll031c - yeast (saccharomycescerevisiae)

CONTIG3955	22525036_c2_5	1920	16023	270	90	S64782	103	0.00019	Saccharomyces cerevisiae	probable membrane protein ylj031c - yeast (saccharomycescerevisiae)
CONTIG490	22447182_c2_2	1921	16024	489	163	S64782	320	1.3(10)-27	Saccharomyces cerevisiae	probable membrane protein ylj031c - yeast (saccharomycescerevisiae)
CONTIG677	20595325_f1_1	1922	16025	792	264	S64783	122	0.00011	Saccharomyces cerevisiae	probable membrane protein ylj032c - yeast (saccharomycescerevisiae)
CONTIG3532	29417632_c1_9	1923	16026	1008	336	S64821	165	3.1(10)-9	Saccharomyces cerevisiae	probable membrane protein ylj001c - yeast (saccharomycescerevisiae)
CONTIG3532	13885817_c3_11	1924	16027	681	227	S64821	118	0.00025	Saccharomyces cerevisiae	probable membrane protein ylj001c - yeast (saccharomycescerevisiae)
CONTIG5361	24413557_f3_4	1925	16028	1185	395	S64821	157	3.2(10)-8	Saccharomyces cerevisiae	probable membrane protein ylj001c - yeast (saccharomycescerevisiae)
CONTIG1738	21540800_f3_4	1926	16029	738	246	S64850	212	1.8(10)-30	Saccharomyces cerevisiae	probable membrane protein ylj023c - yeast (saccharomycescerevisiae)
CONTIG2702	21535661_f2_3	1927	16030	753	251	S61621	497	1.3(10)-47	Saccharomyces cerevisiae	probable membrane protein ylj047c - yeast (saccharomycescerevisiae)
CONTIG3389	30704662_c3_5	1928	16031	231	77	S61621	131	1.2(10)-7	Saccharomyces cerevisiae	probable membrane protein ylj047c - yeast (saccharomycescerevisiae)
CONTIG4951	22378806_c1_11	1929	16032	540	180	S61624	272	9.0(10)-24	Saccharomyces cerevisiae	probable membrane protein ylj050c - yeast (saccharomycescerevisiae)
CONTIG4625	788876_c2_7	1930	16033	840	280	S61637	128	3.1(10)-6	Saccharomyces cerevisiae	probable membrane protein ylj064w - yeast (saccharomycescerevisiae)

CONTIG569	437802_fl_1	1931	16034	528	176	S61637	105	0.00016	Saccharomyces cerevisiae	probable membrane protein ylr064w - yeast (saccharomycescerevisiae)
CONTIG4013	12911436_c2_3	1932	16035	600	200	S61638	134	3.7(10)-9	Saccharomyces cerevisiae	probable membrane protein ylr065c - yeast (saccharomycescerevisiae)
CONTIG2334	12148388_c2_5	1933	16036	837	279	S64909	94	0.00024	Saccharomyces cerevisiae	probable membrane protein ylr077w - yeast (saccharomycescerevisiae)
CONTIG1328	24398567_c1_2	1934	16037	360	120	S64916	110	4.2(10)-5	Saccharomyces cerevisiae	probable membrane protein ylr084c - yeast (saccharomycescerevisiae)
CONTIG2422	24256955_c2_1	1935	16038	1251	417	S64916	113	0.00479	Saccharomyces cerevisiae	probable membrane protein ylr084c - yeast (saccharomycescerevisiae)
CONTIG3100	9803588_c1_3	1936	16039	1428	476	S64916	245	1.0(10)-31	Saccharomyces cerevisiae	probable membrane protein ylr084c - yeast (saccharomycescerevisiae)
CONTIG3100	6702_c3_4	1937	16040	306	102	S64916	98	0.0008	Saccharomyces cerevisiae	probable membrane protein ylr084c - yeast (saccharomycescerevisiae)
CONTIG2569	33245403_fl_1	1938	16041	1158	386	S64921	403	3.3(10)-43	Saccharomyces cerevisiae	probable membrane protein ylr087c - yeast (saccharomycescerevisiae)
CONTIG3051	3179660_c2_3	1939	16042	1173	391	S64921	682	2.0(10)-65	Saccharomyces cerevisiae	probable membrane protein ylr087c - yeast (saccharomycescerevisiae)
CONTIG4581	1204592_c3_9	1940	16043	3516	1172	S64921	522	5.2(10)-70	Saccharomyces cerevisiae	probable membrane protein ylr087c - yeast (saccharomycescerevisiae)
CONTIG5053	26438163_fl_1	1941	16044	1755	585	S64921	470	3.7(10)-62	Saccharomyces cerevisiae	probable membrane protein ylr087c - yeast (saccharomycescerevisiae)

b9x12p78.x	5860930_f2_1	1942	16045	774	258	S64921	259	1.7(10)-20	Saccharomyces cerevisiae	probable membrane protein ylr1087c - yeast (saccharomycescerevisiae)
CONTIG5784	24407557_f3_10	1943	16046	1125	375	S64936	1022	3.0(10)-103	Saccharomyces cerevisiae	probable membrane protein ylr1100w - yeast (saccharomycescerevisiae)
CONTIG3642	24082581_c3_8	1944	16047	435	145	S64940	286	2.8(10)-25	Saccharomyces cerevisiae	probable membrane protein ylr1104w - yeast (saccharomycescerevisiae)
CONTIG1723	2456527_c3_6	1945	16048	555	185	S64942	106	0.02	Saccharomyces cerevisiae	probable membrane protein ylr1106c - yeast (saccharomycescerevisiae)
CONTIG2171	20523377_c1_2	1946	16049	1350	450	S64942	453	7.5(10)-41	Saccharomyces cerevisiae	probable membrane protein ylr1106c - yeast (saccharomycescerevisiae)
CONTIG3775	36523586_c1_5	1947	16050	2103	701	S64942	1778	1.7(10)-181	Saccharomyces cerevisiae	probable membrane protein ylr1106c - yeast (saccharomycescerevisiae)
CONTIG5074	15911718_f1_1	1948	16051	4014	1338	S64942	4108	0	Saccharomyces cerevisiae	probable membrane protein ylr1106c - yeast (saccharomycescerevisiae)
CONTIG822	33242937_f2_1	1949	16052	621	207	S64942	211	3.6(10)-15	Saccharomyces cerevisiae	probable membrane protein ylr1106c - yeast (saccharomycescerevisiae)
b2x10142.x	22367126_c3_2	1950	16053	528	176	S64942	235	1.0(10)-17	Saccharomyces cerevisiae	probable membrane protein ylr1106c - yeast (saccharomycescerevisiae)
CONTIG4818	19569183_f2_3	1951	16054	774	258	S64955	341	4.4(10)-31	Saccharomyces cerevisiae	probable membrane protein ylr1118c - yeast (saccharomycescerevisiae)
CONTIG5000	31444042_c3_10	1952	16055	255	85	S64955	144	3.2(10)-10	Saccharomyces cerevisiae	probable membrane protein ylr1118c - yeast (saccharomycescerevisiae)

CONTIG4241	4980393_fl_1	1953	16056	657	219	S59329	114	4.2(10)-11	Saccharomyces cerevisiae	probable membrane protein ylr137w - yeast (saccharomycescerevisiae)
CONTIG27	22464832_c1_6	1954	16057	441	147	S64994	93	0.00018	Saccharomyces cerevisiae	probable membrane protein ylr145w - yeast (saccharomycescerevisiae)
CONTIG82	35816255_fl_1	1955	16058	624	208	S64994	97	5.4(10)-7	Saccharomyces cerevisiae	probable membrane protein ylr145w - yeast (saccharomycescerevisiae)
CONTIG3333	11804556_c1_3	1956	16059	1584	528	S51422	417	7.2(10)-39	Saccharomyces cerevisiae	probable membrane protein ylr177w - yeast (saccharomycescerevisiae)
CONTIG5437	23546930_c3_20	1957	16060	915	305	S48556	348	7.9(10)-32	Saccharomyces cerevisiae	probable membrane protein ylr205c - yeast (saccharomycescerevisiae)
CONTIG1471	10833318_fl_1	1958	16061	243	81	S51445	178	1.3(10)-12	Saccharomyces cerevisiae	probable membrane protein ylr222c - yeast (saccharomycescerevisiae)
CONTIG3451	4407635_c3_6	1959	16062	693	231	S51445	560	4.5(10)-54	Saccharomyces cerevisiae	probable membrane protein ylr222c - yeast (saccharomycescerevisiae)
CONTIG602	433267_fl_1	1960	16063	744	248	S51445	649	1.0(10)-63	Saccharomyces cerevisiae	probable membrane protein ylr222c - yeast (saccharomycescerevisiae)
CONTIG4367	422500_c1_4	1961	16064	2217	739	S59387	1099	2.5(10)-153	Saccharomyces cerevisiae	probable membrane protein ylr241w - yeast (saccharomycescerevisiae)
CONTIG4897	4688425_c3_5	1962	16065	1989	663	S59387	828	6.7(10)-124	Saccharomyces cerevisiae	probable membrane protein ylr241w - yeast (saccharomycescerevisiae)
CONTIG1938	14219817_c3_7	1963	16066	939	313	S59388	219	6.0(10)-29	Saccharomyces cerevisiae	probable membrane protein ylr242c - yeast (saccharomycescerevisiae)

CONTIG5794	7047711_f2_9	1964	16067	1011	337	SS9389	1059	3.6(10)-107	Saccharomyces cerevisiae	probable membrane protein ylr243w - yeast (saccharomycescerevisiae)
CONTIG4249	14089037_f2_3	1965	16068	1227	409	SS9392	308	8.3(10)-35	Saccharomyces cerevisiae	probable membrane protein ylr246w - yeast (saccharomycescerevisiae)
CONTIG1033	34120706_f1_1	1966	16069	807	269	SS9398	432	1.3(10)-59	Saccharomyces cerevisiae	probable membrane protein ylr253w - yeast (saccharomycescerevisiae)
CONTIG853	10631937_c3_1	1967	16070	660	220	SS9398	609	1.7(10)-59	Saccharomyces cerevisiae	probable membrane protein ylr253w - yeast (saccharomycescerevisiae)
CONTIG5234	24788282_c3_18	1968	16071	957	319	SS0369	475	2.7(10)-45	Saccharomyces cerevisiae	probable membrane protein ylr284c - yeast (saccharomycescerevisiae)
CONTIG705	14629812_c2_4	1969	16072	687	229	SS0369	363	2.0(10)-33	Saccharomyces cerevisiae	probable membrane protein ylr284c - yeast (saccharomycescerevisiae)
CONTIG3605	34042781_c2_4	1970	16073	561	187	SS0370	472	5.7(10)-45	Saccharomyces cerevisiae	probable membrane protein ylr285w - yeast (saccharomycescerevisiae)
CONTIG5400	1273406_f1_3	1971	16074	846	282	SS0370	679	6.7(10)-67	Saccharomyces cerevisiae	probable membrane protein ylr285w - yeast (saccharomycescerevisiae)
CONTIG1981	3956555_c2_5	1972	16075	432	144	SS3401	178	6.9(10)-13	Saccharomyces cerevisiae	probable membrane protein ylr324w - yeast (saccharomycescerevisiae)
CONTIG5688	6069426_f3_10	1973	16076	564	188	SS3401	201	2.2(10)-15	Saccharomyces cerevisiae	probable membrane protein ylr324w - yeast (saccharomycescerevisiae)
CONTIG5245	23851458_c3_25	1974	16077	492	164	SS3403	211	2.6(10)-17	Saccharomyces cerevisiae	probable membrane protein ylr326w - yeast (saccharomycescerevisiae)

CONTIG5756	26192182_f2_10	1975	16078	630	210	S53403	167	1.2(10)-12	Saccharomyces cerevisiae	probable membrane protein ylr326w - yeast (saccharomycescerevisiae)
CONTIG4886	1461032_c3_8	1976	16079	1152	384	S53405	1239	3.0(10)-126	Saccharomyces cerevisiae	probable membrane protein ylr328w - yeast (saccharomycescerevisiae)
CONTIG5803	3172150_f1_3	1977	16080	630	210	S51341	173	5.5(10)-12	Saccharomyces cerevisiae	probable membrane protein ylr335w - yeast (saccharomycescerevisiae)
CONTIG4350	31682632_f1_1	1978	16081	1581	527	S51379	728	4.2(10)-72	Saccharomyces cerevisiae	probable membrane protein ylr361c - yeast (saccharomycescerevisiae)
CONTIG5753	7085932_f3_11	1979	16082	2820	940	S51473	608	3.2(10)-101	Saccharomyces cerevisiae	probable membrane protein ylr386w - yeast (saccharomycescerevisiae)
CONTIG4081	20336503_c2_4	1980	16083	993	331	S55960	91	0.08799	Saccharomyces cerevisiae	probable membrane protein ylr404w - yeast (saccharomycescerevisiae)
CONTIG1974	7125827_c3_8	1981	16084	1422	474	S55965	1270	1.6(10)-129	Saccharomyces cerevisiae	probable membrane protein ylr409c - yeast (saccharomycescerevisiae)
CONTIG762	16609561_f2_1	1982	16085	918	306	S55965	828	1.1(10)-82	Saccharomyces cerevisiae	probable membrane protein ylr409c - yeast (saccharomycescerevisiae)
CONTIG4777	3615881_c3_9	1983	16086	954	318	S59380	115	0.00016	Saccharomyces cerevisiae	probable membrane protein ylr414c - yeast (saccharomycescerevisiae)
CONTIG1923	21504631_c2_1	1984	16087	930	310	S53409	285	1.7(10)-23	Saccharomyces cerevisiae	probable membrane protein ylr422w - yeast (saccharomycescerevisiae)
CONTIG2533	4157252_f2_1	1985	16088	1089	363	S53409	203	6.7(10)-13	Saccharomyces cerevisiae	probable membrane protein ylr422w - yeast (saccharomycescerevisiae)

CONTIG3801	20079760_c3_5	1986	16089	2571	857	S53409	395	5.5(10)-41	Saccharomyces cerevisiae	probable membrane protein ylr422w - yeast (saccharomycescerevisiae)
CONTIG4358	14850025_c3_8	1987	16090	2955	985	S53409	1189	5.7(10)-120	Saccharomyces cerevisiae	probable membrane protein ylr422w - yeast (saccharomycescerevisiae)
CONTIG615	6307812_f3_2	1988	16091	948	316	S53409	371	1.2(10)-32	Saccharomyces cerevisiae	probable membrane protein ylr422w - yeast (saccharomycescerevisiae)
CONTIG5196	3916515_c1_8	1989	16092	981	327	S53413	367	7.7(10)-34	Saccharomyces cerevisiae	probable membrane protein ylr426w - yeast (saccharomycescerevisiae)
CONTIG3427	10351077_f3_4	1990	16093	1383	461	S53414	642	5.5(10)-63	Saccharomyces cerevisiae	probable membrane protein ylr427w - yeast (saccharomycescerevisiae)
CONTIG5801	15893763_f2_8	1991	16094	2040	680	S59408	171	2.6(10)-9	Saccharomyces cerevisiae	probable membrane protein ylr440c - yeast (saccharomycescerevisiae)
CONTIG1242	6093816_c3_5	1992	16095	1395	465	S59413	713	1.3(10)-74	Saccharomyces cerevisiae	probable membrane protein ylr454w - yeast (saccharomycescerevisiae)
CONTIG2220	35708128_f1_1	1993	16096	1149	383	S59413	254	1.8(10)-18	Saccharomyces cerevisiae	probable membrane protein ylr454w - yeast (saccharomycescerevisiae)
CONTIG2264	22322168_f1_1	1994	16097	801	267	S59413	115	5.0(10)-7	Saccharomyces cerevisiae	probable membrane protein ylr454w - yeast (saccharomycescerevisiae)
CONTIG5609	18752_c2_8	1995	16098	1059	353	S61982	498	1.0(10)-47	Saccharomyces cerevisiae	probable membrane protein y0002c - yeast (saccharomycescerevisiae)
CONTIG5711	16831552_c2_10	1996	16099	1347	449	S61981	423	6.0(10)-71	Saccharomyces cerevisiae	probable membrane protein y0003c - yeast (saccharomycescerevisiae)

CONTIG52341	433207_f3_3	1997	16100	1020	340	S66695	177	9.6(10)-13	Saccharomyces cerevisiae	probable membrane protein y0l013c - yeast (saccharomycescerevisiae)
CONTIG438	21657782_c1_2	1998	16101	609	203	S66695	121	1.0(10)-6	Saccharomyces cerevisiae	probable membrane protein y0l013c - yeast (saccharomycescerevisiae)
CONTIG5810	12613926_c3_41	1999	16102	405	135	S66709	136	2.2(10)-9	Saccharomyces cerevisiae	probable membrane protein y0l026c - yeast (saccharomycescerevisiae)
CONTIG5028	4788961_f1_2	2000	16103	1161	387	S66710	746	5.2(10)-74	Saccharomyces cerevisiae	probable membrane protein y0l027c - yeast (saccharomycescerevisiae)
CONTIG1072	471026_f2_1	2001	16104	546	182	S66714	110	0.00033	Saccharomyces cerevisiae	probable membrane protein y0l031c - yeast (saccharomycescerevisiae)
CONTIG5165	24489161_f1_4	2002	16105	852	284	S66733	133	8.5(10)-9	Saccharomyces cerevisiae	probable membrane protein y0l08c - yeast (saccharomycescerevisiae)
CONTIG5483	206562_c3_10	2003	16106	1929	643	S61717	1353	7.0(10)-145	Saccharomyces cerevisiae	probable membrane protein y0l060c - yeast (saccharomycescerevisiae)
CONTIG5791	4070125_f3_15	2004	16107	2277	759	S66755	126	2.1(10)-10	Saccharomyces cerevisiae	probable membrane protein y0l063c - yeast (saccharomycescerevisiae)
CONTIG3291	16835067_f3_4	2005	16108	339	113	S66766	207	8.5(10)-17	Saccharomyces cerevisiae	probable membrane protein y0l073c - yeast (saccharomycescerevisiae)
CONTIG5521	9861083_f1_1	2006	16109	615	205	S66766	123	3.6(10)-6	Saccharomyces cerevisiae	probable membrane protein y0l073c - yeast (saccharomycescerevisiae)
CONTIG5270	19723162_f3_6	2007	16110	948	316	S66770	970	9.6(10)-98	Saccharomyces cerevisiae	probable membrane protein y0l077c - yeast (saccharomycescerevisiae)

CONTIG1978	4807688_c2_1	2008	16111	396	132	S57385	157	3.2(10)-10	Saccharomyces cerevisiae	probable membrane protein y01084w - yeast (saccharomycescerevisiae)
CONTIG3150	4173188_f1_1	2009	16112	984	328	S57377	97	0.025	Saccharomyces cerevisiae	probable membrane protein y01092w - yeast (saccharomycescerevisiae)
CONTIG124	15631555_f1_2	2010	16113	246	82	S51891	93	0.00054	Saccharomyces cerevisiae	probable membrane protein y01107w - yeast (saccharomycescerevisiae)
CONTIG2370	6836502_f1_1	2011	16114	1326	442	S51891	96	0.00021	Saccharomyces cerevisiae	probable membrane protein y01107w - yeast (saccharomycescerevisiae)
CONTIG2884	11767062_c2_5	2012	16115	546	182	S51891	178	2.5(10)-13	Saccharomyces cerevisiae	probable membrane protein y01107w - yeast (saccharomycescerevisiae)
CONTIG700	10162937_c3_2	2013	16116	564	188	S63441	408	3.5(10)-38	Saccharomyces cerevisiae	probable membrane protein y01129w - yeast (saccharomycescerevisiae)
CONTIG1741	4329062_c3_1	2014	16117	1242	414	S66834	264	5.7(10)-37	Saccharomyces cerevisiae	probable membrane protein y01137w - yeast (saccharomycescerevisiae)
CONTIG4573	24298150_c1_10	2015	16118	1518	506	S66834	188	8.5(10)-19	Saccharomyces cerevisiae	probable membrane protein y01137w - yeast (saccharomycescerevisiae)
CONTIG4930	33984693_f1_1	2016	16119	3207	1069	S66835	315	1.1(10)-47	Saccharomyces cerevisiae	probable membrane protein y01138c - yeast (saccharomycescerevisiae)
CONTIG5381	975390_f3_7	2017	16120	648	216	S60390	343	2.7(10)-31	Saccharomyces cerevisiae	probable membrane protein y01146w - yeast (saccharomycescerevisiae)
blx18291.x	14275043_f2_1	2018	16121	507	169	S61984	333	2.6(10)-29	Saccharomyces cerevisiae	probable membrane protein y01001w - yeast (saccharomycescerevisiae)

b3x16041.x	23640785_f3_2	2019	16122	312	104	S61984	194	2.2(10)-14	Saccharomyces cerevisiae	probable membrane protein yor001w - yeast (saccharomycescerevisiae)
CONTIG2420	24615927_f3_2	2020	16123	975	325	S66942	144	2.6(10)-7	Saccharomyces cerevisiae	probable membrane protein yor059c - yeast (saccharomycescerevisiae)
CONTIG4528	5870312_c1_8	2021	16124	669	223	S66942	128	6.5(10)-6	Saccharomyces cerevisiae	probable membrane protein yor059c - yeast (saccharomycescerevisiae)
CONTIG4528	3938875_c3_13	2022	16125	1086	362	S66942	380	3.2(10)-35	Saccharomyces cerevisiae	probable membrane protein yor059c - yeast (saccharomycescerevisiae)
CONTIG5159	2361537_f1_2	2023	16126	669	223	S61645	316	1.8(10)-28	Saccharomyces cerevisiae	probable membrane protein yor084w - yeast (saccharomycescerevisiae)
CONTIG3622	5253760_c2_3	2024	16127	921	307	S61645	236	1.2(10)-19	Saccharomyces cerevisiae	probable membrane protein yor084w - yeast (saccharomycescerevisiae)
CONTIG5177	25581936_f2_2	2025	16128	3081	1027	S61647	852	3.1(10)-85	Saccharomyces cerevisiae	probable membrane protein yor086c - yeast (saccharomycescerevisiae)
CONTIG5747	34064056_c1_31	2026	16129	1923	641	S61648	827	1.3(10)-82	Saccharomyces cerevisiae	probable membrane protein yor088w - yeast (saccharomycescerevisiae)
CONTIG4674	5890885_c3_7	2027	16130	1833	611	S61692	187	2.2(10)-18	Saccharomyces cerevisiae	probable membrane protein yor137c - yeast (saccharomycescerevisiae)
CONTIG5499	33378936_f1_1	2028	16131	1884	628	S61693	101	2.2(10)-7	Saccharomyces cerevisiae	probable membrane protein yor138c - yeast (saccharomycescerevisiae)
CONTIG5076	31331312_f2_2	2029	16132	1629	543	S67042	658	1.1(10)-64	Saccharomyces cerevisiae	probable membrane protein yor154w - yeast (saccharomycescerevisiae)

CONTIG437	477290_f3_7	2030	16133	378	126	S67049	270	7.5(10)-23	Saccharomyces cerevisiae	probable membrane protein yor161c - yeast (saccharomycescerevisiae)
CONTIG3077	5956628_f2_1	2031	16134	2292	764	S67053	1475	3.0(10)-151	Saccharomyces cerevisiae	probable membrane protein yor165w - yeast (saccharomycescerevisiae)
CONTIG4759	34557677_f2_3	2032	16135	453	151	S67054	163	2.2(10)-11	Saccharomyces cerevisiae	probable membrane protein yor166c - yeast (saccharomycescerevisiae)
CONTIG519	4038302_c3_2	2033	16136	885	295	S67054	435	4.7(10)-41	Saccharomyces cerevisiae	probable membrane protein yor166c - yeast (saccharomycescerevisiae)
CONTIG5788	24781502_f1_1	2034	16137	1800	600	S67067	1250	2.1(10)-127	Saccharomyces cerevisiae	probable membrane protein yor175c - yeast (saccharomycescerevisiae)
CONTIG3901	25973936_c3_5	2035	16138	192	64	S67097	102	0.00012	Saccharomyces cerevisiae	probable membrane protein yor205c - yeast (saccharomycescerevisiae)
CONTIG3901	14255287_c3_4	2036	16139	1383	461	S67097	271	8.1(10)-27	Saccharomyces cerevisiae	probable membrane protein yor205c - yeast (saccharomycescerevisiae)
CONTIG404	31274166_c1_3	2037	16140	1020	340	S60954	246	1.3(10)-19	Saccharomyces cerevisiae	probable membrane protein yor227w - yeast (saccharomycescerevisiae)
CONTIG5155	20735907_f2_5	2038	16141	618	206	S60955	154	8.0(10)-11	Saccharomyces cerevisiae	probable membrane protein yor228c - yeast (saccharomycescerevisiae)
CONTIG4877	29303252_c3_7	2039	16142	1065	355	S67133	984	3.2(10)-99	Saccharomyces cerevisiae	probable membrane protein yor240w - yeast (saccharomycescerevisiae)
CONTIG4475	36344386_f1_1	2040	16143	1131	377	S67138	309	6.4(10)-62	Saccharomyces cerevisiae	probable membrane protein yor245c - yeast (saccharomycescerevisiae)

CONTIG1828	3915692_c1_4	2041	16144	603	201	S67139	404	9.1(10)-38	Saccharomyces cerevisiae	probable membrane protein yor246c - yeast (saccharomycescerevisiae)
CONTIG4410	20751950_c2_7	2042	16145	1206	402	S67139	751	1.6(10)-74	Saccharomyces cerevisiae	probable membrane protein yor246c - yeast (saccharomycescerevisiae)
CONTIG5047	6262_c2_7	2043	16146	201	67	S67139	143	1.7(10)-9	Saccharomyces cerevisiae	probable membrane protein yor246c - yeast (saccharomycescerevisiae)
CONTIG175	5083338_f2_1	2044	16147	546	182	S67146	220	3.3(10)-17	Saccharomyces cerevisiae	probable membrane protein yor249c - yeast (saccharomycescerevisiae)
CONTIG568	31812638_f2_1	2045	16148	1110	370	S67146	232	1.7(10)-18	Saccharomyces cerevisiae	probable membrane protein yor249c - yeast (saccharomycescerevisiae)
CONTIG5559	23828436_c3_25	2046	16149	699	233	S67159	734	9.9(10)-73	Saccharomyces cerevisiae	probable membrane protein yor262w - yeast (saccharomycescerevisiae)
CONTIG5559	156640_c2_19	2047	16150	225	75	S67159	249	2.3(10)-21	Saccharomyces cerevisiae	probable membrane protein yor262w - yeast (saccharomycescerevisiae)
CONTIG1508	36365900_f3_1	2048	16151	363	121	S67196	344	2.1(10)-31	Saccharomyces cerevisiae	probable membrane protein yor292c - yeast (saccharomycescerevisiae)
CONTIG5370	4416032_f1_2	2049	16152	1662	554	S67205	177	1.8(10)-27	Saccharomyces cerevisiae	probable membrane protein yor301w - yeast (saccharomycescerevisiae)
CONTIG5068	33439062_c2_10	2050	16153	495	165	S58323	351	3.7(10)-32	Saccharomyces cerevisiae	probable membrane protein yor311c - yeast (saccharomycescerevisiae)
CONTIG5068	46900_c3_12	2051	16154	711	237	S58323	121	2.7(10)-6	Saccharomyces cerevisiae	probable membrane protein yor311c - yeast (saccharomycescerevisiae)

CONTIG4043	31675632_13_2	2052	16155	1368	456	S58330	200	4.4(10)-13	Saccharomyces cerevisiae	probable membrane protein yor322c - yeast (saccharomycescerevisiae)
CONTIG1017	5089681_13_1	2053	16156	372	124	S58333	211	4.2(10)-16	Saccharomyces cerevisiae	probable membrane protein yor322c - yeast (saccharomycescerevisiae)
CONTIG3368	275933_11_1	2054	16157	1512	504	S58333	532	6.7(10)-83	Saccharomyces cerevisiae	probable membrane protein yor322c - yeast (saccharomycescerevisiae)
CONTIG3017	22460778_13_2	2055	16158	1035	345	S67264	127	7.5(10)-10	Saccharomyces cerevisiae	probable membrane protein yor352w - yeast (saccharomycescerevisiae)
CONTIG5361	23933500_11_6	2056	16159	855	285	S67302	238	1.3(10)-26	Saccharomyces cerevisiae	probable membrane protein yor390w - yeast (saccharomycescerevisiae)
CONTIG4922	23831555_13_11	2057	16160	1593	531	S52525	689	2.7(10)-94	Saccharomyces cerevisiae	probable membrane protein ypl006w - yeast (saccharomycescerevisiae)
CONTIG4922	33206313_11_8	2058	16161	1929	643	S52525	547	5.2(10)-104	Saccharomyces cerevisiae	probable membrane protein ypl006w - yeast (saccharomycescerevisiae)
CONTIG4084	15829753_13_1	2059	16162	1722	574	S59681	1309	1.2(10)-133	Saccharomyces cerevisiae	probable membrane protein ypl012w - yeast (saccharomycescerevisiae)
CONTIG2861	33413437_13_2	2060	16163	969	323	S59681	563	1.8(10)-53	Saccharomyces cerevisiae	probable membrane protein ypl012w - yeast (saccharomycescerevisiae)
CONTIG3664	601438_13_9	2061	16164	786	262	S59681	507	1.8(10)-47	Saccharomyces cerevisiae	probable membrane protein ypl012w - yeast (saccharomycescerevisiae)
CONTIG4451	14473413_13_5	2062	16165	2727	909	S62042	409	3.6(10)-35	Saccharomyces cerevisiae	probable membrane protein ypl032c - yeast (saccharomycescerevisiae)

b2x13426.y	32225262_f12_1	2063	16166	495	165	S62034	160	6.5(10)-12	Saccharomyces cerevisiae	probable membrane protein ypl041c - yeast (saccharomycescerevisiae)
CONTIG2908	25677281_f1_1	2064	16167	1470	490	S61114	185	6.7(10)-19	Saccharomyces cerevisiae	probable membrane protein ypl072w - yeast (saccharomycescerevisiae)
CONTIG4426	24261700_f3_4	2065	16168	279	93	S61968	139	1.1(10)-9	Saccharomyces cerevisiae	probable membrane protein ypl098c - yeast (saccharomycescerevisiae)
CONTIG1047	32160156_f1_1	2066	16169	696	232	S61965	448	2.0(10)-42	Saccharomyces cerevisiae	probable membrane protein ypl101w - yeast (saccharomycescerevisiae)
b9x13c67.y	12601016_f1_1	2067	16170	360	120	S61965	188	4.2(10)-14	Saccharomyces cerevisiae	probable membrane protein ypl101w - yeast (saccharomycescerevisiae)
CONTIG4426	2538302_c3_7	2068	16171	1359	453	S61964	741	1.8(10)-73	Saccharomyces cerevisiae	probable membrane protein ypl103c - yeast (saccharomycescerevisiae)
CONTIG3243	4385942_f1_1	2069	16172	1251	417	S62012	1060	8.0(10)-112	Saccharomyces cerevisiae	probable membrane protein ypl109c - yeast (saccharomycescerevisiae)
CONTIG703	24694567_f1_1	2070	16173	912	304	S62009	158	1.3(10)-9	Saccharomyces cerevisiae	probable membrane protein ypl112c - yeast (saccharomycescerevisiae)
CONTIG4453	6650325_c2_4	2071	16174	1497	499	S61996	386	8.3(10)-35	Saccharomyces cerevisiae	probable membrane protein ypl126w - yeast (saccharomycescerevisiae)
CONTIG5473	10628407_f12_2	2072	16175	1035	345	S61996	156	4.5(10)-15	Saccharomyces cerevisiae	probable membrane protein ypl126w - yeast (saccharomycescerevisiae)
CONTIG4949	2929517_c1_6	2073	16176	1056	352	S65173	336	1.5(10)-30	Saccharomyces cerevisiae	probable membrane protein ypl162c - yeast (saccharomycescerevisiae)

CONTIG1969	10165718_f2_1	2074	16177	1002	334	S65195	110	0.0038	Saccharomyces cerevisiae	probable membrane protein ypl183c - yeast (saccharomycescerevisiae)
CONTIG492	36618903_c3_4	2075	16178	933	311	S65195	195	1.3(10)-12	Saccharomyces cerevisiae	probable membrane protein ypl183c - yeast (saccharomycescerevisiae)
b3x12259.y	12897660_c2_5	2076	16179	828	276	S65195	345	2.7(10)-30	Saccharomyces cerevisiae	probable membrane protein ypl183c - yeast (saccharomycescerevisiae)
CONTIG3084	22448317_c3_2	2077	16180	1455	485	S65196	1131	8.4(10)-115	Saccharomyces cerevisiae	probable membrane protein ypl184c - yeast (saccharomycescerevisiae)
b2x12011.y	5285155_f1_1	2078	16181	624	208	S65225	109	3.2(10)-9	Saccharomyces cerevisiae	probable membrane protein ypl206c - yeast (saccharomycescerevisiae)
b1x16281.x	25408182_f3_3	2079	16182	681	227	S65235	109	0.00058	Saccharomyces cerevisiae	probable membrane protein ypl216w - yeast (saccharomycescerevisiae)
CONTIG5569	22462888_f3_4	2080	16183	3561	1187	S65236	1452	7.9(10)-293	Saccharomyces cerevisiae	probable membrane protein ypl217c - yeast (saccharomycescerevisiae)
CONTIG5569	15672192_f1_1	2081	16184	1467	489	S65240	577	4.2(10)-56	Saccharomyces cerevisiae	probable membrane protein ypl221w - yeast (saccharomycescerevisiae)
CONTIG1113	14275011_c1_3	2082	16185	642	214	S65243	165	1.3(10)-11	Saccharomyces cerevisiae	probable membrane protein ypl224c - yeast (saccharomycescerevisiae)
CONTIG5428	511627_c2_13	2083	16186	561	187	S61020	197	1.7(10)-15	Saccharomyces cerevisiae	probable membrane protein ypl244c - yeast (saccharomycescerevisiae)
CONTIG361	4484385_c3_2	2084	16187	630	210	S61018	238	3.6(10)-20	Saccharomyces cerevisiae	probable membrane protein ypl246c - yeast (saccharomycescerevisiae)

CONTIG1801	21640917_c3_3	2085	16188	564	188	S65293	204	1.2(10)-15	Saccharomyces cerevisiae	probable membrane protein ypl260w - yeast (saccharomycescerevisiae)
CONTIG3475	15792062_c1_5	2086	16189	705	235	S65293	441	1.1(10)-41	Saccharomyces cerevisiae	probable membrane protein ypl260w - yeast (saccharomycescerevisiae)
CONTIG1972	24017205_f2_1	2087	16190	1248	416	S65297	647	1.6(10)-63	Saccharomyces cerevisiae	probable membrane protein ypl264c - yeast (saccharomycescerevisiae)
CONTIG4970	24250780_f2_3	2088	16191	2913	971	S54496	164	1.5(10)-20	Saccharomyces cerevisiae	probable membrane protein ypr022c - yeast (saccharomycescerevisiae)
CONTIG5657	12994062_f2_8	2089	16192	303	101	S54496	150	2.1(10)-9	Saccharomyces cerevisiae	probable membrane protein ypr022c - yeast (saccharomycescerevisiae)
CONTIG4752	24407130_c3_8	2090	16193	471	157	S54502	360	4.2(10)-33	Saccharomyces cerevisiae	probable membrane protein ypr028w - yeast (saccharomycescerevisiae)
CONTIG4783	2158316_f1_1	2091	16194	1737	579	S54506	725	5.7(10)-81	Saccharomyces cerevisiae	probable membrane protein ypr032w - yeast (saccharomycescerevisiae)
CONTIG2577	34000177_c2_3	2092	16195	813	271	S54073	102	0.03699	Saccharomyces cerevisiae	probable membrane protein ypr049c - yeast (saccharomycescerevisiae)
CONTIG3870	26773300_f3_2	2093	16196	345	115	S54073	117	7.2(10)-6	Saccharomyces cerevisiae	probable membrane protein ypr049c - yeast (saccharomycescerevisiae)
CONTIG5403	3954028_c3_13	2094	16197	366	122	S54084	159	8.4(10)-12	Saccharomyces cerevisiae	probable membrane protein ypr063c - yeast (saccharomycescerevisiae)
CONTIG5797	12195183_f2_4	2095	16198	2175	725	S59770	347	1.8(10)-28	Saccharomyces cerevisiae	probable membrane protein ypr103c - yeast (saccharomycescerevisiae)

CONTIG3916	15682288_c3_5	2096	16199	1329	443	S59782	407	2.6(10)-36	Saccharomyces cerevisiae	probable membrane protein ypr117w - yeast (saccharomycescerevisiae)
blx19271.y	24321885_c3_3	2097	16200	702	234	S59782	167	8.0(10)-11	Saccharomyces cerevisiae	probable membrane protein ypr117w - yeast (saccharomycescerevisiae)
CONTIG1995	9846041_ft_1	2098	16201	693	231	S58824	492	2.7(10)-46	Saccharomyces cerevisiae	probable membrane protein ypr194c - yeast (saccharomycescerevisiae)
CONTIG4127	402001_ft_3	2099	16202	1041	347	S58824	807	1.8(10)-80	Saccharomyces cerevisiae	probable membrane protein ypr194c - yeast (saccharomycescerevisiae)
CONTIG4140	14720917_c3_7	2100	16203	516	172	S58824	390	2.8(10)-35	Saccharomyces cerevisiae	probable membrane protein ypr194c - yeast (saccharomycescerevisiae)
CONTIG2865	6846082_ft_1	2101	16204	1524	508	S58824	897	5.2(10)-90	Saccharomyces cerevisiae	probable membrane protein ypr194c - yeast (saccharomycescerevisiae)
CONTIG3340	13063143_c3_5	2102	16205	2088	696	S58824	1581	1.7(10)-162	Saccharomyces cerevisiae	probable membrane protein ypr194c - yeast (saccharomycescerevisiae)
CONTIG3983	23626003_c3_7	2103	16206	1023	341	S58824	294	6.0(10)-25	Saccharomyces cerevisiae	probable membrane protein ypr194c - yeast (saccharomycescerevisiae)
CONTIG4488	4708127_c3_4	2104	16207	1407	469	S58824	724	1.1(10)-71	Saccharomyces cerevisiae	probable membrane protein ypr194c - yeast (saccharomycescerevisiae)
CONTIG732	12635400_ft_2	2105	16208	1023	341	S58824	883	1.6(10)-88	Saccharomyces cerevisiae	probable membrane protein ypr194c - yeast (saccharomycescerevisiae)
CONTIG875	23468752_ft_2	2106	16209	615	205	S58824	342	4.2(10)-30	Saccharomyces cerevisiae	probable membrane protein ypr194c - yeast (saccharomycescerevisiae)
CONTIG3031	4876300_c2_6	2107	16210	972	324	S50979	148	9.5(10)-8	Saccharomyces cerevisiae	rhc21 protein - yeast (saccharomycescerevisiae)

CONTIG3166	24412811_f3_6	2108	16211	585	195	S50979	106	0.0022	Saccharomyces cerevisiae	rhc21 protein - yeast (saccharomyces cerevisiae)
CONTIG3179	9954712_f2_1	2109	16212	1425	475	S56295	459	1.2(10)-42	Saccharomyces cerevisiae	sap155 protein - yeast (saccharomyces cerevisiae)
CONTIG4472	23991312_f3_3	2110	16213	729	243	S56295	193	4.0(10)-14	Saccharomyces cerevisiae	sap155 protein - yeast (saccharomyces cerevisiae)
CONTIG2107	20943812_c2_5	2111	16214	1395	465	S64745	210	1.0(10)-13	Saccharomyces cerevisiae	sfl1 protein - yeast (saccharomyces cerevisiae)
CONTIG2904	12145287_f3_2	2112	16215	876	292	S30839	698	6.4(10)-69	Saccharomyces cerevisiae	utr2 protein - yeast (saccharomyces cerevisiae)
CONTIG3856	26423400_f1_1	2113	16216	1335	445	B26955	564	3.3(10)-65	Yarrowia lipolytica	hypothetical protein - yeast (Yarrowia lipolytica) (fragment)
CONTIG5820	5907001_f3_60	2114	16217	699	233	S51503	712	2.1(10)-70	Yarrowia lipolytica	nadh dehydrogenase (ubiquinone) (ec 1.6.5.3) chain 4 - yeast(Yarrowia lipolytica) mitochondrion (sgc2)
CONTIG3215	4406555_f3_3	2115	16218	459	153	JC4589	93	0.00017	Coccidioides immitis	immunoreactive protein - coccidioides immitis this protein is an immunogenic protein, and has the roles in human immunity to coccidioidomycosis.
CONTIG3499	13962542_c3_11	2116	16219	1356	452	JC4589	116	3.7(10)-5	Coccidioides immitis	immunoreactive protein - coccidioides immitis this protein is an immunogenic protein, and has the roles in human immunity to coccidioidomycosis.
CONTIG2529	4823262_c3_4	2117	16220	1434	478	S20466	463	5.2(10)-44	Fusarium oxysporum	hypothetical protein - fungus (Fusarium oxysporum)
CONTIG4977	15672630_c2_10	2118	16221	558	186	S60179	121	6.4(10)-5	Fusarium oxysporum	pol polyprotein homolog - fungus (Fusarium oxysporum)retrotransposon skippy
CONTIG3570	33210062_c3_4	2119	16222	1089	363	S45583	156	1.7(10)-8	Nectria haematococca	pisatin demethylase - fungus (nectria haematococca)

CONTIG3685	32113382_c2_5	2120	16223	747	249	S51577	138	3.3(10)-7	Magnaporthe grisea	transposase - rice blast fungus
CONTIG4956	117793_f3_4	2121	16224	1044	348	S51577	187	4.7(10)-12	Magnaporthe grisea	transposase - rice blast fungus
CONTIG5318	5084575_c3_9	2122	16225	1644	548	S51577	478	1.3(10)-45	Magnaporthe grisea	transposase - rice blast fungus
CONTIG3379	2925687_c3_6	2123	16226	183	61	JC4255	93	0.00087	Neurospora crassa	met-10+ protein - neurospora crassa this protein is involved in methionine biosynthesis, transport and utilization.
CONTIG3478	36337777_f2_2	2124	16227	231	77	A36621	157	1.3(10)-11	Neurospora crassa	nadh dehydrogenase (ubiquinone) (ec 1.6.5.3) 22k chainprecursor - neurospora crassa
CONTIG793	25399213_f2_1	2125	16228	528	176	S59926	499	1.6(10)-47	Neurospora crassa	nadh dehydrogenase (ubiquinone) (ec 1.6.5.3) 78k chainprecursor - neurospora crassa
CONTIG616	16601449_c1_2	2126	16229	618	206	S59926	819	9.6(10)-82	Neurospora crassa	nadh dehydrogenase (ubiquinone) (ec 1.6.5.3) 78k chainprecursor - neurospora crassa
CONTIG5820	22267263_f1_14	2127	16230	807	269	S03127	355	1.3(10)-32	Neurospora crassa	gene cob inttron protein - neurospora crassa mitochondrion(sgc3)
CONTIG4819	24726632_f3_6	2128	16231	1476	492	S49876	1162	4.4(10)-118	Ustilago maydis	gamma-adaptin - smut fungus (ustilago maydis)
CONTIG5046	11025127_c3_7	2129	16232	1275	425	S41649	102	0.12	Plasmodium falciparum	dna polymerase - plasmodium falciparum
CONTIG5330	4307778_c3_13	2130	16233	873	291	S41649	94	0.28	Plasmodium falciparum	dna polymerase - plasmodium falciparum
CONTIG5626	23941882_c2_12	2131	16234	834	278	A45555	91	0.42999	Plasmodium falciparum	glutamate rich protein - plasmodium falciparum
CONTIG1310	24080308_f3_2	2132	16235	564	188	A54523	93	0.001	Plasmodium lophurae	histidine-rich protein - plasmodium lophurae (fragment)
CONTIG5537	29412762_f1_1	2133	16236	282	94	S50099	125	8.8(10)-7	Bufo marinus	h.k-atpase - giant toad
CONTIG3966	3134802_c3_4	2134	16237	1104	368	A57090	380	1.3(10)-40	Homo sapiens	csa protein - human

CONTIG3217	17032510_c3_5	2135	16238	477	159	A48024	121	9.0(10)-8	Homo sapiens	glycosylphosphatidylinositol anchor class h biosynthesisprotein - human
CONTIG3106	32553432_f3_5	2136	16239	939	313	I54209	222	1.8(10)-18	Homo sapiens	hypothetical protein - human (fragment)
CONTIG5607	13672785_f1_2	2137	16240	597	199	A38919	94	0.1	Homo sapiens	hypothetical protein 1 - human
CONTIG1459	33234812_f3_3	2138	16241	738	246	I70160	157	1.6(10)-12	Homo sapiens	pyruvate dehydrogenase kinase - human
CONTIG1996	16287537_f3_1	2139	16242	1041	347	I49272	163	3.5(10)-9	Mus musculus	cd40 receptor-associated factor 1 - mouse
CONTIG4137	3167010_c1_9	2140	16243	3573	1191	S60896	2713	1.3(10)-286	Candida albicans	agglutinin-like protein - yeast (candida albicans)
CONTIG4507	4797561_c3_5	2141	16244	2436	812	S60896	2267	3.5(10)-235	Candida albicans	agglutinin-like protein - yeast (candida albicans)
CONTIG5246	601391_f2_5	2142	16245	900	300	S60896	777	1.7(10)-76	Candida albicans	agglutinin-like protein - yeast (candida albicans)
CONTIG5331	34414057_f3_4	2143	16246	864	288	S20538	1256	4.7(10)-128	Candida albicans	chitin synthase (ec 2.4.1.16) - imperfect fungus (candidaalbicans)
CONTIG2575	10598500_c2_3	2144	16247	909	303	S17517	922	1.2(10)-92	Pichia anomala	hypothetical protein - yeast (pichia anomala)
CONTIG4918	5112925_f1_1	2145	16248	966	322	S17517	759	2.2(10)-75	Pichia anomala	hypothetical protein - yeast (pichia anomala)
CONTIG4050	6820250_f3_3	2146	16249	675	225	S72159	314	3.2(10)-28	Saccharomyces cerevisiae	ribosomal protein y115, mitochondrial - yeast (saccharomycescerevisiae)
b3x16011.y	485135_c3_6	2147	16250	435	145	S63587	126	3.8(10)-7	Aspergillus niger	gene pacc protein - aspergillus niger
CONTIG1874	4425681_f3_1	2148	16251	603	201	S55930	442	8.6(10)-42	Podospora anserina	het-c4 protein - podospora anserina
CONTIG3601	14844627_c1_6	2149	16252	402	134	S23693	110	7.0(10)-6	Plasmodium falci-parum	hypothetical protein 10 - plasmodium falci-parum
CONTIG3050	7078326_f3_1	2150	16253	216	72	S23693	125	1.6(10)-7	Plasmodium falci-parum	hypothetical protein 10 - plasmodium falci-parum

CONTIG1686	26679703_f3_3	2151	16254	282	94	S51376	141	2.7(10)-9	Solanum tuberosum	sucrose cleavage protein - potato
CONTIG592	892752_f3_2	2152	16255	342	114	S57792	129	9.6(10)-8	Mangifera indica	thiolase precursor, peroxisomal - ripe mango
b3x10691.x	4164583_f3_4	2153	16256	471	157	S48094	810	8.6(10)-81	synthetic construct	chloramphenicol o-acetyltransferase (ec 2.3.1.28) - synthetic
CONTIG5474	14541057_c3_18	2154	16257	300	100	S61720	189	5.5(10)-15	Saccharomyces cerevisiae	hypothetical protein orf1224 - yeast (saccharomycescerevisiae)
CONTIG2235	4878400_c2_5	2155	16258	354	118	X70360	105	4.5(10)-6	Azospirillum brasiliense	or:azospirillum brasiliense gn:car le:59 re:580 di:direct nt:orf2
CONTIG3474	10941077_c2_4	2156	16259	372	124	X70360	164	2.5(10)-12	Azospirillum brasiliense	or:azospirillum brasiliense gn:car le:59 re:580 di:direct nt:orf2
CONTIG3446	35834641_f3_1	2157	16260	1761	587	U45424	106	0.00068	Borrelia burgdorferi	or:borrelia burgdorferi gn:rep le:818 re:1303 di:complement sr:lyme disease spirochete strain=297 nt:minus strand repeat motif-containing gene
CONTIG3673	29500325_c2_5	2158	16261	555	185	D49537	189	5.5(10)-15	Clostridium perfringens	or:clostridium perfringens pn:unknown gn:orf18 le:225 re:683 di:direct sr:clostridium perfringens (strain:ncic8237) dna, clone:plsd10
CONTIG5316	2751375_f2_5	2159	16262	477	159	D86544	272	9.0(10)-24	Raistonia pickettii	or:raistonia pickettii pn:hydroxyquinol-1, 2-dioxygenase gn:hac le:2659 re:3606 di:direct sr:burkholderia pickettii (strain:dip0602) dna
CONTIG5723	1050063_c2_25	2160	16263	990	330	D86544	452	7.5(10)-43	Raistonia pickettii	or:raistonia pickettii pn:hydroxyquinol-1, 2-dioxygenase gn:hac le:2659 re:3606 di:direct sr:burkholderia pickettii (strain:dip0602) dna

CONTIG1116	3017257_c3_5	2161	16264	246	82	M26308	102	9.3(10)-6	Plasmid IncF	or:plasmid incf le:3577 re:3894 di:direct sr:plasmid incf dna nt:orf5
CONTIG555	14460883_c1_2	2162	16265	390	130	X97263	91	0.01099	Lactococcus lactis	or:lactococcus lactis gn:abim le:189 re:1931 di:complement
CONTIG3261	3938936_fl_1	2163	16266	687	229	X73834	99	0.0057	Mycoplasma hominis	or:mycoplasma hominis pn:adhesin gn:p50 le:362 re:1765 di:direct
CONTIG2240	3338933_fl_1	2164	16267	564	188	U22020	106	0.0001	Mycoplasma hominis	or:mycoplasma hominis pn:p120 gn:p120 le:1 re:>561 di:direct
CONTIG5813	10322186_f2_15	2165	16268	612	204	L16627	90	0.057	Pasteurella haemolytica	or:pasteurella haemolytica pn:lipoprotein 3 gn:p1pc le:3521 re:4300 di:direct sr:pasteurella haemolytica (strain a1) dna nt:putative
CONTIG5678	10625252_c1_13	2166	16269	2766	922	X94909	103	0.23	Streptococcus pneumoniae	or:streptococcus pneumoniae pn:iga1 protease gn:iga le:259 re:6042 di:direct
CONTIG1197	34242817_c1_2	2167	16270	837	279	U28142	94	0.0073	Streptococcus pyogenes	or:streptococcus pyogenes pn:emm12(a207) gn:emm12(a207) le:1 re:>459 di:direct nt:igg3- binding protein
CONTIG5815	2745675_f3_25	2168	16271	372	124	U63134	91	0.00051	Streptococcus pyogenes	or:streptococcus pyogenes le:<1 re:756 di:complement nt:the 5' end of the open reading frame shows
CONTIG3669	4485750_c2_6	2169	16272	1914	638	Z69926	101	0.039	Yersinia enterocolitica	or:yersinia enterocolitica pn:yopm gn:yopm le:162 re:1265 di:direct
CONTIG3534	4335152_fl_1	2170	16273	732	244	Z83316	92	0.2	Caenorhabditis elegans	or:caenorhabditis elegans pn:b0379.f1e:join(13467 re:13706,13751 di:direct nt:protein predicted using genefinder

CONTIG5300	24804712_c3_9	2171	16274	729	243	Z50109	117	6.7(10)-8	Caenorhabditis elegans	or:caenorhabditis elegans pn:c09h10.6 le:join(35101 re:35213.35265 di:direct nt:similar to histone binding protein; cdna est
CONTIG3861	4001556_f3_6	2172	16275	642	214	Z78540	215	1.8(10)-16	Caenorhabditis elegans	or:caenorhabditis elegans pn:c33g3.4 le:join(19807 re:19939.20519 di:direct nt:protein predicted using genefinder; similarity to
CONTIG4902	33397187_f2_2	2173	16276	408	136	Z74030	130	4.2(10)-8	Caenorhabditis elegans	or:caenorhabditis elegans pn:d1054.14 le:join(36950 re:37074.3726 di:complement nt:protein predicted using genefinder; cdna est
CONTIG4403	23915962_c2_17	2174	16277	609	203	Z66496	151	7.4(10)-10	Caenorhabditis elegans	or:caenorhabditis elegans pn:e04d5.1 le:join(6082 re:6250.6307 di:direct nt:cdna est yk84b6.3 comes from this gene; cdna est
CONTIG710	954507_c3_2	2175	16278	603	201	Z68760	119	0.00011	Caenorhabditis elegans	or:caenorhabditis elegans pn:f36h1.2 le:join(15689 re:15802.16087 di:direct nt:similarity to human ankaryin (sw:ankb_human); cdna
CONTIG3772	35366700_c1_6	2176	16279	582	194	Z49938	161	1.3(10)-11	Caenorhabditis elegans	or:caenorhabditis elegans pn:f38a3.2 le:join(15042 re:15879.1609 di:complement nt:similar to collagen; cdna est yk73f3.5 comes from
CONTIG5062	22063767_c1_6	2177	16280	309	103	Z68218	218	4.7(10)-18	Caenorhabditis elegans	or:caenorhabditis elegans pn:k01h12.1 le:join(7129 re:7235.7495 di:direct

CONTIG2906	1039628_c2_8	2178	16281	492	164	Z78544	90	0.058	Caenorhabditis elegans	or:caenorhabditis elegans pn:k04g11.4 le:join(16299 re:16406,16931 di:direct nt:protein predicted using genefinder; similarity to
CONTIG5019	3985212_f1_1	2179	16282	246	82	Z70284	107	3.2(10)-5	Caenorhabditis elegans	or:caenorhabditis elegans pn:k07f5.14 le:join(28537 re:28761,28876 di:direct nt:cdna est ceesg67r comes from this gene
CONTIG1504	10052018_c3_3	2180	16283	885	295	U61957	123	8.3(10)-5	Caenorhabditis elegans	or:caenorhabditis elegans gn:ac7.2 le:join(2255 re:2437,3752 di:direct sr:caenorhabditis elegans strain=bristol n2 nt:coded for by c. elegans cdna cm06e9; contains
CONTIG1620	15890968_c3_7	2181	16284	636	212	U23453	199	4.9(10)-15	Caenorhabditis elegans	or:caenorhabditis elegans gn:b0252.2 le:join(10366 re:10558,10610 di:direct sr:caenorhabditis elegans strain=bristol n2 nt:similar to sphingomyelin phosphodiesterase
CONTIG4806	26597307_c2_11	2182	16285	1335	445	U80836	109	0.0032	Caenorhabditis elegans	or:caenorhabditis elegans gn:b0432.9 le:join(22295 re:22415,2245 di:complement sr:caenorhabditis elegans strain=bristol n2 nt:contains similarity to a c3hc4-class zinc finger
CONTIG5287	4462_f3_4	2183	16286	1182	394	L07143	105	0.032	Caenorhabditis elegans	or:caenorhabditis elegans gn:b0523.5 le:join(10015 re:10029,1014 di:complement sr:caenorhabditis elegans strain=bristol n2 nt:leu repeats and gelsolin (d. melanogaster

CONTIG549	25446013_c3_4	2184	16287	606	202	U53338	107	0.00051	Caenorhabditis elegans	or:caenorhabditis elegans gn:c05c11.1 le:join(33372 re:33614,33670 di:direct sr:caenorhabditis elegans strain=bristol n2
CONTIG4644	10812676_f3_6	2185	16288	366	122	U61947	155	2.2(10)-11	Caenorhabditis elegans	or:caenorhabditis elegans gn:c06g3.11 le:join(30495 re:30534,3072 di:complement sr:caenorhabditis elegans strain=bristol n2
CONTIG3689	12994052_f2_2	2186	16289	1503	501	U56965	90	0.41999	Caenorhabditis elegans	or:caenorhabditis elegans gn:c15h9.4 le:join(12284 re:12437,12488 di:direct sr:caenorhabditis elegans strain=bristol n2
CONTIG5058	21994161_c2_6	2187	16290	666	222	U23169	193	8.3(10)-15	Caenorhabditis elegans	or:caenorhabditis elegans gn:c29h12.2 le:join(19961 re:20183,20227 di:direct sr:caenorhabditis elegans strain=bristol n2 nt:coded for by c. elegans cdna cm14g11
b2x10185.x	10991428_f2_1	2188	16291	492	164	U88314	93	0.017	Caenorhabditis elegans	or:caenorhabditis elegans gn:c46h1.2 le:join(30376 re:30456,30710 di:direct sr:caenorhabditis elegans strain=bristol n2 nt:coded for by c. elegans cdna yk167c11.5; coded for
CONTIG3886	6650763_f3_2	2189	16292	2115	705	U80445	461	3.8(10)-45	Caenorhabditis elegans	or:caenorhabditis elegans gn:c50f2.3 le:join(771 re:836,884 di:direct sr:caenorhabditis elegans strain=bristol n2 nt:coded for by c. elegans cdna yk13g5.3; coded for by

CONTIG5264	10938957_f3_3	2190	16293	744	248	U39996	102	0.028	Caenorhabditis elegans	or:caenorhabditis elegans gn:c56e6.6 le:join(28904 re:29200,2925 di:complement sr:caenorhabditis elegans strain=bristol n2 nt:coded for by c. elegans cdna yk132e5.5; coded for
CONTIG5283	34657540_f3_7	2191	16294	1569	523	U13070	353	1.1(10)-31	Caenorhabditis elegans	or:caenorhabditis elegans gn:f01f1.1 le:join(37237 re:37241,37471 di:direct sr:caenorhabditis elegans strain=bristol n2 nt:coded for by c. elegans cdna ceesb68f; coded for by
CONTIG52036	21523378_c3_5	2192	16295	939	313	U40029	174	5.7(10)-14	Caenorhabditis elegans	or:caenorhabditis elegans gn:f10g7.2 le:join(22509 re:22942,23020 di:direct sr:caenorhabditis elegans strain=bristol n2 nt:similar to human 100 kda coactivator (u22055)
CONTIG5638	2908260_f2_11	2193	16296	663	221	U88176	149	3.5(10)-19	Caenorhabditis elegans	or:caenorhabditis elegans gn:f18f11.1 le:join(12152 re:12273,12319 di:direct sr:caenorhabditis elegans strain=bristol n2
CONTIG2278	10735912_c1_2	2194	16297	1554	518	U53343	179	1.8(10)-10	Caenorhabditis elegans	or:caenorhabditis elegans gn:f22f4.3 le:join(4805 re:4831,6545 di:direct sr:caenorhabditis elegans strain=bristol n2 nt:coded for by c. elegans cdna yk53e5.3; coded for by

b3x12379.x	26252252_c1_2	2195	16298	834	278	U40934	91	0.34999	Caenorhabditis elegans	or:caenorhabditis elegans gn:f35h10.4 le:join(8199 re:8315,8607 di:direct sr:caenorhabditis elegans strain=bristol n2 nt:coded for by c. elegans cdna yk49d12.5; similar to
CONTIG3153	36366526_f3_2	2196	16299	843	281	U41996	117	6.0(10)-5	Caenorhabditis elegans	or:caenorhabditis elegans gn:f38e1.9 le:join(7863 re:8099,814 di:complement sr:caenorhabditis elegans strain=bristol n2
b9x10190.x	36573918_c3_8	2197	16300	486	162	U55366	90	0.00097	Caenorhabditis elegans	or:caenorhabditis elegans gn:f41f3.4 le:join(13544 re:14272,1433 di:complement sr:caenorhabditis elegans strain=bristol n2 nt:similar to cuticle collagen
CONTIG5810	14630378_f1_4	2198	16301	972	324	U50313	470	9.3(10)-45	Caenorhabditis elegans	or:caenorhabditis elegans gn:f44c4.5 le:join(17781 re:17978,1819 di:complement sr:caenorhabditis elegans strain=bristol n2 nt:similar to palmitoyl-protein thioesterase
CONTIG2346	5120306_c3_4	2199	16302	228	76	U88173	277	2.6(10)-24	Caenorhabditis elegans	or:caenorhabditis elegans gn:f46f11.4 le:join(6769 re:6877,756 di:complement sr:caenorhabditis elegans strain=bristol n2 nt:weak similarity to arabidopsis thaliana

CONTIG2566	21495953_c2_4	2200	16303	888	296	U41109	91	0.5	Caenorhabditis elegans	or:caenorhabditis elegans gn:f52e1.4 le:join(5058 re:5105,5154 di:direct sr:caenorhabditis elegans strain=bristol n2 nt:coded for by c. elegans cdna yk11c7.3; coded for by
CONTIG5603	859388_c2_10	2201	16304	1017	339	U80436	96	0.29999	Caenorhabditis elegans	or:caenorhabditis elegans gn:f55c7.7 le:join(24700 re:24729,2533 di:complement sr:caenorhabditis elegans strain=bristol n2 nt:strong similarity to human proto-oncogene dbl
CONTIG5500	16408425_c1_9	2202	16305	894	298	U51993	304	3.6(10)-27	Caenorhabditis elegans	or:caenorhabditis elegans gn:f56f10.3 le:join(10544 re:10633,1068 di:complement sr:caenorhabditis elegans strain=bristol n2 nt:coded for by c. elegans cdna cm7a8; similar to
CONTIG5785	2343930_f1_6	2203	16306	546	182	U70856	100	0.0067	Caenorhabditis elegans	or:caenorhabditis elegans gn:f57f4.1 le:join(13373 re:13441,13488 di:direct sr:caenorhabditis elegans strain=bristol n2 nt:weak similarity to rat cytosolic acyl coenzyme a
CONTIG2224	9798431_c2_2	2204	16307	969	323	U41625	112	0.00169	Caenorhabditis elegans	or:caenorhabditis elegans gn:k03a1.2 le:join(15437 re:15775,16143 di:direct sr:caenorhabditis elegans strain=bristol n2 nt:coded for by c. elegans cdna yk133e1.5; coded for

CONTIG4454	23626542_c3_3	2205	16308	780	260	Z66523	417	3.8(10)-39	Caenorhabditis elegans	or:caenorhabditis elegans pn:m05d6.7 le:join(17855 re:17891,17945 di:direct nt:similar to gamma-butyrobetaine,2-oxoglutarate
CONTIG5572	20353186_c2_14	2206	16309	2445	815	Z50796	92	0.51	Caenorhabditis elegans	or:caenorhabditis elegans pn:i05a6.4 le:join(20406 re:20458,2062 di:complement nt:weak similarity to some rna directed
CONTIG4770	33632632_f3_5	2207	16310	990	330	Z73098	103	0.032	Caenorhabditis elegans	or:caenorhabditis elegans pn:i21c9.2 le:join(446 re:548,59 di:complement nt:weak similarity to the yeast kipl protein (swiss
CONTIG5325	32437842_f1_1	2208	16311	303	101	Z54238	117	1.5(10)-5	Caenorhabditis elegans	or:caenorhabditis elegans pn:i28c6.7 le:join(21186 re:21335,21383 di:direct nt:weak similarity to myosin proteins; cdna est
CONTIG2858	4329057_c1_2	2209	16312	1293	431	U19615	392	1.8(10)-35	Caenorhabditis elegans	or:caenorhabditis elegans pn:let 858 gn:let-858 le:6 re:2699 di:direct
CONTIG3977	12131875_c2_7	2210	16313	684	228	U33058	95	0.38	Caenorhabditis elegans	or:caenorhabditis elegans pn:unc-89 gn:unc-89 le:join(4920 re:4969,5656 di:direct nt:giant ig superfamily member located in the middle
CONTIG5001	2166663_f1_1	2211	16314	1410	470	U33058	114	5.0(10)-5	Caenorhabditis elegans	or:caenorhabditis elegans pn:unc-89 gn:unc-89 le:join(4920 re:4969,5656 di:direct nt:giant ig superfamily member located in the middle

CONTIG5153	34086007_fl_1	2212	16315	216	72	Z49969	90	0.0035	Caenorhabditis elegans	or:caenorhabditis elegans pn:w01c9.3 le:join(8547 re:8589,8876 di:direct nt:cdna est yk13c5.3 comes from this gene; cdna est
CONTIG3992	2157913_fl_2	2213	16316	495	165	Z50029	102	0.00068	Caenorhabditis elegans	or:caenorhabditis elegans pn:zc504.3 le:join(15177 re:15381,1546 di:complement nt:cell division cycle 2-like protein; cdna est
CONTIG3043	22551877_c3_14	2214	16317	351	117	Z47357	137	1.8(10)-8	Caenorhabditis elegans	or:caenorhabditis elegans pn:zk1128.1 le:join(1289 re:1558,165 di:complement nt:cdna est ceesj77r comes from this gene; cdna est
CONTIG5679	12126285_c3_22	2215	16318	1425	475	Z47357	270	1.8(10)-29	Caenorhabditis elegans	or:caenorhabditis elegans pn:zk1128.1 le:join(1289 re:1558,165 di:complement nt:cdna est ceesj77r comes from this gene; cdna est
CONTIG5721	24104657_fl_1	2216	16319	198	66	Z69385	112	8.0(10)-7	Caenorhabditis elegans	or:caenorhabditis elegans pn:zk593.7 le:join(23733 re:23738,23793 di:direct nt:similarity to yeast jta107 protein (pir acc. no.
CONTIG3814	9942177_fl_1	2217	16320	678	226	Z73899	90	0.07499	Caenorhabditis elegans	or:caenorhabditis elegans pn:zk829.5 le:join(8904 re:9055,9109 di:direct
CONTIG3229	5892176_fl_1	2218	16321	612	204	U07817	119	2.8(10)-5	Dictyostelium discoideum	or:dictyostelium discoideum pn:glutamine-asparagine rich protein le:<1 re:2165 di:direct

CONTIG3405	24609468_f1_2	2219	16322	273	91	U75467	110	2.2(10)-5	Drosophila melanogaster	or:drosophila melanogaster pn:atu gn:atu le:join(78 re:1373,147 nt:complement sr:fruit fly nt:contains arg-ser and ser-arg dipeptides; c-terminal
CONTIG468	1953125_f1_1	2220	16323	1041	347	U23930	105	0.0019	Drosophila simulans	or:drosophila simulans pn:ref(2)p protein gn:dsimref(2)p le:join(137 re:308,949 di:direct nt:allele: im2
CONTIG5388	30344201_f2_5	2221	16324	432	144	X15081	104	3.5(10)-5	Crithidia fasciculata	or:mitochondrion crithidia fasciculata le:856 re:1898 di:direct sr:crithidia fasciculata nt:tmuf2 protein (aa 1-348)
b2x14270.y	4063377_c3_1	2222	16325	480	160	U43145	91	0.03599	Plasmodium chabaudi	or:plasmodium chabaudi pn:repeat organellar protein le:2158 re:7977 di:direct nt:rope
CONTIG4004	21662662_f2_3	2223	16326	279	93	L04161	105	0.0004	Plasmodium falciparum	or:plasmodium falciparum pn:pfg377 le:43 re:9402 di:direct sr:malaria parasite nt:gametocyte specific antigen
CONTIG3019	4725375_f3_1	2224	16327	1431	477	L27838	90	0.96999	Plasmodium yoelii	or:plasmodium yoelii pn:rhoptry protein le:76 re:6885 di:direct sr:plasmodium yoelii (strain ym) dna
CONTIG3018	20350786_c1_1	2225	16328	972	324	X95276	105	0.01499	Plasmodium falciparum	or:plasmodium falciparum gn:cp (c?) le:10926 re:13226 di:direct sr:malaria parasite
CONTIG4690	25805_f2_2	2226	16329	912	304	Z26314	94	0.13	Plasmodium falciparum	or:plasmodium falciparum pn:stap antigen le:join(735 re:806,982 di:direct sr:malaria parasite
CONTIG5672	12687510_c3_23	2227	16330	564	188	Z26314	100	0.01099	Plasmodium falciparum	or:plasmodium falciparum pn:stap antigen le:join(735 re:806,982 di:direct sr:malaria parasite

CONTIG4156	13781552_f2_2	2228	16331	1005	335	Z30339	101	0.029	Plasmodium reichenowi	or:plasmodium reichenowi pn:starp antigen le:join(1 re:72,243 di:direct
CONTIG5768	1992062_f2_8	2229	16332	1314	438	U36927	131	0.00012	Plasmodium yoelii	or:plasmodium yoelii pn:rhoptry protein le:<1 re:7206 di:direct
CONTIG4431	9805287_f1_1	2230	16333	2718	906	D28811	165	1.8(10)-8	Schistosoma japonicum	or:schistosoma japonicum pn:paramyosin le:50 re:2650 di:direct sr:schistosoma japonicum (strain japanese) adult cdna to mma, cion
b3x16066.y	36019206_f1_1	2231	16334	585	195	D83125	333	9.3(10)-30	Sarcophaga peregrina	or:sarcophaga peregrina pn:secretory component le:169 re:1830 di:direct sr:sarcophaga peregrina cell_line:nih-sape-4 cdna to mma
CONTIG1784	25195312_c2_12	2232	16335	279	93	U22376	298	1.2(10)-25	Homo sapiens	or:homo sapiens gn:c-myb le:join(2226 re:2248,6595 di:direct sr:human nt:alternatively spliced product using exon 13a
CONTIG5675	29891911_c2_16	2233	16336	2046	682	U57758	262	2.2(10)-21	Drosophila melanogaster	or:drosophila melanogaster pn:putative thyroid receptor interacting protein gn:alien le:58 re:140 di:direct sr:fruit fly
CONTIG1713	9845311_c2_4	2234	16337	1035	345	L03534	113	0.0067	Entamoeba histolytica	or:entamoeba histolytica pn:myosin heavy chain gn:mhca le:368 re:6787 di:direct
CONTIG5429	3946957_f2_2	2235	16338	648	216	D89205	321	5.7(10)-29	Schizosaccharomyces pombe	or:schizosaccharomyces pombe le:88 re:1089 di:direct sr:schizosaccharomyces pombe (strain:pr745) cdna to mma nt:similar to saccharomyces cerevisiae auxin-induced

CONTIG389	4865706_f2_4	2236	16339	558	186	D89240	108	0.00024	Schizosaccharo myces pombe	or:schizosaccharomyces pombe le:<1 re:854 di:direct sr:schizosaccharomyces pombe (strain:pr745) cdna to mma nt:unnamed protein product
CONTIG4741	36360002_c3_14	2237	16340	1200	400	D89245	282	9.3(10)-24	Schizosaccharo myces pombe	or:schizosaccharomyces pombe le:<1 re:1549 di:direct sr:schizosaccharomyces pombe (strain:pr745) cdna to mma nt:similar to human protein kinase c substrate, 80kd
CONTIG4969	12554680_c3_11	2238	16341	519	173	X86470	309	1.1(10)-27	Saccharomyces cerevisiae	or:saccharomyces cerevisiae pn:unknown gn:odp2 le:19206 re:19571 di:complement sr:baker's yeast nt:n2375, len:121, cai:0.089
CONTIG5614	9876532_c1_18	2239	16342	198	66	Z81038	184	1.8(10)-14	Caenorhabditis elegans	or:caenorhabditis elegans pn:c25a1.6 le:join(19836 re:20021,20161 di:direct nt:protein predicted using genefinder
CONTIG1841	12582563_c2_2	2240	16343	372	124	Z83125	92	0.0011	Caenorhabditis elegans	or:caenorhabditis elegans pn:i15d6.12 le:join(27950 re:28052,2810 di:complement
CONTIG4717	12582563_f2_3	2241	16344	402	134	Z83125	102	8.9(10)-5	Caenorhabditis elegans	or:caenorhabditis elegans pn:i15d6.12 le:join(27950 re:28052,2810 di:complement
CONTIG2959	3319087_c2_7	2242	16345	636	212	Z92770	102	0.00095	Mycobacterium tuberculosis	or:mycobacterium tuberculosis pn:unknown gn:mtci5.07 le:6144 re:6749 di:direct nt:mtci5.07, len: 201 aa, most similar to puac_srlp
CONTIG5443	86593_c3_9	2243	16346	1386	462	Z92770	100	0.00013	Mycobacterium tuberculosis	or:mycobacterium tuberculosis pn:unknown gn:mtci5.07 le:6144 re:6749 di:direct nt:mtci5.07, len: 201 aa, most similar to puac_srlp

CONTIG1249	35601452_c1_2	2244	16347	1176	392	Z92770	740	2.2(10)-73	Mycobacterium tuberculosis	or:mycobacterium tuberculosis pn:unknown gn:mtc15.28c lc:27262 re:28473 di:complement nt:mtc15.28c, len: 403 aa, c-terminal region similar
CONTIG3069	30250078_c3_3	2245	16348	1269	423	Z83333	439	1.1(10)-40	Emmericella nidulans	or:emmericella nidulans gn:pala lc:join(491 re:498,548 di:direct
CONTIG5315	4782782_f1_3	2246	16349	1086	362	Z83333	549	6.2(10)-53	Emmericella nidulans	or:emmericella nidulans gn:pala lc:join(491 re:498,548 di:direct
CONTIG5820	13937550_f3_46	2247	16350	297	99	Z72500	345	3.0(10)-31	Pytaella littoralis	or:mitochondrion pytaella littoralis pn:cytochrome oxidase, subunit i gn:cox1 ec:1.9.3.1 lc:join(1 re:817.3252 di:direct sr:pytaella littoralis
CONTIG1578	2914063_c3_4	2248	16351	972	324	X98130	179	4.4(10)-11	Arabidopsis thaliana	or:arabidopsis thaliana pn:non-1r retrotransposon reverse gn:orf1 le:37009 re:39690 di:complement sr:thale cress nt:premature stop codon - likely pseudogene
CONTIG1447	2353325_f2_1	2249	16352	702	234	Y07867	428	2.6(10)-40	Homo sapiens	or:homo sapiens pn:pirin lc:205 re:1077 di:direct sr:human
CONTIG1289	7038417_f2_1	2250	16353	252	84	Y07867	131	2.6(10)-8	Homo sapiens	or:homo sapiens pn:pirin lc:205 re:1077 di:direct sr:human
CONTIG2607	23836552_c3_6	2251	16354	588	196	Y07867	341	4.4(10)-31	Homo sapiens	or:homo sapiens pn:pirin lc:205 re:1077 di:direct sr:human
CONTIG5442	3001301_c2_19	2252	16355	804	268	Y07867	438	2.2(10)-41	Homo sapiens	or:homo sapiens pn:pirin lc:205 re:1077 di:direct sr:human
CONTIG5442	9797327_c1_10	2253	16356	1146	382	Y07867	576	5.5(10)-56	Homo sapiens	or:homo sapiens pn:pirin lc:205 re:1077 di:direct sr:human
CONTIG4664	26362552_c3_8	2254	16357	1587	529	U46857	94	0.029	Anolis pulchellus	or:anolis pulchellus pn:vitellogenin lc:<1 re:>546 di:direct nt:apvlg5, similar to chicken and xenopus phosvitin

CONTIG4190	13931927_c2_9	2255	16358	2334	778	U34662	95	0.34999	Danio rerio	or:danio rerio pn:complement factor b le:15 re:2228 di:direct sr:zebrafish
CONTIG5650	2218826_f2_11	2256	16359	711	237	X95074	150	1.8(10)-9	Gallus gallus	or:gallus gallus pn:translin le:5 re:694 di:direct sr:chicken
CONTIG5427	24296937_f2_3	2257	16360	2883	961	A08564	3639	0	unidentified	or:unidentified pn:glucoamylase le:323 re:3199 di:direct
CONTIG5305	16832785_f3_6	2258	16361	1476	492	U78721	95	0.09199	Arabidopsis thaliana	or:arabidopsis thaliana pn:hypothetical protein gn:i01b08.6 le:join(24846 re:25193,2558 di:complement sr:thale cress
CONTIG1962	11727291_f2_1	2259	16362	876	292	D83006	424	1.3(10)-38	Saccharomyces cerevisiae	or:saccharomyces cerevisiae gn:mn4 le:419 re:3955 di:direct sr:saccharomyces cerevisiae (strain:s288c) dna, clone:atcc70798 nt:gene required for phosphorylation of
CONTIG2573	3017188_f2_1	2260	16363	1230	410	D83006	330	3.0(10)-34	Saccharomyces cerevisiae	or:saccharomyces cerevisiae gn:mn4 le:419 re:3955 di:direct sr:saccharomyces cerevisiae (strain:s288c) dna, clone:atcc70798 nt:gene required for phosphorylation of
CONTIG2738	9769380_c2_2	2261	16364	909	303	D83006	177	6.7(10)-17	Saccharomyces cerevisiae	or:saccharomyces cerevisiae gn:mn4 le:419 re:3955 di:direct sr:saccharomyces cerevisiae (strain:s288c) dna, clone:atcc70798 nt:gene required for phosphorylation of

CONTIG3780	22071885_c1_4	2262	16365	924	308	D83006	188	8,6(10)-22	Saccharomyces cerevisiae	or:saccharomyces cerevisiae gn:mn4 le:419 re:3955 di:direct sr:saccharomyces cerevisiae (strain:s288c) dna, clone:atcc70798 nt:gene required for phosphorylation of
CONTIG3780	4409760_c1_3	2263	16366	1005	335	D83006	164	5,0(10)-9	Saccharomyces cerevisiae	or:saccharomyces cerevisiae gn:mn4 le:419 re:3955 di:direct sr:saccharomyces cerevisiae (strain:s288c) dna, clone:atcc70798 nt:gene required for phosphorylation of
CONTIG4825	20413430_f1_1	2264	16367	2043	681	D83006	460	5,0(10)-56	Saccharomyces cerevisiae	or:saccharomyces cerevisiae gn:mn4 le:419 re:3955 di:direct sr:saccharomyces cerevisiae (strain:s288c) dna, clone:atcc70798 nt:gene required for phosphorylation of
CONTIG5641	175092_f1_3	2265	16368	2310	770	D83006	324	1,6(10)-25	Saccharomyces cerevisiae	or:saccharomyces cerevisiae gn:mn4 le:419 re:3955 di:direct sr:saccharomyces cerevisiae (strain:s288c) dna, clone:atcc70798 nt:gene required for phosphorylation of
CONTIG2347	10048961_c3_4	2266	16369	258	86	M59935	147	3,3(10)-10	Emericella nidulans	or:emerichella nidulans le:join(1138 re:1735,179 di:complement sr:emerichella nidulans (strain fgsc a4) (clone:117e5) cdna to murra nt:unidentified gene; orf
CONTIG4984	5128276_c2_9	2267	16370	783	261	U19882	253	9,1(10)-22	Emericella nidulans	or:emerichella nidulans pn:flbd gn:flbd le:1278 re:2222 di:direct nt:myb-like dna binding protein
CONTIG2706	4329830_f3_2	2268	16371	432	144	X95888	106	3,5(10)-6	Kluyveromyces lacticus	or:kluyveromyces lacticus gn:som1 le:218 re:433 di:direct nt:putative

CONTIG5025	554511_c3_12	2269	16372	819	273	U48413	462	6.5(10)-44	Kluyveromyces lactis	or:kluyveromyces lactis pn:golgi upd-glcnac transporter mnn2-2p gn:kl.mnn2-2 le:244 re:1230 di:direct sr:kluyveromyces lactis strain=mg1/2
CONTIG5384	14333137_c3_20	2270	16373	798	266	L35053	184	5.4(10)-13	Magnaporthe grisea	or:magnaporthe grisea pn:reverse transcriptase gn:pol le:1757 re:5357 di:direct sr:magnaporthe grisea dna nt:homologue of retroviral pol genes; protease;
CONTIG5603	26445192_B_6	2271	16374	3369	1123	L35053	578	9.0(10)-53	Magnaporthe grisea	or:magnaporthe grisea pn:reverse transcriptase gn:pol le:1757 re:5357 di:direct sr:magnaporthe grisea dna nt:homologue of retroviral pol genes; protease;
CONTIG5820	35991431_c2_74	2272	16375	312	104	X75679	323	3.5(10)-29	Candida parapsilosis	or:mitochondrion candida parapsilosis pn:cytochrome oxidase subunit 3 gn:cox3 le:62 re:871 di:direct sr:candida parapsilosis
CONTIG647	14490811_c3_2	2273	16376	519	173	X95547	374	1.3(10)-34	Neurospora crassa	or:neurospora crassa pn:ferredoxin- like iron-sulfur subunit of ec:1.6.5.3 le:139 re:798 di:direct
CONTIG5820	19819050_B_49	2274	16377	393	131	U02970	244	8.3(10)-21	Prototheca wickerhamii	or:mitochondrion prototheca wickerhamii gn:al1 orf = ymf44 le:7715 re:8491 di:complement sr:prototheca wickerhamii nt:cox1 intron 1 orf, group 1 intronic orf
CONTIG5738	23915932_B_7	2275	16378	1176	392	SS9774	1022	3.0(10)-103	Saccharomyces cerevisiae	or:saccharomyces cerevisiae le:2422 re:3582 di:direct sr:baker's yeast nt:description: stil stress-inducible protein homolog;

CONTIG5549	23610625_f1_1	2276	16379	3033	1011	S78624	339	3.7(10)-46	Saccharomyces cerevisiae	or:saccharomyces cerevisiae gn:yer592 le:1695 re:5375 di:direct sr:baker's yeast nt:this sequence comes from fig3.
CONTIG4957	4774050_f1_1	2277	16380	1536	512	X04288	499	9.0(10)-55	Saccharomyces cerevisiae	or:saccharomyces cerevisiae gn:cdc37 sp:p06101 le:150 re:1499 di:direct sr:baker's yeast nt:cdc37 gene product (aa 1-440)
CONTIG5774	23472885_f3_13	2278	16381	327	109	X95258	126	2.6(10)-8	Saccharomyces cerevisiae	or:saccharomyces cerevisiae pn:unknown protein gn:smf1 le:3530 re:3901 di:direct sr:baker's yeast nt:internal to smf1
CONTIG1618	12516577_c2_4	2279	16382	243	81	X87941	114	5.0(10)-7	Saccharomyces cerevisiae	or:saccharomyces cerevisiae gn:orf143 le:14608 re:15039 di:complement sr:baker's yeast
CONTIG4735	190692_f3_2	2280	16383	1035	345	L13655	97	0.014	Saccharum sp.	or:saccharum sp. pn:membrane protein le:123 re:1100 di:direct sr:saccharum sp. (strain h65-7052) leaf cdna to mma nt:putative
b3x16985.y	30165686_c3_2	2281	16384	594	198	X69881	328	4.4(10)-29	Saccharomyces cerevisiae	or:saccharomyces cerevisiae le:2051 re:>3811 di:complement sr:baker's yeast nt:orf2
CONTIG5154	493762_c1_13	2282	16385	819	273	X62105	353	2.2(10)-32	Saccharomyces cerevisiae	or:saccharomyces cerevisiae gn:tfi51 sp:p14306 le:639 re:1298 di:direct sr:baker's yeast
CONTIG1315	19703438_f3_2	2283	16386	474	158	U01878	420	1.8(10)-39	Saccharomyces cerevisiae	or:saccharomyces cerevisiae pn:unknown le:1365 re:1793 di:complement sr:baker's yeast
CONTIG3863	29475017_f2_2	2284	16387	1950	650	U05211	626	2.7(10)-61	Saccharomyces cerevisiae	or:saccharomyces cerevisiae pn:tip1p gn:tip1 le:222 re:2015 di:direct sr:baker's yeast nt:putative

CONTIG4502	29320413_f2_1	2285	16388	582	194	U09129	257	4.9(10)-21	Saccharomyces cerevisiae	or:saccharomyces cerevisiae pn:mkt1p gn:mkt1 le:311 re:2764 di:direct sr:baker's yeast
CONTIG4993	875002_c2_7	2286	16389	1011	337	U09129	144	6.7(10)-7	Saccharomyces cerevisiae	or:saccharomyces cerevisiae pn:mkt1p gn:mkt1 le:311 re:2764 di:direct sr:baker's yeast
CONTIG1554	35789040_f3_1	2287	16390	1017	339	U59224	125	7.0(10)-5	Schizosaccharomyces pombe	or:schizosaccharomyces pombe pn:byr4p gn:byr4 le:636 re:2633 di:direct sr:fission yeast
CONTIG5187	19963927_f1_4	2288	16391	1680	560	L04488	653	4.2(10)-117	Trichosporon cutaneum	or:trichosporon cutaneum pn:phenol hydroxylase le:1 re:1998 di:direct sr:trichosporon cutaneum (library: atcc 46490) cdna to mma
CONTIG2460	35629507_c2_1	2289	16392	795	265	L12045	1172	3.7(10)-119	Candida albicans	or:candida albicans pn:cyclic nucleotide phosphodiesterase gn:pdcl le:300 re:1580 di:direct sr:candida albicans (strain b792) dna
CONTIG5103	1210311_c1_6	2290	16393	1182	394	L12450	1990	7.9(10)-206	Candida albicans	or:candida albicans pn:secreted aspartyl proteinase 1 gn:sap1 le:1325 re:2500 di:direct sr:candida albicans (strain) dna
CONTIG2263	9860450_f2_1	2291	16394	1149	383	L13380	1761	1.5(10)-181	Candida albicans	or:candida albicans pn:trna ligase le:121 re:2619 di:direct sr:candida albicans (strain sc5314) dna nt:putative
CONTIG4894	1975931_f1_1	2292	16395	1794	598	D38310	575	8.6(10)-61	Saccharomyces cerevisiae	or:saccharomyces cerevisiae pn:boi2p gn:boi2 le:79 re:3201 di:direct sr:saccharomyces cerevisiae dna nt:encoding sh3 domain, proline-rich sequence for sh3

CONTIG399	2743877_f2_3	2293	16396	576	192	M88172	216	7.7(10)-18	Saccharomyces cerevisiae	or:saccharomyces cerevisiae le:757 re:1362 di:complement sr:saccharomyces cerevisiae (library: lambda emb13 sau3a partia nt:orf2
CONTIG2445	13835937_c2_2	2294	16397	1041	347	M88172	354	1.8(10)-32	Saccharomyces cerevisiae	or:saccharomyces cerevisiae le:1614 re:2555 di:complement sr:saccharomyces cerevisiae (library: lambda emb13 sau3a partia nt:orf3
CONTIG3948	33707167_c3_8	2295	16398	264	88	L37084	131	6.2(10)-8	Schizosaccharomyces pombe	or:schizosaccharomyces pombe pn:phosphopyruvate hydratase ec:4.2.1.11 le:2 re:1342 di:complement sr:schizosaccharomyces pombe cdna to mma
CONTIG3588	4328812_f2_3	2296	16399	1248	416	D30801	94	0.07099	Zinnia elegans	or:zinnia elegans pn:ted3 le:264 re:1223 di:direct sr:zinnia elegans xylem tracheary element cdna to mma
CONTIG4873	12010012_c3_10	2297	16400	3216	1072	U68408	716	1.6(10)-68	Zea mays	or:zea mays gn:pol le:3696 re:6902 di:direct sr:maize nt:5' end not determined experimentally
CONTIG4571	10344801_c2_5	2298	16401	897	299	D42138	407	4.4(10)-38	Homo sapiens	or:homo sapiens pn:pig-b le:45 re:1709 di:direct sr:homo sapiens cell_line:39 cdna to mma, clone_lib:human p3 nt:involvement of gpi-anchor biosynthesis
CONTIG5493	3915625_f2_5	2299	16402	747	249	D63484	230	4.7(10)-18	Homo sapiens	or:homo sapiens gn:kiaa0150 le:<2 re:2836 di:direct sr:homo sapiens male myeloblast cell_line:kg-1 cdna to mma nt:the kiaa0150 gene product is novel.

CONTIG5167	26601525_c2_14	2300	16403	453	151	D84307	209	1.3(10)-16	Homo sapiens	or:homo sapiens pn:phosphoethanolamine cytidyltransferase le:67 re:1236 di:direct sr:homo sapiens glioblastoma cdna nt:cp
CONTIG3102	10975925_c2_3	2301	16404	801	267	Z54367	93	0.73999	Homo sapiens	or:homo sapiens pn:pleclin le:1 re:14055 di:direct sr:human
CONTIG2984	24617002_f2_3	2302	16405	1740	580	U22055	408	3.3(10)-37	Homo sapiens	or:homo sapiens pn:100 kda coactivator le:268 re:2925 di:direct sr:human
CONTIG5716	16875_f1_1	2303	16406	393	131	U66616	95	0.00169	Homo sapiens	or:homo sapiens pn:swi/snf complex 170 kda subunit gn:baf170 le:23 re:3664 di:direct sr:human nt:similar to human baf155 and yeast swi3; contains a
CONTIG5442	14881583_c1_11	2304	16407	342	114	D26018	114	5.0(10)-6	Homo sapiens	or:homo sapiens gn:kiaa0039 le:<1 re:1476 di:direct sr:homo sapiens male myeloblast cell_line kg-1 cdna to mrna
CONTIG2286	33382873_f2_1	2305	16408	753	251	M31467	686	1.2(10)-67	Homo sapiens	or:homo sapiens le:1 re:576 di:direct sr:human teratocarcinoma cell line ntera2/d1, cdna to mrna, clon nt:ras-like protein
CONTIG2994	26594078_c1_4	2306	16409	1455	485	S47242	149	1.2(10)-7	Homo sapiens	or:homo sapiens gn:son le:1 re:1233 di:direct sr:human placenta nt:description: putative dna binding protein; this
CONTIG3666	3914090_f2_1	2307	16410	1254	418	U76374	165	2.8(10)-9	Mus musculus	or:mus musculus pn:skm-bop2 gn:bop le:1452 re:2885 di:direct sr:house mouse nt:allele b; alternatively spliced form lacking exon

CONTIG1843	6909425_f1_1	2308	16411	555	185	M36227	94	9.4(10)-5	Mus musculus	or:imms musculus pn:immunoglobulin heavy chain v- region gn:igh le:<1 re:>345 di:direct sr:mouse (strain balb/c), cdna to mna, from hybridoma h35-c7
CONTIG1785	25959837_f1_1	2309	16412	330	110	U32575	94	0.00119	Rattus norvegicus	or:rattus norvegicus gn:rsc6 le:1 re:>2265 di:direct sr:norway rat nt:similar to yeast sec6p, swiss-prot accession number
CONTIG5339	6679633_c2_9	2310	16413	1308	436	U83119	221	7.7(10)-15	Rattus norvegicus	or:rattus norvegicus le:<1 re:3903 di:direct sr:norway rat nt:orf2 consensus sequence encoding endonuclease and
CONTIG5606	14648437_f2_16	2311	16414	885	295	U20341	94	0.33	Cassava vein mosaic virus	or:cassava vein mosaic virus le:30 re:4148 di:direct nt:orf1
CONTIG5789	23886702_c2_28	2312	16415	885	295	X93351	100	0.025	Little cherry closterovirus	or:little cherry closterovirus gn:orf2, unknown le:1834 re:3387 di:direct
blx10404.x	2400633_f2_1	2313	16416	759	253	U26458	192	1.3(10)-13	Snakehead retrovirus	or:snakehead retrovirus pn:gag-pol polyprotein gn:gag-pol le:337 re:6390 di:direct nt:the pol protein is presumed to be derived from the
CONTIG5718	40877_c1_14	2314	16417	1245	415	Q45423	94	0.08599	Burkholderia sp.	
CONTIG1735	433207_f2_1	2315	16418	1002	334	Z66567	105	0.01099	Caenorhabditis elegans	zk455.4,,
CONTIG3993	16587782_c3_10	2316	16419	1143	381	Z66567	92	0.26	Caenorhabditis elegans	zk455.4,,
CONTIG3823	17132_c2_11	2317	16420	765	255	Y11066	93	0.17	Drosophila melanogaster	„klu
b3x16054.y	24081942_c3_5	2318	16421	765	255	Y09542	1196	1.1(10)-121	Aspergillus fumigatus	„chsc

CONTIG3619	21484438_f1_1	2319	16422	411	137	U72633	208	1.0(10)-21	Saccharomyces cerevisiae	rna annealing protein yral p.,yral
b9x12s39.x	10198957_f1_1	2320	16423	594	198	P74208	93	0.05	Synechocystis sp.	ctp synthase, \u(udp--ammonia ligase\)(ctp synthetase\),
CONTIG3934	9878567_f1_1	2321	16424	420	140	Q12024	428	2.6(10)-40	Saccharomyces cerevisiae	microtubule-associated protein ytm1,
CONTIG3970	10634687_f1_3	2322	16425	486	162	Q12024	411	1.7(10)-38	Saccharomyces cerevisiae	microtubule-associated protein ytm1,
CONTIG4650	23611307_f1_3	2323	16426	612	204	P55441	321	5.7(10)-29	Rhizobium sp.	hypothetical monoxygenase y4fc,,
CONTIG5510	29315900_f1_3	2324	16427	1095	365	P55487	328	6.7(10)-29	Rhizobium sp.	probable monoxygenase y4fd,,
CONTIG5690	4797161_c3_23	2325	16428	1116	372	Q00319	371	2.8(10)-34	Candida boidinii	peroxisomal membrane protein pmp47b,
CONTIG4877	29298187_f1_1	2326	16429	855	285	Q12380	215	9.8(10)-18	Saccharomyces cerevisiae	autophagy protein apg5,
CONTIG4764	4882763_f3_3	2327	16430	1404	468	Q92262	275	1.1(10)-23	Pichia pastoris	peroxisomal membrane protein pas2 \u(peroxin-3\),
CONTIG5710	16228311_c3_23	2328	16431	375	125	Q92262	113	5.7(10)-6	Pichia pastoris	peroxisomal membrane protein pas2 \u(peroxin-3\),
CONTIG5411	23600651_c3_15	2329	16432	1218	406	Q01962	226	6.0(10)-16	Pichia pastoris	peroxisomal protein per3 precursor \u(peroxin-8\),
CONTIG4573	26379635_c1_11	2330	16433	198	66	Q08446	167	6.0(10)-12	Saccharomyces cerevisiae	sgt1 protein,
CONTIG3702	26066076_f3_3	2331	16434	1284	428	Q01961	500	8.0(10)-60	Pichia pastoris	peroxisome assembly protein pas10 \u(peroxin-12\),
CONTIG3716	4696890_c1_6	2332	16435	354	118	S72314	167	1.2(10)-12	Saccharomyces cerevisiae	,
CONTIG3861	22845337_c1_7	2333	16436	480	160	JC5096	152	4.5(10)-10	Cochliobolus carbonum	,
CONTIG5143	26272827_c3_20	2334	16437	798	266	S74287	510	5.4(10)-49	Saccharomyces cerevisiae	,
CONTIG922	13704080_c3_3	2335	16438	594	198	S74280	545	3.2(10)-52	Saccharomyces cerevisiae	,

CONTIG5673	22079077_c2_30	2336	16439	2436	812	S74291	452	5.7(10)-46	Saccharomyces cerevisiae	,
CONTIG5038	11759430_c2_6	2337	16440	2277	759	S74293	249	2.5(10)-17	Saccharomyces cerevisiae	,
CONTIG1877	6523431_f2_3	2338	16441	582	194	Z95151	92	0.07	Mycobacterium leprae	purI,,purI,mleB5.30, purI, phosphoribosylformylglycinamide
CONTIG5464	9891030_f1_3	2339	16442	1377	459	U97002	269	1.8(10)-20	Caenorhabditis elegans	„k09h11.1,coded for by c. elegans cdna yk4418.5; coded for by
CONTIG4767	10625702_f1_1	2340	16443	453	151	U97552	258	2.7(10)-22	Caenorhabditis elegans	„w05h7.3,coded for by c. elegans cdna yk165e3.3; coded for
CONTIG4901	3940880_f2_1	2341	16444	732	244	U97405	192	2.7(10)-15	Caenorhabditis elegans	„i09b4.10,coded for by c. elegans cdna ccesu71r; contains
CONTIG5388	30195287_c3_11	2342	16445	1482	494	U92879	221	3.7(10)-16	Schizosaccharomyces pombe	cyclin c homolog 1,,pch1,similar to rattus rattus cyclin c encoded by the
CONTIG1770	511452_f3_1	2343	16446	534	178	U79010	245	2.2(10)-20	Borago officinalis	delta 6 desaturase,,,
CONTIG5746	1173436_f3_9	2344	16447	735	245	U93563	236	1.7(10)-18	Homo sapiens	putative p150,,orf2
CONTIG5472	13847552_f1_2	2345	16448	1149	383	U80223	93	0.60999	Drosophila melanogaster	eukaryotic initiation factor eif-2 alpha kinase,,similar to yeast gcn2 protein kinase; dgcn2
CONTIG1655	4694025_c2_3	2346	16449	219	73	AF002109	96	0.00019	Arabidopsis thaliana	„i29m21.1,5,26s proteasome regulatory subunit s12 isolog
CONTIG1812	15632252_c3_6	2347	16450	1299	433	AF003148	126	6.7(10)-5	Caenorhabditis elegans	„f32b5.7,coded for by c. elegans cdna yk93g1.3; coded for by
CONTIG3216	32101663_f1_1	2348	16451	948	316	AF003148	106	0.00779	Caenorhabditis elegans	„f32b5.7,coded for by c. elegans cdna yk93g1.3; coded for by
CONTIG3280	25437566_c3_9	2349	16452	912	304	AF003148	96	0.083	Caenorhabditis elegans	„f32b5.7,coded for by c. elegans cdna yk93g1.3; coded for by
CONTIG5131	22367135_f2_1	2350	16453	2043	681	AF003148	120	0.00085	Caenorhabditis elegans	„f32b5.7,coded for by c. elegans cdna yk93g1.3; coded for by
CONTIG5318	34017252_c1_6	2351	16454	1992	664	AF003148	141	4.0(10)-6	Caenorhabditis elegans	„f32b5.7,coded for by c. elegans cdna yk93g1.3; coded for by

CONTIG5404	511501_f1_1	2352	16455	1788	596	AF003148	117	0.0015	Caenorhabditis elegans	„f32b5.7, coded for by c. elegans cdna yk93g1.3; coded for by
CONTIG5817	29297186_f3_20	2353	16456	2127	709	AF003148	131	4.7(10)-5	Caenorhabditis elegans	„f32b5.7, coded for by c. elegans cdna yk93g1.3; coded for by
CONTIG5803	24812816_f3_15	2354	16457	1059	353	AF003148	103	0.025	Caenorhabditis elegans	„f32b5.7, coded for by c. elegans cdna yk93g1.3; coded for by
CONTIG2676	9867915_c2_2	2355	16458	1260	420	AB003310	1035	1.3(10)-104	Candida albicans	chitin synthase regulatory factor,,
CONTIG190	14460082_c2_2	2356	16459	699	233	D21852	90	0.31	Homo sapiens	„kia0029,
CONTIG4687	4095138_f1_3	2357	16460	690	230	Y12314	729	3.2(10)-72	Schizosaccharomyces pombe	gfpase,, spg1,
CONTIG3299	35156555_f2_1	2358	16461	522	174	Y12886	156	1.8(10)-11	Amanita muscaria	dopa-dioxygenase,, doda,
CONTIG4483	26462787_c2_15	2359	16462	381	127	Y12886	147	1.6(10)-10	Amanita muscaria	dopa-dioxygenase,, doda,
CONTIG4458	4022651_f1_1	2360	16463	1215	405	Z95395	390	3.0(10)-48	Schizosaccharomyces pombe	unknown,, spac3a12.11c, spac3a12.11c, unknown, len
CONTIG1170	22772832_f1_1	2361	16464	816	272	Z95395	213	2.2(10)-16	Schizosaccharomyces pombe	unknown,, spac3a12.15, spac3a12.15, unknown, len
CONTIG3726	11725652_c3_8	2362	16465	606	202	Z95396	197	7.9(10)-16	Schizosaccharomyces pombe	unknown,, spac57a7.01, spac57a7.01, unknown; partial, len
CONTIG2188	20563588_f2_1	2363	16466	702	234	Z95396	114	0.0014	Schizosaccharomyces pombe	unknown,, spac57a7.05, spac57a7.05, unknown, len
CONTIG5524	33595927_c3_19	2364	16467	3447	1149	Z95396	424	1.8(10)-52	Schizosaccharomyces pombe	unknown,, spac57a7.05, spac57a7.05, unknown, len
CONTIG5015	22443762_c3_3	2365	16468	813	271	Z95397	399	3.1(10)-37	Schizosaccharomyces pombe	unknown,, spbc25h2.06c, spbc25h2.06c, hypothetical integral membrane
CONTIG4131	16132692_f2_2	2366	16469	1746	582	AC001645	103	0.039	Arabidopsis thaliana	„t02o04.10, jasmonate inducible protein isolog
CONTIG601	10833550_f2_2	2367	16470	870	290	X97908	114	0.00095	Vicia faba	transcription factor,, putative
CONTIG5653	16488950_c3_21	2368	16471	987	329	AF003137	522	2.8(10)-50	Caenorhabditis elegans	„c27a12.8,

CONTIG4524	14485962_f1_1	2369	16472	1881	627	U97106	119	0.00239	Arabidopsis thaliana	downy mildew resistance protein rpp5,,rpp5,
CONTIG2134	14457525_c3_5	2370	16473	870	290	Z95586	265	1.3(10)-22	Mycobacterium tuberculosis	unknown,,mcy336.12,mcy336.12.
CONTIG2491	1181561_f2_4	2371	16474	858	286	Z95586	274	1.2(10)-23	Mycobacterium tuberculosis	unknown,,mcy336.12,mcy336.12.
CONTIG4177	30116378_c2_5	2372	16475	1272	424	Z95586	405	7.2(10)-38	Mycobacterium tuberculosis	unknown,,mcy336.12,mcy336.12.
CONTIG4394	22265877_c3_7	2373	16476	1404	468	Z95586	332	9.4(10)-36	Mycobacterium tuberculosis	unknown,,mcy336.12,mcy336.12.
CONTIG4449	11910930_f2_2	2374	16477	687	229	Z95586	235	2.7(10)-19	Mycobacterium tuberculosis	unknown,,mcy336.12,mcy336.12.
CONTIG4449	24335137_f3_4	2375	16478	798	266	Z95586	142	2.8(10)-7	Mycobacterium tuberculosis	unknown,,mcy336.12,mcy336.12.
CONTIG4509	1181561_c3_7	2376	16479	1386	462	Z95586	353	2.2(10)-32	Mycobacterium tuberculosis	unknown,,mcy336.12,mcy336.12.
CONTIG4587	662505_c2_7	2377	16480	1266	422	Z95586	388	4.5(10)-36	Mycobacterium tuberculosis	unknown,,mcy336.12,mcy336.12.
CONTIG5106	1048127_f2_2	2378	16481	816	272	Z95586	91	0.17999	Mycobacterium tuberculosis	unknown,,mcy336.12,mcy336.12.
CONTIG5214	24609633_c3_20	2379	16482	882	294	Z95586	158	1.5(10)-13	Mycobacterium tuberculosis	unknown,,mcy336.12,mcy336.12.
CONTIG5593	10751268_f2_3	2380	16483	1314	438	Z95586	385	9.5(10)-36	Mycobacterium tuberculosis	unknown,,mcy336.12,mcy336.12.
CONTIG5722	19640702_f2_4	2381	16484	801	267	Z95586	366	9.8(10)-34	Mycobacterium tuberculosis	unknown,,mcy336.12,mcy336.12.
CONTIG5722	4773400_f2_5	2382	16485	585	195	Z95586	104	0.0028	Mycobacterium tuberculosis	unknown,,mcy336.12,mcy336.12.
CONTIG629	10391885_f3_2	2383	16486	609	203	Z95586	219	1.7(10)-17	Mycobacterium tuberculosis	unknown,,mcy336.12,mcy336.12.

CONTIG3337	22348461_f3_2	2384	16487	573	191	S77615	423	7.0(10)-39	Saccharomyces cerevisiae	[PN:hypothetical protein YJL204c:hypothetical protein J0318:hypothetical protein J0320:hypothetical protein YJL205c] [MP:10L]
CONTIG3158	22301376_c1_7	2385	16488	747	249	P97998	795	3.3(10)-79	Candida albicans	[GN:MDL1] [SR:YEAST] [DE:ATP-DEPENDENT PERMEASE MDL1] [SP:P97998]
CONTIG4519	12678325_c3_5	2386	16489	1524	508	P79001	1097	3.3(10)-111	Saccharomyces pastorianus	[GN:PELL1:YCLUN3W] [SR:YEAST] [EC:2.7.8.8] [DE:(EC 2.7.8.8) (PHOSPHATIDYL SERINE SYNTHASE)] [SP:P79001]
CONTIG3423	21640885_c3_9	2387	16490	186	62	P79024	121	8.0(10)-7	Candida tropicalis	[GN:CIT] [SR:YEAST] [EC:4.1.3.7] [DE:CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR.] [SP:P79024]
CONTIG3630	4789680_c2_5	2388	16491	426	142	Q64359	115	4.9(10)-6	Rattus norvegicus	[SR:RAT] [DE:CYCLIC-NUCLEOTIDE-GATED OLFACTORY CHANNEL OCN2 SUBUNIT] [SP:Q64359]
CONTIG2579	21882686_c3_7	2389	16492	1107	369	Q99042	526	1.1(10)-50	Trigonopsis variabilis	[EC:1.4.3.3] [DE:D-AMINO ACID OXIDASE, (DAMOXY) (DAO) (DAO)] [SP:Q99042]
b3x16009 y	6370807_f1_2	2390	16493	198	66	P78954	127	2.7(10)-8	Schizosaccharomyces pombe	[GN:TIF45:TIF1] [SR:FISSION YEAST] [DE:CAP-BINDING PROTEIN] (EIF-4F 25 KD SUBUNIT)] [SP:P78954]
CONTIG5179	4079510_c2_16	2391	16494	867	289	Q07651	304	3.6(10)-27	Saccharomyces cerevisiae	[GN:YDL222C] [SR:BAKER'S YEAST] [DE:HYPOTHETICAL 34.1 KD PROTEIN IN CDC13-GCSI INTERGENIC REGION] [SP:Q07651]

CONTIG4657	1978136_f2_3	2392	16495	702	234	P78588	119	0.00012	Candida albicans	[GN:CFL1] [SR: YEAST] [DE:PROBABLE FERRIC REDUCTASE TRANSMEMBRANE COMPONENT] [SP:P78588]
CONTIG4681	47011_c1_1	2393	16496	813	271	P78588	125	8.8(10)-13	Candida albicans	[GN:CFL1] [SR: YEAST] [DE:PROBABLE FERRIC REDUCTASE TRANSMEMBRANE COMPONENT] [SP:P78588]
CONTIG4739	13954437_c3_4	2394	16497	2166	722	P78588	2911	0	Candida albicans	[GN:CFL1] [SR: YEAST] [DE:PROBABLE FERRIC REDUCTASE TRANSMEMBRANE COMPONENT] [SP:P78588]
CONTIG4876	20488905_f2_2	2395	16498	1368	456	P78588	1576	5.9(10)-162	Candida albicans	[GN:CFL1] [SR: YEAST] [DE:PROBABLE FERRIC REDUCTASE TRANSMEMBRANE COMPONENT] [SP:P78588]
CONTIG660	4148317_f2_1	2396	16499	513	171	P78588	402	5.5(10)-37	Candida albicans	[GN:CFL1] [SR: YEAST] [DE:PROBABLE FERRIC REDUCTASE TRANSMEMBRANE COMPONENT] [SP:P78588]
CONTIG312	898578_c2_2	2397	16500	501	167	Q06706	367	2.0(10)-32	Saccharomyces cerevisiae	[GN:IK13:YLR384C.L3502.7] [SR:BAKER'S YEAST] [DE:IK13 PROTEIN] [SP:Q06706:O00036]
CONTIG4748	1057925_f1_1	2398	16501	264	88	Q06706	285	1.1(10)-23	Saccharomyces cerevisiae	[GN:IK13:YLR384C.L3502.7] [SR:BAKER'S YEAST] [DE:IK13 PROTEIN] [SP:Q06706:O00036]

CONTIG4901	16113803_f2_2	2399	16502	1302	434	Q06706	983	4.0(10)-99	Saccharomyces cerevisiae	[GN:IKI3:YLR384C.L3502.7] [SR:BAKER'S YEAST] [DE:IKI3 PROTEIN] [SP:Q06706:000036]
CONTIG64	6048438_c2_2	2400	16503	501	167	Q06706	339	1.8(10)-29	Saccharomyces cerevisiae	[GN:IKI3:YLR384C.L3502.7] [SR:BAKER'S YEAST] [DE:IKI3 PROTEIN] [SP:Q06706:000036]
blx15502.y	9921942_c2_2	2401	16504	912	304	Q06706	515	3.1(10)-48	Saccharomyces cerevisiae	[GN:IKI3:YLR384C.L3502.7] [SR:BAKER'S YEAST] [DE:IKI3 PROTEIN] [SP:Q06706:000036]
CONTIG4363	15112562_c1_7	2402	16505	402	134	P78587	611	1.1(10)-59	Candida albicans	[GN:CGT1] [SR:YEAST] [EC:2.7.7.50] [DE:(GTP--RNA GUANYLYLTRANSFERASE)] [SP:P78587]
CONTIG718	6673506_c2_4	2403	16506	807	269	P78587	1376	9.1(10)-141	Candida albicans	[GN:CGT1] [SR:YEAST] [EC:2.7.7.50] [DE:(GTP--RNA GUANYLYLTRANSFERASE)] [SP:P78587]
CONTIG4324	33320135_f1_1	2404	16507	213	71	Q02820	109	1.7(10)-6	Saccharomyces cerevisiae	[GN:NCE1:YIL205BC] [SR:BAKER'S YEAST] [DE:NON-CLASSICAL EXPORT PROTEIN NCE1] [SP:Q02820:000038:000037]
CONTIG5127	11876385_f1_1	2405	16508	195	65	P80967	96	4.0(10)-5	Saccharomyces cerevisiae	[GN:TOM5] [SR:BAKER'S YEAST] [DE:MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM5] [SP:P80967]
CONTIG2633	13789075_f2_1	2406	16509	459	153	Q12277	155	4.7(10)-17	Saccharomyces cerevisiae	[GN:RRP42:YDL111C] [SR:BAKER'S YEAST] [DE:RRP42 PROTEIN] [SP:Q12277]

b9x12123.y	16601562_f1_1	2407	16510	333	111	Q12277	208	5.4(10)-17	Saccharomyces cerevisiae	[GN:RRP42.YDL111C] [SR:BAKER'S YEAST] [DE:RRP42 PROTEIN] [SP:Q12277]
b9x12123.y	3227187_f3_2	2408	16511	354	118	Q12277	154	4.7(10)-11	Saccharomyces cerevisiae	[GN:RRP42.YDL111C] [SR:BAKER'S YEAST] [DE:RRP42 PROTEIN] [SP:Q12277]
CONTIG2256	1057031_c3_4	2409	16512	1269	423	Q07878	826	1.1(10)-80	Saccharomyces cerevisiae	[GN:VPS13.S011.YLL040C] [SR:BAKER'S YEAST] [DE:VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13] [SP:Q07878]
CONTIG2550	25916316_f2_1	2410	16513	939	313	Q07878	751	9.9(10)-73	Saccharomyces cerevisiae	[GN:VPS13.S011.YLL040C] [SR:BAKER'S YEAST] [DE:VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13] [SP:Q07878]
CONTIG3456	33672567_c1_5	2411	16514	1959	653	Q07878	829	5.0(10)-81	Saccharomyces cerevisiae	[GN:VPS13.S011.YLL040C] [SR:BAKER'S YEAST] [DE:VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13] [SP:Q07878]
CONTIG3489	4072587_f1_1	2412	16515	660	220	Q07878	294	3.3(10)-24	Saccharomyces cerevisiae	[GN:VPS13.S011.YLL040C] [SR:BAKER'S YEAST] [DE:VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13] [SP:Q07878]
CONTIG3489	23925277_f2_2	2413	16516	1464	488	Q07878	824	1.7(10)-80	Saccharomyces cerevisiae	[GN:VPS13.S011.YLL040C] [SR:BAKER'S YEAST] [DE:VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13] [SP:Q07878]

CONTIG5809	25400262_f1_7	2414	16517	2394	798	Q07878	1141	5.2(10)-169	Saccharomyces cerevisiae	[GN:VPS13;SOIL:YLL040C] [SR:BAKER'S YEAST] [DE:VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13] [SP:Q07878]
CONTIG5346	10581527_f2_5	2415	16518	1368	456	P78599	2102	1.1(10)-217	Candida albicans	[GN:SPE1] [SR: YEAST] [EC:4.1.1.17] [DE:ORNITHINE DECARBOXYLASE, (ODC)] [SP:P78599;P78592]
CONTIG3488	7165888_f1_1	2416	16519	771	257	Q07953	693	2.2(10)-68	Saccharomyces cerevisiae	[GN:YLR022C] [SR:BAKER'S YEAST] [DE:HYPOTHETICAL 28.3 KD PROTEIN IN PPR1-SNF7 INTERGENIC REGION] [SP:Q07953]
CONTIG1585	164663_f2_2	2417	16520	492	164	Q08647	167	2.0(10)-22	Saccharomyces cerevisiae	[GN:YOR243C;O5254] [SR:BAKER'S YEAST] [DE:HYPOTHETICAL 77.0 KD PROTEIN IN HES1-SEC63 INTERGENIC REGION] [SP:Q08647]
CONTIG2186	1956552_f1_1	2418	16521	819	273	Q08647	167	7.2(10)-24	Saccharomyces cerevisiae	[GN:YOR243C;O5254] [SR:BAKER'S YEAST] [DE:HYPOTHETICAL 77.0 KD PROTEIN IN HES1-SEC63 INTERGENIC REGION] [SP:Q08647]
blx11180.y	1347531_f1_1	2419	16522	513	171	Q08647	361	1.8(10)-32	Saccharomyces cerevisiae	[GN:YOR243C;O5254] [SR:BAKER'S YEAST] [DE:HYPOTHETICAL 77.0 KD PROTEIN IN HES1-SEC63 INTERGENIC REGION] [SP:Q08647]

CONTIG1795	23844400_c3_7	2420	16523	936	312	P78609	963	5.2(10)-97	Pichia jadinii	[SR:YEAST:CANDIDA UTILIS] [EC:1.7.3.3] [DE:URICASE, (URATE OXIDASE)] [SP:P78609]
CONTIG3707	15820192_c2_3	2421	16524	1842	614	S75787	94	0.062	Synechocystis sp.	[PN:hypothetical protein] [OR:Synechocystis sp.] [SR:PCC 6803, PCC 6803] [SR:PCC 6803,]
CONTIG4731	19922051_c3_15	2422	16525	432	144	S76221	96	0.00309	Synechocystis sp.	[PN:hypothetical protein] [OR:Synechocystis sp.] [SR:PCC 6803, PCC 6803] [SR:PCC 6803,]
b2x19077.y	14266580_c2_4	2423	16526	600	200	S77003	121	1.2(10)-6	Synechocystis sp.	[PN:hypothetical protein] [OR:Synechocystis sp.] [SR:PCC 6803, PCC 6803] [SR:PCC 6803,]
CONTIG2249	33235057_f1_1	2424	16527	1134	378	S77453	196	2.3(10)-13	Synechocystis sp.	[PN:hypothetical protein] [OR:Synechocystis sp.] [SR:PCC 6803, PCC 6803] [SR:PCC 6803,]
CONTIG5506	3150677_c1_10	2425	16528	585	195	S74956	96	0.00073	Synechocystis sp.	[PN:spore protein sp21;protein sll1514;protein sll1514] [GN:hspA] [OR:Synechocystis sp.] [SR:PCC 6803, PCC 6803] [SR:PCC 6803,]
CONTIG2983	13722130_c1_3	2426	16529	753	251	S77699	141	9.4(10)-10	Saccharomyces cerevisiae	[PN:inner cell wall mannoprotein ICWP:protein YLR390w-a] [GN:ICWP] [MP:12R]
CONTIG4885	24220165_f3_8	2427	16530	288	96	S77567	157	1.3(10)-11	Saccharomyces cerevisiae	[PN:ribosomal protein S37, mitochondrial]

CONTIG3379	23475401_c1_4	2428	16531	1209	403	AF009672	179	2.1(10)-25	Acinetobacter calcoaceticus	[PN:unknown] [DE:Acinetobacter calcoaceticus ADP1 vanillate demethylase region, vanillate demethylase (vanB) and vanillate demethylase (vanA) genes, complete cds.] [NT:putative oxo-ketoglutarate dioxigenase; ORF3] [LE:2783] [RE:3784] [D]
b9x11006.y	11775402_f3_2	2429	16532	834	278	U71377	107	0.0097	Staphylococcus epidermidis	[PN:auto-lysins AtIE] [DE:Staphylococcus epidermidis auto-lysins AtIE and putative transcriptional regulator AtIR genes, complete cds.] [NT:primary attachment to a polystyrene surface] [LE:2620] [RE:6627] [DI:direct]
CONTIG5779	585458_c2_23	2430	16533	777	259	U82227	92	0.02599	Sulfolobus solfataricus	[PN:unknown] [GN:c0859] [DE:Sulfolobus solfataricus leucyl-tRNA synthetase (leuS) gene, partialcds, histidine biosynthesis operon hisCGABdFDEH1, (hisC, hisG,hisBd, hisF, hisD, hisE, hisH and hisI) genes, complete cds and seryl-tRNA syn
CONTIG4836	7039187_f3_2	2431	16534	552	184	AB001078	287	2.2(10)-25	Bombyx mori	[PN:Multiprotein bridging factor 1] [SR:Bombyx mori cDNA to mRNA] [DE:Bombyx mori mRNA for Multiprotein bridging factor 1, complete cds.] [NT:MBF1] [LE:101] [RE:541] [DI:direct]

CONTIG5264	21504376_f2_2	2432	16535	1167	389	Z81098	108	0.012	Caenorhabditis elegans	[PN:K07A12.2] [DE:Caenorhabditis elegans cosmid K07A12.] [NT:Similarity to Rat insulin-like growth factor binding] [LE:11543:11843:12923] [RE:11765:12861:13591] [DI:complementoin]
CONTIG1953	12694837_f1_2	2433	16536	426	142	AF016448	256	4.4(10)-22	Caenorhabditis elegans	[GN:F41E6.9] [SR:Caenorhabditis elegans strain=Bristol N2] [DE:Caenorhabditis elegans cosmid F41E6.] [NT:similar to Saccharomyces cerevisiae nuclear protein] [LE:13138:13445:13811] [RE:13323:13715:14007] [DI:complementoin]
CONTIG4964	23526686_g2_13	2434	16537	765	255	AF016687	113	0.0015	Caenorhabditis elegans	[GN:T21D12.9b] [SR:Caenorhabditis elegans strain=Bristol N2] [DE:Caenorhabditis elegans cosmid T21D12.] [NT:coded for by C. elegans cDNA yk6g3.3; coded for by] [LE:4395:4847:5306] [RE:4712:5123:5384] [DI:complementoin]
CONTIG4711	14742907_g2_6	2435	16538	2475	825	U49332	646	4.0(10)-68	Dictyostelium discoideum	[PN:150-kD protein] [GN:cluA] [DE:Dictyostelium discoideum 150-kD protein (cluA) mRNA, complete cds.] [NT:protein required for proper dispersion of] [LE:224] [RE:4189] [DI:direct]

CONTIG5013	26359692_ft_2	2436	16539	1236	412	U87912	90	0.45	Dictyostelium discoideum	[PN:MAP kinase protein DdMEK1] [GN:mekA] [FN:regulator of chemotaxis] [DE:Dictyostelium discoideum MAP kinase protein DdMEK1 (mekA)mRNA, complete cds.] [LE:1] [RE:1983] [DI:direct]
CONTIG4907	25_c3_11	2437	16540	609	203	AB004535	101	0.00589	Schizosaccharo myces pombe	[GN:pi021] [SR:Schizosaccharomyces pombe (strain:972 h-) DNA, clone_lib:Mizukami] [DE:Schizosaccharomyces pombe 42.8 kb genomic DNA, clone c973.] [NT:similar to S.pombe unknown protein : DDBJ ACC#] [LE:15395] [RE:16642] [DI:direct]
CONTIG1951	4797252_ft_2	2438	16541	747	249	AB004535	114	0.00062	Schizosaccharo myces pombe	[PN:HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5] [GN:pi030] [SR:Schizosaccharomyces pombe (strain:972 h-) DNA, clone_lib:Mizukami] [DE:Schizosaccharomyces pombe 42.8 kb genomic DNA, clone c973.] [NT:similar to S.cerevisiae HYPOTHETICAL

CONTIG3680	23867125_c2_6	2439	16542	1620	540	AB004535	262	8.6(10)-21	Schizosaccharo myces pombe	[PN:HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5] [GN:pi030] [SR:Schizosaccharomyces pombe (strain:972 h-) DNA, clone_lib:Mizukam] [DE:Schizosaccharomyces pombe 42.8 kb genomic DNA, clone c973.] [NT:similar to S. cerevisiae HYPOTHETICAL
CONTIG2299	14179686_f1_1	2440	16543	993	331	AB004537	327	1.3(10)-29	Schizosaccharo myces pombe	[PN:HYPOTHETICAL 47.4KD PROTEIN IN SHP1-SEC17] [GN:pi038] [SR:Schizosaccharomyces pombe (strain:972 h-) DNA, clone_lib:Mizukam] [DE:Schizosaccharomyces pombe 37 kb genomic DNA, clone c213.] [NT:similar to S. cerevisiae HYPOTHETICAL 47.
CONTIG3583	1460067_f2_2	2441	16544	663	221	AB004537	181	1.8(10)-13	Schizosaccharo myces pombe	[PN:HLJ1 PROTEIN] [GN:pi041] [SR:Schizosaccharomyces pombe (strain:972 h-) DNA, clone_lib:Mizukam] [DE:Schizosaccharomyces pombe 37 kb genomic DNA, clone c213.] [NT:similar to S. cerevisiae HLJ1 PROTEIN: SWISS_PROT] [LE:11111:11194:116

CONTIG5568	14267312_c3_21	2442	16545	372	124	AC000348	101	0.00044	Arabidopsis thaliana	[PN:T7N9.2] [SR:thale cress] [DE:Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence.] [NT:TA1-like retrotransposon] [LE:9987:1109:12764] [RE:11012:12706:13970] [DI:complementoin]
CONTIG3772	5879385_f2_2	2443	16546	1485	495	AF001978	1057	5.7(10)-107	Candida albicans	[GN:ECE2] [DE:Candida albicans ECE2 gene, complete cds.] [NT:differentially expressed in relation to the extent] [LE:151] [RE:2055] [DI:direct]
CONTIG5229	21953577_c1_14	2444	16547	1083	361	AF004731	135	3.0(10)-6	Saccharomyces cerevisiae	[PN:Stp22p] [GN:STP22] [FN:required for vacuolar targeting of] [SR:baker's yeast] [DE:Saccharomyces cerevisiae Stp22p (STP22) gene, complete cds.] [NT:similar to the mouse and human Tsg101 tumor] [LE:383] [RE:1540] [DI:direct]
CONTIG2426	4726567_f3_1	2445	16548	1314	438	AF004880	102	0.017	Lycopersicon esculentum	[PN:resistance complex protein 12C-3] [GN:12C-3] [FN:confers resistance against Fusarium oxysporum] [SR:tomato] [DE:Lycopersicon esculentum resistance complex protein 12C-3 (12C-3)mRNA, partial cds.] [LE:<1] [RE:1122] [DI:direct]

CONTIG944	21994032_13_1	2446	16549	546	182	AF007873	611	1.1(10)-59	Schizosaccharo myces pombe	[PN:dolichol monophosphate mannose synthase] [GN:dpm1+] [FN:transfers mannose from GDP- mannose to dolichol] [SR:fission yeast] [DE:Schizosaccharomyces pombe dolichol monophosphate mannose synthase(dpm1+) mRNA, complete cds.] [LE:47] [
CONTIG2873	14573430_c1_7	2447	16550	720	240	AF011386	746	5.2(10)-74	Candida albicans	[PN:pH-regulated protein 2] [GN:PHR2] [DE:Candida albicans pH-regulated protein 2 (PHR2) gene, complete cds.] [LE:52] [RE:1692] [DI:direct]
CONTIG1784	10056376_c1_10	2448	16551	348	116	Y11969	90	0.0016	Arabidopsis thaliana	[PN:dnaI-like protein] [GN:J10] [SR:thale cress] [DE:A.thaliana mRNA for dnaI-like protein.] [LE:149] [RE:1429] [DI:direct]
CONTIG1597	23470281_13_1	2449	16552	627	209	U74294	163	3.0(10)-11	Botryotinia fueckeliana	[PN:transposase] [DE:Botryotinia fueckeliana Flippase transposable element transposasegene, complete cds.] [LE:149] [RE:1747] [DI:direct]
CONTIG3861	24819811_c3_10	2450	16553	717	239	U74294	173	2.5(10)-12	Botryotinia fueckeliana	[PN:transposase] [DE:Botryotinia fueckeliana Flippase transposable element transposasegene, complete cds.] [LE:149] [RE:1747] [DI:direct]
CONTIG5685	412806_c3_10	2451	16554	1635	545	U74294	585	6.0(10)-57	Botryotinia fueckeliana	[PN:transposase] [DE:Botryotinia fueckeliana Flippase transposable element transposasegene, complete cds.] [LE:149] [RE:1747] [DI:direct]

CONTIG3424	3990760_f2_1	2452	16555	915	305	Y13973	867	8.0(10)-87	Candida sp.	[PN:CIP1 protein] [GN:CIP1] [OR:Candida sp.] [SR:Candida sp] [DE:Candida sp. CIP1 gene.] [NT:cadmium induced] [LE:1676] [RE:2566] [DI:direct]
b2x17229.x	23603827_f3_2	2453	16556	192	64	D88815	125	1.8(10)-6	Candida albicans	[PN:beta-1,3-glucan synthase catalytic subunit 1] [GN:GSC1] [SR:Candida albicans DNA] [DE:Candida albicans gene for beta- 1,3-glucan synthase catalyticsubunit 1, complete cds.] [LE:708] [RE:6401] [DI:direct]
CONTIG5371	905162_c3_18	2454	16557	2079	693	AC000132	124	0.00027	Arabidopsis thaliana	[GN:F21M12.21] [SR:thale cress] [DE:Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence.] [NT:Similar to N. tabacum salt- inducible protein] [LE:77480] [RE:79300] [DI:complement]
CONTIG3904	1178387_f1_1	2455	16558	642	214	AC001229	259	2.1(10)-22	Arabidopsis thaliana	[GN:F5114.18] [SR:thale cress] [DE:Sequence of BAC F5114 from Arabidopsis thaliana chromosome 1, complete sequence.] [NT:ESTs gb T45673.gb N37512 come from this gene.] [LE:94242:95089:95364] [RE:95006:95191:95410] [DI:complement/oin]

CONTIG4669	14062943_c3_11	2456	16559	282	94	AC001229	175	4.7(10)-13	Arabidopsis thaliana	[GN:F5114.18] [SR:thale cress] [DE:Sequence of BAC F5114 from Arabidopsis thaliana chromosome 1, complete sequence.] [NT:EST's gb T45673;gb N37512 come from this gene.] [LE:94242:95089:95364] [RE:95006:95191:95410] [DI:complementoin]
CONTIG3681	35421936_c1_5	2457	16560	504	168	Y13139	559	3.5(10)-54	Saccharomyces cerevisiae	[gn:yip3] [sr:baker's yeast] [db:genbank-sac] [de:saccharomyces cerevisiae chromosome xiv.] [nt:orf ynl044w]
CONTIG2135	994002_f1_1	2458	16561	537	179	Z97208	155	2.8(10)-10	Schizosaccharo myces pombe	[PN:hypothetical protein] [GN:SPAC15A10.13] [SR:fission yeast] [DE:S. pombe chromosome 1 cosmid c15A10.] [NT:SPAC15A10.13, unknown, len:637aa, similar eg. to C.] [LE:35343:35518:35710:35864] [RE:35468:35658:35811:36724] [DI:directioin]
CONTIG4777	24260903_c1_6	2459	16562	591	197	Z97210	134	5.2(10)-7	Schizosaccharo myces pombe	[PN:beta-transducin] [GN:SPAC29A4.08c] [SR:fission yeast] [DE:S. pombe chromosome 1 cosmid c29A4.] [NT:SPAC29A4.08c, unknown; beta-transducin; some] [LE:11807:13596:13741] [RE:13110:13700:13798] [DI:complementoin]

CONTIG5566	2817637_f2_10	2460	16563	705	235	Z98056	297	2.0(10)-26	Schizosaccharo myces pombe	[PN:hypothetical protein] [GN:SPAC5D6.06c] [SR:fission yeast] [DE:S.pombe chromosome I cosmid c5D6.] [NT:SPAC5D6.06c, unknown, len:210aa, similar eg. to] [LE:9149:9363] [RE:9316:9827] [DI:complementoin]
CONTIG5606	183187_f3_27	2461	16564	669	223	Z97204	341	4.4(10)-31	Schizosaccharo myces pombe	[PN:hypothetical protein] [GN:SPBC31F10.03] [SR:fission yeast] [DE:S.pombe chromosome II cosmid c31F10.] [NT:SPBC31F10.03, unknown, len:203aa, similar eg. to] [LE:1913] [RE:2524] [DI:direct]
CONTIG5650	31772188_c2_19	2462	16565	2202	734	Z97204	438	5.7(10)-38	Schizosaccharo myces pombe	[PN:hypothetical protein] [GN:SPBC31F10.14c] [SR:fission yeast] [DE:S.pombe chromosome II cosmid c31F10.] [NT:SPBC31F10.14c, unknown, len:1586aa, some similarity] [LE:23034] [RE:27926] [DI:complement]
CONTIG3986	11886303_c2_10	2463	16566	738	246	Z97052	134	2.7(10)-6	Schizosaccharo myces pombe	[PN:hypothetical protein] [GN:SPCC4G3.10c] [SR:fission yeast] [DE:S.pombe chromosome III cosmid c4G3.] [NT:SPCC4G3.10c, putative dna repair protein.] [LE:19546] [RE:21606] [DI:complement]

CONTIG4931	9773402_c3_18	2464	16567	336	112	X86179	111	2.3(10)-5	Schizosaccharo myces pombe	[PN:phosphoprotein] [GN:cdc15] [FN:colonises with f actin at mitosis but not in] [SR:fission yeast] [DE:S.pombe cdc15 gene.] [LE:376:515:799:3293] [RE:456:606:3236:3465] [DI:directioin]
CONTIG1872	24257682_c2_7	2465	16568	204	68	L47210	234	2.6(10)-18	Candida albicans	[PN:serine/threonine kinase] [FN:hyphal formation] [DE:Candida albicans serine/threonine protein kinase gene, complete cds.] [LE:355] [RE:4047] [DI:direct]
CONTIG3788	867055_c3_4	2466	16569	519	173	AF006087	604	5.9(10)-59	Homo sapiens	[PN:p20-Arc] [GN:ARC20] [SR:human] [DE:Homo sapiens Arp2/3 protein complex subunit p20-Arc (ARC20) mRNA, complete cds.] [NT:20 kD subunit of the Arp2/3 protein complex] [LE:16] [RE:522] [DI:direct]
CONTIG4018	23448436_c1_2	2467	16570	285	95	Z24459	117	2.3(10)-7	Homo sapiens	[PN:p8MTCPI protein] [GN:MTCPI] [SR:human] [DE:H.sapiens MTCPI gene, exons 2A to 7 (and joined mRNA).] [LE:2888:5587] [RE:2945:5735] [DI:directioin]
CONTIG4396	22744525_f2_5	2468	16571	354	118	AF003348	192	8.1(10)-14	Mus musculus	[PN:NPCI] [GN:Npci] [SR:house mouse] [DE:Mus musculus NPCI (Npci) mRNA, complete cds.] [NT:mutations within this gene are responsible for the] [LE:124] [RE:3960] [DI:direct]

CONTIG470	4407527_f2_3	2469	16572	399	133	D88364	122	1.8(10)-7	Rattus norvegicus	[PN:PIG-L] [FN:phosphatidylinositol glycan class L] [SR:Rattus norvegicus glial cell_line:C6 cDNA to mRNA] [DE:Rat mRNA for PIG-L, complete cds.] [LE:391] [RE:1149] [DI:direct]
CONTIG4294	546887_f3_2	2470	16573	960	320	Q06598	625	3.5(10)-61	Saccharomyces cerevisiae	[gn:acr3:ypj201w:p9677.2] [sr:baker's yeast] [de:arsenical-resistance protein acr3] [sp:q06598] [db:swissprot-sp_new]
CONTIG4847	4535312_f2_2	2471	16574	1653	551	P89105	632	4.2(10)-61	Saccharomyces cerevisiae	[gn:ctr9:yoi145c] [sr:baker's yeast] [de:ctr9 protein] [sp:p89105:q08292:q07332] [db:swissprot-sp_new]
CONTIG5381	32454650_c3_16	2472	16575	1278	426	P89105	389	5.9(10)-35	Saccharomyces cerevisiae	[gn:ctr9:yoi145c] [sr:baker's yeast] [de:ctr9 protein] [sp:p89105:q08292:q07332] [db:swissprot-sp_new]
CONTIG2666	23672000_f1_2	2473	16576	210	70	P56091	157	1.2(10)-10	Candida albicans	[gn:gal1] [sr:yeast] [ec:2.7.1.6] [de:galactokinase.] [sp:p56091] [db:swissprot-sp_new]
CONTIG4512	23943787_f3_3	2474	16577	444	148	P56091	578	3.3(10)-56	Candida albicans	[gn:gal1] [sr:yeast] [ec:2.7.1.6] [de:galactokinase.] [sp:p56091] [db:swissprot-sp_new]
b1x16820.x	10721974_c1_1	2475	16578	513	171	P56091	691	3.6(10)-68	Candida albicans	[gn:gal1] [sr:yeast] [ec:2.7.1.6] [de:galactokinase.] [sp:p56091] [db:swissprot-sp_new]
CONTIG1672	12128388_f1_1	2476	16579	261	87	P56090	314	3.2(10)-28	Candida albicans	[gn:his3] [sr:yeast] [ec:4.2.1.19] [de:imidazoleglycerol-phosphate dehydratase, (igpd)] [sp:p56090] [db:swissprot-sp_new]

b2x10243.x	9958514_c1_3	2477	16580	465	155	P87323	120	1.2(10)-6	Schizosaccharo myces pombe	[gn:mc54] [sr:,fission yeast] [dc:response regulator mc54 (mitotic catastrophe suppressor 4)] [sp:p87323] [db:swissprot-sp_new]
CONTIG3202	1995175_c3_4	2478	16581	1158	386	P87207	1939	2.0(10)-200	Candida albicans	[gn:mt3] [sr:,yeast] [ec:2.4.1.131] [dc:probable mannosyltransferase mt3_] [sp:p87207] [db:swissprot- sp_new]
CONTIG5796	33379011_c2_18	2479	16582	297	99	Q07842	185	1.5(10)-14	Neurospora crassa	[gn:mno-10.5] [ec:1.6.5.3:1.6.99.3] [dc:(ec 1.6.99.3) (complex i) (ci)] [sp:q07842] [db:swissprot-sp_new]
CONTIG931	19531518_f1_2	2480	16583	525	175	P78723	189	1.3(10)-28	Pichia angusta	[gn:pex14.per10] [sr:,yeast:hansenula polymorpha] [dc:peroxisomal membrane protein per10 (peroxin-14)] [sp:p78723] [db:swissprot-sp_new]
CONTIG734	33336050_c2_2	2481	16584	825	275	P87200	133	5.7(10)-6	Yarrowia lipolytica	[gn:pex17] [sr:,candida lipolytica] [dc:peroxisomal membrane protein pex17 (peroxin-17)] [sp:p87200] [db:swissprot-sp_new]
CONTIG2128	117055_c1_3	2482	16585	681	227	P87020	1003	3.1(10)-101	Candida albicans	[gn:pra1] [sr:,yeast] [dc:ph- regulated antigen pra1 precursor (fibrinogen binding protein)] [sp:p87020:p78598] [db:swissprot- sp_new]
CONTIG1684	9799180_c2_3	2483	16586	360	120	Q08096	417	3.8(10)-39	Saccharomyces cerevisiae	[gn:rc1.yo1010w] [sr:,baker's yeast] [ec:6.5.1.4] [dc:cyclase] (ma cyclase)] [sp:q08096] [db:swissprot- sp_new]

CONTIG5808	3964827_ft_1	2484	16587	711	237	Q08096	765	5.0(10)-76	Saccharomyces cerevisiae	[gn:rtcl.yo1010w] [sr:.baker's yeast] [ec:6.5.1.4] [de:cyclase] (ma cyclase)] [sp:q08096] [db:swissprot-sp_new]
CONTIG5787	35164063_ft_10	2485	16588	1662	554	Q12460	1669	8.1(10)-172	Saccharomyces cerevisiae	[gn:sik1.yf197w:18167.9] [sr:.baker's yeast] [de:sik1 protein] [sp:q12460] [db:swissprot-sp_new]
CONTIG5152	2922062_c3_8	2486	16589	1806	602	P87024	2785	4.5(10)-290	Candida albicans	[gn:skn1] [sr:.yeast] [de:beta-glucan synthesis-associated protein skn1] [sp:p87024] [db:swissprot-sp_new]
CONTIG2960	235902_c3_15	2487	16590	465	155	P87219	424	7.0(10)-40	Candida albicans	[gn:sou1] [sr:.yeast] [de:sorbitol utilization protein sou1] [sp:p87219] [db:swissprot-sp_new]
CONTIG347	7160882_ft_1	2488	16591	336	112	P87219	533	2.0(10)-51	Candida albicans	[gn:sou1] [sr:.yeast] [de:sorbitol utilization protein sou1] [sp:p87219] [db:swissprot-sp_new]
CONTIG5783	1988500_ft_17	2489	16592	873	291	P87219	544	1.3(10)-52	Candida albicans	[gn:sou1] [sr:.yeast] [de:sorbitol utilization protein sou1] [sp:p87219] [db:swissprot-sp_new]
CONTIG2960	15031327_c1_10	2490	16593	927	309	P87218	1358	7.4(10)-139	Candida albicans	[gn:sou2] [sr:.yeast] [de:sorbitol utilization protein sou2] [sp:p87218] [db:swissprot-sp_new]
CONTIG5262	23602181_c2_9	2491	16594	480	160	Q03446	99	4.2(10)-5	Saccharomyces cerevisiae	[gn:ssh5.ydr003w.ydr8119.09] [sr:.baker's yeast] [de:ssh5 protein] [sp:q03446] [db:swissprot-sp_new]

CONTIG2331	10052012_f3_1	2492	16595	1026	342	P87078	1356	1.2(10)-138	Candida albicans	[gn:top2] [sr:yeast] [ec:5.99.1.3] [de:dna topoisomerase ii.] [sp:p87078] [db:swissprot-sp_new]
CONTIG5703	22112812_c1_28	2493	16596	504	168	P56093	417	3.8(10)-39	Candida albicans	[gn:tup1] [sr:yeast] [de:transcriptional repressor tup1] [sp:p56093] [db:swissprot-sp_new]
CONTIG4527	4397588_c2_10	2494	16597	486	162	Q94535	270	1.5(10)-23	Drosophila melanogaster	[gn:u2a38] [sr:fruit fly] [de:subunit (u2 snmp auxiliary factor small subunit)] [sp:q94535] [db:swissprot-sp_new]
CONTIG1603	2535930_c2_5	2495	16598	573	191	Q29350	161	5.2(10)-12	Sus scrofa	[gn:u2a11] [sr:pig] [de:subunit (u2 snmp auxiliary factor small subunit) (fragment)] [sp:q29350] [db:swissprot-sp_new]
CONTIG4527	19957125_c2_9	2496	16599	606	202	Q09176	165	2.0(10)-12	Schizosaccharo myces pombe	[sr:fission yeast] [de:subunit (u2 snmp auxiliary factor small subunit) (u2a123)] [sp:q09176] [db:swissprot-sp_new]
b3x16048.y	2081926_c3_5	2497	16600	198	66	Q92353	97	0.00032	Schizosaccharo myces pombe	[gn:spac6g.08] [sr:fission yeast] [ec:3.1.2.15] [de:(deubiquitinating enzyme)] [sp:q92353] [db:swissprot-sp_new]
CONTIG5780	4414061_f1_6	2498	16601	870	290	Q12499	1062	1.7(10)-107	Saccharomyces cerevisiae	[gn:yor310c:o6108] [sr:baker's yeast] [de:hyposphthal 57.0 kd protein] [sp:q12499] [db:swissprot-sp_new]
CONTIG5780	7063507_f1_7	2499	16602	690	230	Q12499	585	6.0(10)-57	Saccharomyces cerevisiae	[gn:yor310c:o6108] [sr:baker's yeast] [de:hyposphthal 57.0 kd protein] [sp:q12499] [db:swissprot-sp_new]

CONTIG1788	31287937_f3_1	2500	16603	1296	432	Q06053	566	1.2(10)-81	Saccharomyces cerevisiae	[gn:yl401c:18084.19] [sr:baker's yeast] [de:hypothetical 69.8 kd protein in bdf1-sfp1 intergenic region] [sp:q06053] [db:swissprot-sp_new]
CONTIG5484	12523285_f1_1	2501	16604	294	98	Q06063	248	3.1(10)-21	Saccharomyces cerevisiae	[gn:yl405w:18084.2] [sr:baker's yeast] [de:hypothetical 41.7 kd protein in sfp1-ctr3 intergenic region] [sp:q06063] [db:swissprot-sp_new]
CONTIG5484	7322336_f2_4	2502	16605	765	255	Q06063	674	2.2(10)-66	Saccharomyces cerevisiae	[gn:yl405w:18084.2] [sr:baker's yeast] [de:hypothetical 41.7 kd protein in sfp1-ctr3 intergenic region] [sp:q06063] [db:swissprot-sp_new]
CONTIG3442	32531905_f3_3	2503	16606	834	278	Q07821	528	6.7(10)-51	Saccharomyces cerevisiae	[gn:yl1027w] [sr:baker's yeast] [de:hypothetical 27.7 kd protein in prp19-hsp104 intergenic region] [sp:q07821] [db:swissprot-sp_new]
CONTIG4075	13925182_f3_8	2504	16607	861	287	Q12524	393	1.3(10)-36	Saccharomyces cerevisiae	[gn:yl151c:19634.8] [sr:baker's yeast] [de:hypothetical 39.8 kd protein in mpt4-acs2 intergenic region] [sp:q12524] [db:swissprot-sp_new]
CONTIG5707	4884437_f1_1	2505	16608	1200	400	Q06218	1027	8.8(10)-104	Saccharomyces cerevisiae	[gn:yl276c:19328.3] [sr:baker's yeast] [de:putative atp-dependent rna helicase ylr276c] [sp:q06218] [db:swissprot-sp_new]
CONTIG5707	4188562_f1_2	2506	16609	525	175	Q06218	545	1.1(10)-52	Saccharomyces cerevisiae	[gn:yl276c:19328.3] [sr:baker's yeast] [de:putative atp-dependent rna helicase ylr276c] [sp:q06218] [db:swissprot-sp_new]

CONTIG5714	24396086_c2_21	2507	16610	1158	386	Q12094	888	4.7(10)-89	Saccharomyces cerevisiae	[gn:yor006c:und313] [sr:baker's yeast] [de:hyprothetical 35.7 kd protein in dna1-slg1 intergenic region] [sp:q12094] [db:swissprot-sp_new]
CONTIG2961	24797785_c3_9	2508	16611	2331	777	Q08960	1666	1.7(10)-171	Saccharomyces cerevisiae	[gn:yp1207w] [sr:baker's yeast] [de:hyprothetical 89.8 kd protein yp1207w] [sp:q08960] [db:swissprot-sp_new]
CONTIG4215	110900_f3_4	2509	16612	600	200	AF020657	110	0.00025	Borrelia burgdorferi	[pn:erpx protein] [gn:erpx] [sr:lyme disease spirochete] [db:genpept-bc] [de:borrelia burgdorferi plasmid lp56 erpx protein (erpx) gene,complete cds.]
CONTIG1392	32542706_f1_1	2510	16613	1074	358	D31792	94	0.14999	Streptomyces griseus	[pn:serine/threonine protein kinase] [gn:pksg1] [sr:streptomyces griseus (strain:b2682) dna] [db:genpept-bc] [de:streptomyces griseus dna for serine/threonine protein kinases,complete cds.]
CONTIG4864	2616537_f3_7	2511	16614	1053	351	A1001073	128	2.0(10)-5	Thermotoga maritima	[pn:beta-fructosidase] [gn:bfa] [fn:hydrolysis of sucrose, raffinose, inulin.] [db:genpept-bc] [ec:3.2.1.26] [de:thermotoga maritima bfa gene and orf1.]
CONTIG5544	19957186_c1_13	2512	16615	1710	570	Z81074	466	6.9(10)-73	Caenorhabditis elegans	[pn:f32b6.8] [db:genpept-inv] [de:caenorhabditis elegans cosmid f32b6.] [nt:protein predicted using genefinder; similarity to]
CONTIG1317	19788276_f1_1	2513	16616	630	210	AF026212	94	0.03699	Caenorhabditis elegans	[gn:f52g3.5] [sr:caenorhabditis elegans strain=bristol n2] [db:genpept-inv] [de:caenorhabditis elegans cosmid f52g3.]

CONTIG4752	10728407_f1_1	2514	16617	744	248	AF025472	107	0.0023	Caenorhabditis elegans	[gn:zk250.8] [sr:caenorhabditis elegans strain=bristol n2]
CONTIG4582	21484377_c1_3	2515	16618	414	138	U95996	111	5.2(10)-6	Cryptosporidium parvum	[pn:unknown] [db:genpept-inv] [de:cryptosporidium parvum unknown protein, complete cds.] [nt:similar to jnk protein kinases; small segment]
CONTIG5496	1223160_f1_1	2516	16619	1737	579	U94410	99	0.17999	Dictyostelium discoideum	[pn:rep protein] [gn:rep] [db:genpept-inv] [de:dictyostelium discoideum plasmid ddp6 rep protein (rep) gene, complete cds.]
CONTIG5513	22144535_f3_7	2517	16620	3786	1262	AF012898	5109	0	Candida albicans	[pn:protein phosphatase ssd1 homolog] [gn:ssd1] [db:genpept-pln] [de:candida albicans protein phosphatase ssd1 homolog (ssd1) gene, complete cds.] [nt:cassd1; similar to saccharomyces cerevisiae ssd1]
CONTIG5266	22891927_f1_3	2518	16621	942	314	AF013799	1475	3.0(10)-151	Candida albicans	[pn:aur1 homolog] [db:genpept-pln] [de:candida albicans aur1 homolog gene, complete cds.]
CONTIG1877	1433277_f1_1	2519	16622	621	207	AF015771	112	7.0(10)-6	Magnaporthe grisea	[pn:putative transcriptional regulator] [gn:con7] [fn:controls germ tube growth and pathogenicity of] [db:genpept-pln] [de:magnaporthe grisea putative transcriptional regulator (con7) gene, complete cds.] [nt:has zinc-finger motif and

CONTIG2705	26226412_f1_2	2520	16623	1212	404	AC002332	91	0.23999	Arabidopsis thaliana	[gn:f4p9.9] [sr:thale cress] [db:genpept-pin] [de:arabidopsis thaliana chromosome ii bac f4p9 genomic sequence,complete sequence.] [nt:hyptothetical protein]
CONTIG4174	12791652_c3_8	2521	16624	3183	1061	Y13975	4117	0	Candida albicans	[pn:phospholipase c] [gn:plc1] [db:genpept-pin] [de:candida albicans plc1 gene.]
CONTIG4434	4015803_c1_5	2522	16625	216	72	U60973	334	2.3(10)-29	Candida albicans	[pn:opt1p] [gn:opt1] [fn:membrane protein mediating transport of] [db:genpept-pin] [de:candida albicans oligopeptide transporter (opt1) gene, completecds.] [nt:oligopeptide transporter]
CONTIG4856	11992132_f1_1	2523	16626	2301	767	U60973	653	3.7(10)-64	Candida albicans	[pn:opt1p] [gn:opt1] [fn:membrane protein mediating transport of] [db:genpept-pin] [de:candida albicans oligopeptide transporter (opt1) gene, completecds.] [nt:oligopeptide transporter]
CONTIG5662	6835052_f2_6	2524	16627	1161	387	U60973	1847	1.1(10)-190	Candida albicans	[pn:opt1p] [gn:opt1] [fn:membrane protein mediating transport of] [db:genpept-pin] [de:candida albicans oligopeptide transporter (opt1) gene, completecds.] [nt:oligopeptide transporter]

CONTIG5640	34175152_f2_3	2525	16628	2106	702	U87996	1476	1.8(10)-227	Candida albicans	[pn:claf protein kinase homolog] [fn:hyphal formation and virulence; morphological] [db:genpept-pin] [de:candida albicans claf protein kinase homolog gene, complete cds.]
CONTIG5530	24084426_c2_12	2526	16629	483	161	U23425	103	0.00012	Neurospora crassa	[gn:ropy-2] [db:genpept-pin] [de:neurospora crassa ropy-2 gene, complete cds.]
blx16210.y	36453425_f2_1	2527	16630	489	163	Z98951	258	3.6(10)-20	Schizosaccharo myces pombe	[pn:hypothetical protein] [gn:spac10d6.03c] [sr:fission yeast] [db:genpept-pin] [de:s.pombe chromosome i cosmid c10d6.] [nt:spac10d6.03c, unknown; probable motor protein.]
CONTIG5373	6676332_c1_4	2528	16631	648	216	Z98951	139	5.5(10)-12	Schizosaccharo myces pombe	[pn:hypothetical protein] [gn:spac10d6.04] [sr:fission yeast] [db:genpept-pin] [de:s.pombe chromosome i cosmid c10d6.] [nt:spac10d6.04, unknown, len:660aa, similar eg. to]
CONTIG5621	6113177_f1_5	2529	16632	600	200	Z98595	135	2.8(10)-9	Schizosaccharo myces pombe	[pn:hypothetical protein] [gn:spac11e3.10] [sr:fission yeast] [db:genpept-pin] [de:s.pombe chromosome i cosmid c11e3.] [nt:spac11e3.10, unknown, len:187aa]

CONTIG2424	30085805_c3_3	2530	16633	1086	362	Z98595	190	3.3(10)-12	Schizosaccharo myces pombe	[pn:hypothetical protein] [gn:spac11e3.11c] [sr:fission yeast] [db:genpept-pfn] [de:s.pombe chromosome i cosmid c11e3.] [nt:spac11e3.11c, unknown, len:942aa, some similarity]
CONTIG2826	10972337_c1_3	2531	16634	1554	518	Z98596	737	4.7(10)-73	Schizosaccharo myces pombe	[pn:hypothetical protein] [gn:spac14c4.11] [sr:fission yeast] [db:genpept-pfn] [de:s.pombe chromosome i cosmid c14c4.] [nt:spac14c4.11, unknown, len:734aa, similar eg. to]
CONTIG5011	10162510_f3_2	2532	16635	633	211	Z98529	211	2.6(10)-17	Schizosaccharo myces pombe	[pn:hypothetical protein] [gn:spac16e8.02] [sr:fission yeast] [db:genpept-pfn] [de:s.pombe chromosome i cosmid c16e8.] [nt:spac16e8.02, unknown, len:223aa, similar eg. to]
CONTIG5817	26568763_c1_40	2533	16636	225	75	Z98529	101	0.00014	Schizosaccharo myces pombe	[pn:hypothetical protein] [gn:spac16e8.13] [sr:fission yeast] [db:genpept-pfn] [de:s.pombe chromosome i cosmid c16e8.] [nt:spac16e8.13, unknown; zinc finger containing.]
CONTIG3295	4102300_c3_9	2534	16637	1305	435	Z99292	435	4.7(10)-41	Schizosaccharo myces pombe	[pn:flavoprotein] [gn:spac17a2.05] [sr:fission yeast] [db:genpept-pfn] [de:s.pombe chromosome i cosmid c17a2.] [nt:spac17a2.05, putative oxidoreductase; flavoprotein.]

CONTIG4027	9954677_f2_3	2535	16638	666	222	Z98849	110	1.5(10)-7	Schizosaccharo myces pombe	[pn:hypothetical protein] [gn:spac17a5.09c] [sr:fission yeast] [db:genpept-pin] [de:s.pombe chromosome i cosmid c17a5.] [nt:spac17a5.09c, unknown, len:310aa]
CONTIG5614	2756682_c3_26	2536	16639	984	328	Z98849	348	5.2(10)-31	Schizosaccharo myces pombe	[pn:hypothetical protein] [sr:fission yeast] [db:genpept-pin] [de:s.pombe chromosome i cosmid c17a5.] [nt:spac17a5.12, unknown; may need n terminal]
CONTIG5009	2353135_f3_2	2537	16640	3195	1065	Z98849	113	2.2(10)-9	Schizosaccharo myces pombe	[pn:hypothetical protein] [gn:spac17a5.16] [sr:fission yeast] [db:genpept-pin] [de:s.pombe chromosome i cosmid c17a5.] [nt:spac17a5.16, unknown, len:921aa, similar eg. to c.]
CONTIG4109	4703130_c3_8	2538	16641	1200	400	Z99162	234	9.3(10)-21	Schizosaccharo myces pombe	[pn:hypothetical protein] [gn:spac17g6.05c] [sr:fission yeast] [db:genpept-pin] [de:s.pombe chromosome i cosmid c17g6.] [nt:spac17g6.05c, unknown, len:775aa, similar eg. to]
CONTIG768	22470177_f1_1	2539	16642	693	231	Z99162	130	5.7(10)-6	Schizosaccharo myces pombe	[pn:hypothetical protein] [gn:spac17g6.12] [sr:fission yeast] [db:genpept-pin] [de:s.pombe chromosome i cosmid c17g6.] [nt:spac17g6.12, putative cell division control]

CONTIG2361	25433303_f2_1	2540	16643	684	228	Z98597	110	0.001	Schizosaccharo myces pombe	[pn:hyposhethcal protein] [gn:spac17h9.20] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c17h9.] [nt:spac17h9.20, partial; unknown, len:563aa, some]
CONTIG3822	5890767_f1_1	2541	16644	234	78	Z98974	120	1.1(10)-7	Schizosaccharo myces pombe	[pn:hyposhethcal protein] [gn:spac19a8.09] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c19a8.] [nt:spac19a8.09, unknown, len:81aa]
CONTIG4079	803212_f2_2	2542	16645	432	144	Z98974	108	6.4(10)-6	Schizosaccharo myces pombe	[pn:hyposhethcal protein] [gn:spac19a8.11c] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c19a8.] [nt:spac19a8.11c, unknown, len:246aa]
CONTIG1426	33644591_f2_1	2543	16646	834	278	Z98598	190	4.9(10)-14	Schizosaccharo myces pombe	[pn:hyposhethcal protein] [gn:spac1b3.05] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c1b3.] [nt:spac1b3.05, probable transcriptional regulator.]
CONTIG3514	16615683_c2_3	2544	16647	282	94	Z98598	126	8.5(10)-8	Schizosaccharo myces pombe	[pn:hyposhethcal protein] [gn:spac1b3.06c] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c1b3.] [nt:spac1b3.06c, unknown, len:278aa, some similarity]

CONTIG4070	25803812_f1_2	2545	16648	1116	372	Z98598	192	2.2(10)-16	Schizosaccharo myces pombe	[pn:hy:pothetical protein] [gn:spac1b3.08] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c1b3.] [nt:spac1b3.08, unknown, len:424aa, similar eg. to c.]
CONTIG3736	14246016_f2_2	2546	16649	699	233	Z98598	125	1.0(10)-5	Schizosaccharo myces pombe	[pn:hy:pothetical protein] [gn:spac1b3.08] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c1b3.] [nt:spac1b3.08, unknown, len:424aa, similar eg. to c.]
CONTIG5498	10970438_f3_7	2547	16650	1512	504	Z98598	970	9.6(10)-98	Schizosaccharo myces pombe	[pn:hy:pothetical protein] [gn:spac1b3.16c] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c1b3.] [nt:spac1b3.16c, possible transporter, len:568aa.]
CONTIG4818	15712755_f2_2	2548	16651	558	186	Z99295	167	1.2(10)-11	Schizosaccharo myces pombe	[pn:phosphatidyl synthase] [gn:spac22a12.08c] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c22a12.] [nt:spac22a12.08c, unknown; putative phosphatidyl]
CONTIG2123	25431652_c2_8	2549	16652	789	263	Z99295	125	1.7(10)-11	Schizosaccharo myces pombe	[pn:pre-mrna splicing factor] [gn:spac22a12.09c] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c22a12.] [nt:spac22a12.09c, putative pre- mna splicing factor,]

b2x10952.y	36334443_c1_1	2550	16653	690	230	Z98559	145	1.1(10)-13	Schizosaccharo myces pombe	[pn:hyprothetical protein] [gn:spac23c11.01] [sr:fission yeast] [db:genpept-pin] [de:s.pombe chromosome i cosmid c23c11.] [nt:spac23c11.01, unknown, len:441aa, some similarity]
CONTIG3360	6261265_c1_7	2551	16654	702	234	Z98559	231	6.4(10)-19	Schizosaccharo myces pombe	[pn:hyprothetical protein] [gn:spac23c11.04c] [sr:fission yeast] [db:genpept-pin] [de:s.pombe chromosome i cosmid c23c11.] [nt:spac23c11.04c, unknown, len:421aa, similar eg. to]
CONTIG5477	35956467_f1_1	2552	16655	684	228	Z98559	216	5.0(10)-31	Schizosaccharo myces pombe	[pn:hyprothetical protein] [gn:spac23c11.04c] [sr:fission yeast] [db:genpept-pin] [de:s.pombe chromosome i cosmid c23c11.] [nt:spac23c11.04c, unknown, len:421aa, similar eg. to]
CONTIG4786	2816316_c1_6	2553	16656	1338	446	Z99753	395	8.3(10)-37	Schizosaccharo myces pombe	[pn:hyprothetical protein] [gn:spac23c4.16c] [sr:fission yeast] [db:genpept-pin] [de:s.pombe chromosome i cosmid c23c4.] [nt:spac23c4.16c, unknown, len:424aa, similar eg. to a]
CONTIG1811	4428750_c2_4	2554	16657	819	273	Z99163	186	2.1(10)-20	Schizosaccharo myces pombe	[pn:hyprothetical protein] [gn:spac23h3.04] [sr:fission yeast] [db:genpept-pin] [de:s.pombe chromosome i cosmid c23h3.] [nt:spac23h3.04, unknown, len:349aa]

CONTIG368	2147513_f1_1	2555	16658	312	104	Z98977	139	2.3(10)-8	Schizosaccharo myces pombe	[pn:hyprothetical protein] [gn:spac23h4.14] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c23h4.] [nt:spac23h4.14, unknown, len:905aa, contains ps00307]
CONTIG4912	23953887_f2_2	2556	16659	2037	679	Z98601	325	2.3(10)-32	Schizosaccharo myces pombe	[pn:hyprothetical protein] [gn:spac24c9.05c] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c24c9.] [nt:spac24c9.05c, unknown, len:730aa]
CONTIG5803	9957510_f3_14	2557	16660	2607	869	Z98601	695	1.3(10)-68	Schizosaccharo myces pombe	[pn:hyprothetical protein] [gn:spac24c9.11] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c24c9.] [nt:spac24c9.11, unknown, len:775aa, similar eg. to]
CONTIG3472	1210258_f3_3	2558	16661	396	132	Z99126	148	1.2(10)-10	Schizosaccharo myces pombe	[pn:hyprothetical protein] [gn:spac26h5.14] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c26h5.] [nt:spac26h5.14, unknown, len:166aa, similar eg. to pig]
CONTIG2971	25861411_c2_3	2559	16662	1449	483	Z98978	608	2.2(10)-59	Schizosaccharo myces pombe	[pn:cell division protein] [gn:cde1] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c27e2.] [nt:spac27e2.05, cdc1, cell division protein.]

CONTIG4757	19589556_f2_2	2560	16663	627	209	Z99164	101	0.0008	Schizosaccharo myces pombe	[pn:hypothetical protein] [gn:spac29b12.11c] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c29b12.] [nt:spac29b12.11c, unknown, len:174aa, similar eg. to]
CONTIG5489	798562_c3_10	2561	16664	432	144	Z98887	204	1.3(10)-16	Schizosaccharo myces pombe	[pn:hypothetical protein] [gn:spac2c6.07] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c2c6.] [nt:spac2c6.07, unknown, len:101aa]
CONTIG4354	266381_c3_8	2562	16665	486	162	Z98850	190	4.4(10)-15	Schizosaccharo myces pombe	[pn:hypothetical protein] [gn:spac2e11.03c] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c2e11.] [nt:spac2e11.03c, unknown, len:124aa]
CONTIG5008	24783428_f2_3	2563	16666	2217	739	Z99165	680	2.1(10)-73	Schizosaccharo myces pombe	[pn:hypothetical protein] [gn:spac2f3.16] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c2f3.] [nt:spac2f3.16, unknown, (splicing may be incorrectly)]
CONTIG5340	31345378_f3_3	2564	16667	2082	694	Z98979	991	5.7(10)-100	Schizosaccharo myces pombe	[pn:hypothetical protein] [gn:spac31g5.20c] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c31g5.] [nt:author-given protein sequence is in conflict with]

CONTIG4504	12789064_c1_7	2565	16668	1803	601	Z95395	100	0.039	Schizosaccharo myces pombe	[pn:unknown] [gn:spac3a12.01c] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c3a12.] [nt:spac3a12.01c, unknown; partial, len:371aa, similar]
CONTIG3109	36643128_f2_1	2566	16669	1308	436	Z99568	146	5.7(10)-7	Schizosaccharo myces pombe	[pn:hypothetical protein] [gn:spac3c7.04] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c3c7.] [nt:spac3c7.04, putative transcriptional control.]
CONTIG201	30258317_f3_1	2567	16670	609	203	Z99568	93	0.033	Schizosaccharo myces pombe	[pn:hypothetical protein] [gn:spac3c7.05c] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c3c7.] [nt:spac3c7.05c, unknown, len:442aa]
CONTIG2732	22461713_c2_4	2568	16671	471	157	Z99568	136	1.8(10)-8	Schizosaccharo myces pombe	[pn:hypothetical protein] [gn:spac3c7.05c] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c3c7.] [nt:spac3c7.05c, unknown, len:442aa]
CONTIG5511	4297340_c2_19	2569	16672	306	102	Z99568	114	4.2(10)-6	Schizosaccharo myces pombe	[pn:hypothetical protein] [gn:spac3c7.05c] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c3c7.] [nt:spac3c7.05c, unknown, len:442aa]

CONTIG5767	36386575_c1_37	2570	16673	1371	457	Z99568	164	3.2(10)-9	Schizosaccharo myces pombe	[pn:hypothetical protein] [gn:spac3c7.05c] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c3c7.] [nt:spac3c7.05c, unknown, len:442aa]
CONTIG5106	23440952_c1_6	2571	16674	1623	541	Z99568	204	7.9(10)-20	Schizosaccharo myces pombe	[pn:hypothetical protein] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c3c7.] [nt:spac3c7.15c, partial; unknown, len:<397aa]
CONTIG2105	4807168_f1_1	2572	16675	660	220	Z98560	186	1.7(10)-14	Schizosaccharo myces pombe	[pn:hypothetical protein] [gn:spac4c5.03] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c4c5.] [nt:spac4c5.03, unknown, len:302aa]
CONTIG1550	34416332_c2_2	2573	16676	867	289	Z98602	120	3.7(10)-5	Schizosaccharo myces pombe	[pn:hypothetical protein] [gn:spac4d7.11] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c4d7.] [nt:spac4d7.11, unknown, len:281aa]
CONTIG5158	6750753_c3_16	2574	16677	2388	796	Z98980	325	3.7(10)-26	Schizosaccharo myces pombe	[pn:hypothetical protein] [gn:spac4f10.07c] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c4f10.] [nt:spac4f10.07c, unknown, len:758aa, some similarity]
CONTIG5721	4722536_c1_22	2575	16678	1494	498	Z98531	530	3.8(10)-62	Schizosaccharo myces pombe	[pn:hypothetical protein] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c6b12.] [nt:spac6b12.07c, unknown; dna binding, len:456aa.]

CONTIG5699	5860137_13_17	2576	16679	492	164	Z98531	160	6.5(10)-12	Schizosaccharo myces pombe	[pn:hy:pothetical protein] [gn:spac6b12.13] [sr:fission yeast] [db:genpept-pin] [de:s.pombe chromosome i cosmid c6b12.] [nt:spac6b12.13, unknown, len:104aa, similar eg. to]
CONTIG1271	276561_c3_4	2577	16680	933	311	Z98981	353	2.2(10)-32	Schizosaccharo myces pombe	[pn:hy:pothetical protein] [gn:spac6f6.04c] [sr:fission yeast] [db:genpept-pin] [de:s.pombe chromosome i cosmid c6f6.] [nt:spac6f6.04c, unknown, len:489aa]
b1x18631.x	23829751_c3_4	2578	16681	555	185	Z98981	127	2.0(10)-7	Schizosaccharo myces pombe	[pn:hy:pothetical protein] [gn:spac6f6.04c] [sr:fission yeast] [db:genpept-pin] [de:s.pombe chromosome i cosmid c6f6.] [nt:spac6f6.04c, unknown, len:489aa]
b9x12169.x	30475931_c1_1	2579	16682	234	78	Z98603	178	4.5(10)-13	Schizosaccharo myces pombe	[pn:hy:pothetical protein] [gn:spac6g10.03c] [sr:fission yeast] [db:genpept-pin] [de:s.pombe chromosome i cosmid c6g10.] [nt:spac6g10.03c, unknown, len:428aa, similar eg. to]
CONTIG5458	5288942_13_7	2580	16683	639	213	Z98603	117	0.0004	Schizosaccharo myces pombe	[pn:hy:pothetical protein] [gn:spac6g10.05c] [sr:fission yeast] [db:genpept-pin] [de:s.pombe chromosome i cosmid c6g10.] [nt:spac6g10.05c, unknown, len:1210aa, similar eg. to]

CONTIG2887	1175267_f3_3	2581	16684	1806	602	Z99532	110	0.01	Schizosaccharo myces pombe	[pn:hypothetical protein] [gn:spac7d4.03c] [sr:fission yeast] [db:genpept-pin] [de:s.pombe chromosome i cosmid c7d4.] [nt:spac7d4.03c, unknown; serine rich, len:886aa]
CONTIG4209	24336641_c1_5	2582	16685	1590	530	Z99532	1021	3.6(10)-107	Schizosaccharo myces pombe	[pn:hypothetical protein] [gn:spac7d4.12c] [sr:fission yeast] [db:genpept-pin] [de:s.pombe chromosome i cosmid c7d4.] [nt:spac7d4.12c, unknown, len:759aa, similar eg.]
CONTIG4813	0_f2_4	2583	16686	603	201	Z99262	92	0.085	Schizosaccharo myces pombe	[pn:hypothetical protein] [gn:spac9e9.10c] [sr:fission yeast] [db:genpept-pin] [de:s.pombe chromosome i cosmid c9e9.] [nt:spac9e9.10c, unknown, len:514aa, similar eg. to]
CONTIG3949	190637_f1_1	2584	16687	408	136	Z99759	104	5.7(10)-6	Schizosaccharo myces pombe	[pn:hypothetical protein] [gn:spbc16e9.01c] [sr:fission yeast] [db:genpept-pin] [de:s.pombe chromosome ii cosmid c16e9.] [nt:spbc16e9.01c, partial; unknown, len:<161aa]
CONTIG1905	26175937_f2_1	2585	16688	591	197	Z99759	144	5.7(10)-9	Schizosaccharo myces pombe	[pn:hypothetical protein] [gn:spbc16e9.10c] [sr:fission yeast] [db:genpept-pin] [de:s.pombe chromosome ii cosmid c16e9.] [nt:spbc16e9.10c, unknown, len:779aa, similar eg. to]

CONTIG449	480016_f3_2	2586	16689	819	273	Z99759	92	0.0018	Schizosaccharo myces pombe	[pn:hyptothetical protein] [gn:spbc16e9.16c] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c16e9.] [nt:spbc16e9.16c, unknown; splicing prediction may be]
CONTIG1321	5953825_c2_4	2587	16690	291	97	U48234	122	1.1(10)-7	Schizosaccharo myces pombe	[pn:spu2af23] [sr:fission yeast] [db:genpept-pln] [de:schizosaccharomyces pombe small subunit of u2af splicing factorspu2af23 gene, complete cds.] [nt:small subunit of u2af splicing factor]
CONTIG2863	24615675_f2_1	2588	16691	891	297	AJ001414	329	7.0(10)-29	Yarrowia lipolytica	[pn:gpase activating protein] [gn:gyP7] [db:genpept-pln] [de:yarrowia lipolytica gyp7 gene.]
CONTIG5253	24252057_f3_8	2589	16692	936	312	U54559	264	6.2(10)-23	Homo sapiens	[pn:ei3-p40] [sr:human] [db:genpept-pr12] [de:human translation initiation factor ei3 p40 subunit mma, completecds.] [nt:translation initiation factor ei3 p40 subunit]
CONTIG3093	22550753_f1_1	2590	16693	624	208	AF015297	108	0.0053	Human herpesvirus 6 (strain Uganda- 1102)	[pn:ie2hom] [gn:ie2hom] [or:human herpesvirus 6 (strain uganda-1102)] [db:genpept-vrl] [de:human herpesvirus 6 (strain uganda-1102) ie2hom mma, complete cds.] [nt:similar to the immediate-early 2 protein of human]

CONTIG1420	1047135_f2_1	2591	16694	693	231	AF022372	1089	2.3(10)-110	Candida albicans	[pn:proteinase] [gn:kex2] [db:genpept] [de:candida albicans proteinase (kex2) gene, complete cds.] [nt:convertase; probably in trans golgi network]
CONTIG4441	1047135_c2_4	2592	16695	1155	385	AF022372	1920	2.1(10)-198	Candida albicans	[pn:proteinase] [gn:kex2] [db:genpept] [de:candida albicans proteinase (kex2) gene, complete cds.] [nt:convertase; probably in trans golgi network]
CONTIG177	15631938_c3_3	2593	16696	528	176	AF025429	707	9.9(10)-69	Candida albicans	[pn:agglutinin-like adhesin] [gn:ala1] [fn:cell adhesion protein] [db:genpept] [de:candida albicans agglutinin-like adhesin (ala1) gene, complete cds.]
CONTIG4256	15865762_f1_1	2594	16697	1710	570	AF025429	1505	2.0(10)-154	Candida albicans	[pn:agglutinin-like adhesin] [gn:ala1] [fn:cell adhesion protein] [db:genpept] [de:candida albicans agglutinin-like adhesin (ala1) gene, complete cds.]
CONTIG5246	14095436_f1_1	2595	16698	690	230	AF025429	800	1.0(10)-78	Candida albicans	[pn:agglutinin-like adhesin] [gn:ala1] [fn:cell adhesion protein] [db:genpept] [de:candida albicans agglutinin-like adhesin (ala1) gene, complete cds.]
CONTIG5486	12301431_c1_11	2596	16699	2472	824	AF025429	1327	1.3(10)-186	Candida albicans	[pn:agglutinin-like adhesin] [gn:ala1] [fn:cell adhesion protein] [db:genpept] [de:candida albicans agglutinin-like adhesin (ala1) gene, complete cds.]
CONTIG5486	14187555_c3_15	2597	16700	234	78	AF025429	267	9.5(10)-22	Candida albicans	[pn:agglutinin-like adhesin] [gn:ala1] [fn:cell adhesion protein] [db:genpept] [de:candida albicans agglutinin-like adhesin (ala1) gene, complete cds.]

CONTIG5486	839688_c3_14	2598	16701	1941	647	AF025429	1817	1.7(10)-187	Candida albicans	[pn:agglutinin-like adhesin] [gn:ala1] [fn:cell adhesion protein] [db:genpept] [de:candida albicans agglutinin-like adhesin (ala1) gene, complete cds.]
CONTIG5515	3167010_c2_10	2599	16702	2340	780	AF025429	2740	2.6(10)-285	Candida albicans	[pn:agglutinin-like adhesin] [gn:ala1] [fn:cell adhesion protein] [db:genpept] [de:candida albicans agglutinin-like adhesin (ala1) gene, complete cds.]
CONTIG5648	1062887_f2_4	2600	16703	1390	530	AF025429	102	0.0057	Candida albicans	[pn:agglutinin-like adhesin] [gn:ala1] [fn:cell adhesion protein] [db:genpept] [de:candida albicans agglutinin-like adhesin (ala1) gene, complete cds.]
CONTIG4507	5118942_f3_1	2601	16704	1128	376	AF025429	119	0.00068	Candida albicans	[pn:agglutinin-like adhesin] [gn:ala1] [fn:cell adhesion protein] [db:genpept] [de:candida albicans agglutinin-like adhesin (ala1) gene, complete cds.]
CONTIG1863	1281513_f3_2	2602	16705	882	294	AF025429	90	0.58999	Dictyostelium discoideum	[pn:multifunctional protein] [db:genpept] [de:dictyostelium discoideum retrotransposable element tdd-3, complete sequence] [fn:multifunctional protein including en domain and]
b9x12147.y	24895453_c1_7	2603	16706	666	222	AF025995	99	0.00076	Mycobacterium genavense	[pn:hyphothetical 21 kda protein] [db:genpept] [de:mycobacterium genavense hyphothetical 21 kda protein gene, complete cds.] [nt:p21]
CONTIG4308	25971886_f3_4	2604	16707	522	174	U69696	712	2.1(10)-70	Candida albicans	[pn:sec65] [gn:sec65] [db:genpept] [de:candida albicans sec65 (sec65) gene, complete cds, and ura5 (ura5)gene, partial cds.]

CONTIG4308	4320302_f1_2	2605	16708	354	118	U69696	488	1.2(10)-46	Candida albicans	[pn:sec65] [gn:sec65] [db:genpep] [de:candida albicans sec65 (sec65) gene, complete cds, and ura5 (ura5) gene, partial cds.]
CONTIG1784	21505030_c1_11	2606	16709	246	82	AF012106	128	1.6(10)-8	Homo sapiens	[pn:dnaj protein] [gn:hsp72] [sr:human] [db:genpep] [de:homo sapiens dnaj protein (hsp72) mrna, complete cds.]
CONTIG1784	29792326_c2_14	2607	16710	411	137	AF012106	432	9.9(10)-41	Homo sapiens	[pn:dnaj protein] [gn:hsp72] [sr:human] [db:genpep] [de:homo sapiens dnaj protein (hsp72) mrna, complete cds.]
CONTIG3993	1178140_c2_6	2608	16711	363	121	AF020554	113	1.1(10)-5	Candida albicans	[pn:translation release factor 3] [gn:sup35] [db:genpep] [de:candida albicans translation release factor 3 (sup35) gene, complete cds.] [nr:erf3; translation termination factor; putative]
CONTIG2653	9799166_c2_8	2609	16712	1344	448	AF029885	1374	1.5(10)-140	Emmericella nidulans	[pn:putative homoserine o-acetyltransferase] [gn:cysc] [db:genpep] [de:emmericella nidulans putative homoserine o-acetyltransferase (cysc) gene, complete cds.]
CONTIG4195	4335256_c1_4	2610	16713	363	121	AF030343	113	3.2(10)-6	Mus musculus	[pn:ech1p] [gn:ech1] [sr:house mouse] [db:genpep] [de:mus musculus peroxisomal/mitochondrial dienoyl-coa isomerase ech1p(ech1) mrna, complete cds.] [nr:peroxisomal/mitochondrial dienoyl-coa isomerase]

CONTIG5744	22276390_f2_9	2611	16714	888	296	U78082	195	1.3(10)-15	Homo sapiens	[pn:ma polymerase transcriptional regulation] [gn:h-med6] [sr:human] [db:genpept] [de:human ma polymerase transcriptional regulation mediator (h-med6)mma, complete cds.] [nt:h-med6p]
CONTIG5813	24226632_c2_45	2612	16715	954	318	AF027728	92	0.81999	Xenopus laevis	[pn:kinesin-related protein] [gn:xceup-e] [sr:african clawed frog] [db:genpept] [de:xenopus laevis kinesin-related protein (xceup-e) mma, completecds.] [nt:kinetochore-associated; plus end-directed]
b9x11m31.y	34400702_c2_3	2613	16716	207	69	AF030861	90	0.005	Debaryomyces occidentalis	[pn:p-type atpase 2] [gn:ena2] [db:genpept] [de:debaryomyces occidentalis p-type atpase 2 (ena2) gene, completecds.]
CONTIG1818	476384_c1_4	2614	16717	1407	469	AF030861	1551	2.6(10)-159	Debaryomyces occidentalis	[pn:p-type atpase 2] [gn:ena2] [db:genpept] [de:debaryomyces occidentalis p-type atpase 2 (ena2) gene, completecds.]
CONTIG957	13772010_f2_2	2615	16718	576	192	AJ002030	165	2.0(10)-12	Homo sapiens	[pn:progesterone binding protein] [sr:human] [db:genpept] [de:homo sapiens mma for putative progesterone binding protein.] [nt:putative]
CONTIG1432	16287535_f2_1	2616	16719	909	303	AC002983	90	0.46999	Arabidopsis thaliana	[pn:predicted protein] [gn:t3f12.8] [sr:thale cress] [db:genpept] [de:a thaliana bac t3f12 from chromosome iv, likely from the long arm, complete sequence.] [nt:strongly similar to t21b4.1 (pid:2191190); an]

CONTIG5336	5271877_f2_6	2617	16720	1305	435	AF030693	95	0.27	Plasmodium falciparum	[pn:cg2] [gn:cg2] [in:chloroquine resistance gene candidate] [sr:malaria parasite] [db:genpept-inv] [de:plasmodium falciparum strain hb3 cg2 (cg2) gene, complete cds.] [nt:detected by monoclonal antibody]
CONTIG3828	3907752_c2_3	2618	16721	753	251	AF030694	98	0.066	Plasmodium falciparum	[pn:cg7] [gn:cg7] [sr:malaria parasite] [db:genpept-inv] [de:plasmodium falciparum strain dd2 heat shock protein 86 (hsp86), ol(o1), o3 (o3), o2 (o2), cg8 (cg8), cg4 (cg4), cg3 (cg3), cg9 (cg9), cg1 (cg1), cg6 (cg6), chloroquine resist
CONTIG3914	2847027_c3_7	2619	16722	1404	468	AF007776	143	3.2(10) ⁻⁷	Candida albicans	[pn:gag protein] [db:genpept-pln] [de:candida albicans retrotransposon pcal, complete sequence.] [nt:orf1]
CONTIG5122	9819075_f1_1	2620	16723	1014	338	AF007776	1448	2.2(10) ⁻¹⁴⁸	Candida albicans	[pn:gag protein] [db:genpept-pln] [de:candida albicans retrotransposon pcal, complete sequence.] [nt:orf1]
CONTIG962	2788182_f1_1	2621	16724	270	90	AF007776	207	8.9(10) ⁻¹⁷	Candida albicans	[pn:gag protein] [db:genpept-pln] [de:candida albicans retrotransposon pcal, complete sequence.] [nt:orf1]
CONTIG1327	35799058_f1_1	2622	16725	987	329	AF007776	1510	5.7(10) ⁻¹⁵⁵	Candida albicans	[pn:pol protein] [db:genpept-pln] [de:candida albicans retrotransposon pcal, complete sequence.] [nt:orf2]
CONTIG3732	15672567_f1_1	2623	16726	555	185	AF007776	231	7.5(10) ⁻¹⁸	Candida albicans	[pn:pol protein] [db:genpept-pln] [de:candida albicans retrotransposon pcal, complete sequence.] [nt:orf2]

CONTIG3732	3008442_f1_2	2624	16727	573	191	AF007776	538	1.5(10)-50	Candida albicans	[pn:pol protein] [db:genpept-pln] [dc:candida albicans retrotransposon pcal, complete sequence.] [nt:orf2]
CONTIG2840	24725930_c3_5	2625	16728	1425	475	AF007776	146	1.8(10)-6	Candida albicans	[pn:pol protein] [db:genpept-pln] [dc:candida albicans retrotransposon pcal, complete sequence.] [nt:orf2]
CONTIG3054	860338_c2_5	2626	16729	2637	879	AF007776	4183	0	Candida albicans	[pn:pol protein] [db:genpept-pln] [dc:candida albicans retrotransposon pcal, complete sequence.] [nt:orf2]
CONTIG4386	56587_c2_6	2627	16730	258	86	AF007776	154	1.2(10)-9	Candida albicans	[pn:pol protein] [db:genpept-pln] [dc:candida albicans retrotransposon pcal, complete sequence.] [nt:orf2]
CONTIG5122	15913437_f1_2	2628	16731	507	169	AF007776	843	3.6(10)-83	Candida albicans	[pn:pol protein] [db:genpept-pln] [dc:candida albicans retrotransposon pcal, complete sequence.] [nt:orf2]
CONTIG962	15913437_f1_2	2629	16732	708	236	AF007776	1150	8.1(10)-117	Candida albicans	[pn:pol protein] [db:genpept-pln] [dc:candida albicans retrotransposon pcal, complete sequence.] [nt:orf2]
CONTIG224	25600324_c1_2	2630	16733	624	208	AF007776	854	2.3(10)-84	Candida albicans	[pn:pol protein] [db:genpept-pln] [dc:candida albicans retrotransposon pcal, complete sequence.] [nt:orf2]
CONTIG1165	22851388_c1_1	2631	16734	1167	389	U89714	1576	5.9(10)-162	Candida albicans	[pn:opaque-specific abc transporter] [gn:cdt3] [db:genpept-pln] [dc:candida albicans opaque- specific abc transporter (cdt3) gene, complete cds.]

CONTIG1739	471040_f3_2	2632	16735	345	115	U89714	507	2.7(10)-47	Candida albicans	[pn:opaque-specific abc transporter] [gn:cdt3] [db:genpept-pfn] [de:candida albicans opaque-specific abc transporter (cdt3) gene, complete cds.]
CONTIG1806	36516561_c3_6	2633	16736	783	261	U89714	1229	3.5(10)-125	Candida albicans	[pn:opaque-specific abc transporter] [gn:cdt3] [db:genpept-pfn] [de:candida albicans opaque-specific abc transporter (cdt3) gene, complete cds.]
CONTIG3175	30258442_c1_3	2634	16737	234	78	AL001726	103	3.0(10)-5	Neurospora crassa	[pn:complex i intermediate associated protein cia35] [gn:cia35] [db:genpept-pfn] [de:neurospora crassa cia35 gene.]
CONTIG5047	19554627_f2_4	2635	16738	495	165	AL001726	213	1.6(10)-17	Neurospora crassa	[pn:complex i intermediate associated protein cia35] [gn:cia35] [db:genpept-pfn] [de:neurospora crassa cia35 gene.]
CONTIG4800	4798127_f2_2	2636	16739	525	175	AL009197	131	7.2(10)-18	Schizosaccharo myces pombe	[pn:hypothetical protein] [gn:vip1] [sr:fission yeast] [db:genpept-pfn] [de:s.pombe chromosome i cosmid c10f6.] [nt:spac10f6.06, vip1; unknown, len:257aa, identical to]
CONTIG3451	23539000_c3_5	2637	16740	1539	513	AL009197	676	1.3(10)-66	Schizosaccharo myces pombe	[pn:hypothetical protein] [gn:spac10f6.14c] [sr:fission yeast] [db:genpept-pfn] [de:s.pombe chromosome i cosmid c10f6.] [nt:spac10f6.14c, unknown, len:535aa, similar eg. to]

CONTIG5754	15662777_c1_25	2638	16741	2739	913	Z99296	604	7.2(10)-68	Schizosaccharo myces pombe	[pn:hypothetical protein] [gn:spac3h5.08c] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c3h5.] [nt:spac3h5.08c, unknown, len:855aa, some similarity]
CONTIG2859	899012_c1_3	2639	16742	720	240	Z99262	253	9.1(10)-22	Schizosaccharo myces pombe	[pn:cell-cycle regulatory protein] [gn:wos2] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c9e9.] [nt:spac9e9.13c, wos2; cell cycle regulatory protein]
CONTIG2466	14244652_c2_8	2640	16743	720	240	AF006514	94	0.23	Homo sapiens	[pn:chd2] [gn:chd2] [sr:human] [db:genpept-pri2] [de:homo sapiens chd2 mrra, complete cds.]
CONTIG5320	4018761_c1_6	2641	16744	1050	350	AF001688	318	9.0(10)-28	Mus musculus	[pn:u4/u6 snmp 90 kda protein] [sr:house mouse] [db:genpept-rod] [de:mus musculus u4/u6 snmp 90 kda protein gene, complete cds.]
CONTIG2886	35165687_f3_2	2642	16745	1944	648	AF013614	154	1.8(10)-10	Fugu rubripes	[gn:isc2] [db:genpept-vrt] [de:fugu rubripes cosmid 259c6, complete sequence.] [nt:f_259c6.1]
CONTIG4108	5195337_f1_2	2643	16746	1149	383	AE001153	126	0.00032	Borrelia burgdorferi	[pn:b. burgdorferi predicted coding region bb0512] [gn:bb0512] [sr:lyme disease spirochete] [db:genbank] [de:borrelia burgdorferi (section 39 of 70) of the complete genome.] [nt:hypothetical protein, identified by genemark.]

CONTIG4977	31428803_f1_1	2644	16747	783	261	AE001153	117	2.6(10)-5	Borrelia burgdorferi	[pn:b. burgdorferi predicted coding region bb0512] [gn:bb0512] [sr:lyme disease spirochete] [db:genbank] [dc:borrelia burgdorferi (section 39 of 70) of the complete genome.] [nt:hypothetical protein; identified by genemark;]
CONTIG5055	29329517_c1_10	2645	16748	339	113	AE000788	90	0.00096	Borrelia burgdorferi	[pn:b. burgdorferi predicted coding region bbk23] [gn:bbk23] [sr:lyme disease spirochete] [db:genbank] [dc:borrelia burgdorferi plasmid lp36, complete plasmid sequence.] [nt:hypothetical protein; identified by genemark;]
CONTIG5388	24852276_c2_10	2646	16749	1245	415	adhB	317	1.5(10)-28	Bacillus subtilis	[ui:adhB] [pn:alcohol dehydrogenase] [gtcf:1.1:1.8:2.2:3.5:5.12:8.1] [keggfc:1.1:1.8:2.2:3.5:5.12:8.1] [bsorfc:2.6.1] [db:gtc-bacillus subtilis]
CONTIG4019	14710432_f2_1	2647	16750	1383	461	acol	109	0.00449	Bacillus subtilis	[ui:acol] [pn:acetoin dehydrogenase e3 component: dihydrolipoamide dehydrogenase] [gn:yfjh] [gtcf:1.1] [keggfc:14.2] [bsorfc:2.4.1] [db:gtc-bacillus subtilis]

CONTIG5346	4491625_c2_19	2648	16751	993	331	acol	103	0.01299	Bacillus subtilis	[ui:acol] [pn:acetoin dehydrogenase e3 component: dihydroliipoamide dehydrogenase] [gn:yfjh] [gctc:1.1] [keggfc:14.2] [bsorffc:2.4.1] [db:gct-bacillus subtilis]
CONTIG5018	23453909_c2_14	2649	16752	957	319	aldX	403	1.2(10)-37	Bacillus subtilis	[ui:aldx] [pn:aldehyde dehydrogenase:probable aldehyde dehydrogenase yxas] [gn:yxas:yxbe:ve7fr] [gctc:1.1] [ec:1.2.1.3] [keggfc:14.1] [bsorffc:2.4.1] [db:gct-bacillus subtilis]
CONTIG2774	10658208_c3_4	2650	16753	948	316	ywdH	282	1.7(10)-24	Bacillus subtilis	[ui:ywdh] [pn:hypothetical protein:probable aldehyde dehydrogenase ywdh] [gn:ipa-58r] [gctc:1.10.1.11:1.7.1.8.3.2.3.5.5.10 :5.11:5.12:5.14:5.6:5.9:6.1:8.1:14.1] [ec:1.2.1.3] [keggfc:1.7.1.8.1.10:1.11:3.2.3.5.5.6:5.9:5.10:5.11:5.12:5.1]
CONTIG4021	23598500_c1_10	2651	16754	1485	495	ywdH	404	1.3(10)-48	Bacillus subtilis	[ui:ywdh] [pn:hypothetical protein:probable aldehyde dehydrogenase ywdh] [gn:ipa-58r] [gctc:1.10.1.11:1.7.1.8.3.2.3.5.5.10 :5.11:5.12:5.14:5.6:5.9:6.1:8.1:14.1] [ec:1.2.1.3] [keggfc:1.7.1.8.1.10:1.11:3.2.3.5.5.6:5.9:5.10:5.11:5.12:5.1]

CONTIG5498	4459628_f2_3	2652	16755	606	202	gutB	106	0.00093	Bacillus subtilis	[ui:gutB] [pn:sorbitol dehydrogenase:l-iditol 2-dehydrogenase] [gctc:1.4:1.5] [ec:1.1.1.14] [keggfc:1.5] [bsorffc:2.1.1] [db:gic-bacillus subtilis]
CONTIG553	191877_f2_1	2653	16756	426	142	gutB	149	4.4(10)-10	Bacillus subtilis	[ui:gutB] [pn:sorbitol dehydrogenase:l-iditol 2-dehydrogenase] [gctc:1.4:1.5] [ec:1.1.1.14] [keggfc:1.5] [bsorffc:2.1.1] [db:gic-bacillus subtilis]
CONTIG5522	26425177_c3_24	2654	16757	873	291	kduD	418	3.0(10)-39	Bacillus subtilis	[ui:kduD] [pn:2-keto-3-deoxygluconate oxidoreductase:2-deoxy-d-gluconate 3-dehydrogenase:2-keto-3-deoxygluconate oxydoreductase] [gctc:1.4] [ec:1.1.1.125] [keggfc:14.1] [bsorffc:2.1.1] [db:gic-bacillus subtilis]
b3x16037.y	16219543_f3_5	2655	16758	282	94	mmgC	201	9.4(10)-16	Bacillus subtilis	[ui:mmgC] [pn:acyl-coa dehydrogenase] [gn:yqin] [gctc:1.8:2.2] [ec:1.3.99.-] [keggfc:14.1] [bsorffc:2.6.1:2.6.2] [db:gic-bacillus subtilis]
CONTIG5614	25507180_c2_22	2656	16759	1635	545	aspB	234	4.5(10)-17	Bacillus subtilis	[ui:aspB] [pn:aspartate aminotransferase:transaminase a:aspA] [gctc:2.4:5.1:5.10:5.15:5.2:5.5] [ec:2.6.1.1] [keggfc:2.3:5.1:5.2:5.5:10:5.15] [bsorffc:3.1.2] [db:gic-bacillus subtilis]

CONTIG3790	1069136_c2_5	2657	16760	615	205	hmp	306	2.2(10)-27	Bacillus subtilis	[ui:hmp] [pn:flavohemoprotein:haemoglobin- like protein:flavohemoglobin] [gn:ykia:anc3] [gctc:2.8] [keggfc:14.2] [bsorffc:2.7.1] [db:gct-bacillus subtilis]
CONTIG3790	15672827_c2_4	2658	16761	300	100	hmp	112	6.0(10)-6	Bacillus subtilis	[ui:hmp] [pn:flavohemoprotein:haemoglobin- like protein:flavohemoglobin] [gn:ykia:anc3] [gctc:2.8] [keggfc:14.2] [bsorffc:2.7.1] [db:gct-bacillus subtilis]
CONTIG4338	5907500_f2_3	2659	16762	1269	423	hmp	511	4.2(10)-49	Bacillus subtilis	[ui:hmp] [pn:flavohemoprotein:haemoglobin- like protein:flavohemoglobin] [gn:ykia:anc3] [gctc:2.8] [keggfc:14.2] [bsorffc:2.7.1] [db:gct-bacillus subtilis]
CONTIG5015	35573416_f3_1	2660	16763	924	308	fabD	324	2.7(10)-29	Bacillus subtilis	[ui:fabD] [pn:malonyl coa-acyl carrier protein transacylase:mcI] [gn:y/peI] [gctc:3.1.9.5] [ec:2.3.1.39] [keggfc:3.1] [bsorffc:3.4.9] [db:gct-bacillus subtilis]
CONTIG2545	23984576_f1_1	2661	16764	789	263	fabG	249	2.3(10)-21	Bacillus subtilis	[ui:fabG] [pn:3-oxoacyl-acyl-carrier protein reductase:3-ketoacyl-acyl carrier protein reductase] [gn:y/pf] [gctc:3.1.9.5] [ec:1.1.1.100] [keggfc:3.1] [bsorffc:3.4.9] [db:gct- bacillus subtilis]

CONTIG3469	4882813_f2_2	2662	16765	1083	361	yusK	589	2.2(10)-57	Bacillus subtilis	[ui:yusK] [pn:hypothetical protein:similar to acetyl-coa c-acyltransferase] [gicf:3.1:3.2:3.5:5.13:5.6:14.1] [ec:2.3.1.16] [keggf:3.1:3.2:3.5:5.6:5.13] [bsorffc:8.1.1] [db:gic-bacillus subtilis]
b3x14056.y	12924199_c1_2	2663	16766	582	194	yxE	576	5.5(10)-56	Bacillus subtilis	[ui:yxE] [pn:hypothetical protein:probable succinyl-coa:3-ketoacid-coenzyme a transferase subunit b:succinyl coa:3-oxoacid coa-transferase:oxct b] [gn:scob:n151] [gicf:5.13:14.1] [keggf:5.13] [bsorffc:8.1.1] [db:gic-bacillus subtil]
CONTIG3457	24650402_c1_6	2664	16767	909	303	yxD	344	8.0(10)-56	Bacillus subtilis	[ui:yxD] [pn:hypothetical protein:probable succinyl-coa:3-ketoacid-coenzyme a transferase subunit a:succinyl coa:3-oxoacid coa-transferase:oxct a] [gn:scob:n15k] [gicf:5.13:14.1] [keggf:5.13] [bsorffc:8.1.1] [db:gic-bacillus subtil]
CONTIG5713	21875341_f3_5	2665	16768	1209	403	metS	708	5.5(10)-70	Bacillus subtilis	[ui:metS] [pn:methionyl-trna synthetase:methionine--trna ligase:metS] [gicf:10.6] [ec:6.1.1.10] [keggf:5.4:6.4:10.1:10.2] [bsorffc:4.3.1] [db:gic-bacillus subtilis]

CONTIG2734	480152_c3_8	2666	16769	903	301	ykWC	142	1.5(10)-7	Bacillus subtilis	[ui:ykwc] [pn:hypothetical protein:similar to 3-hydroxyisobutyrate dehydrogenase] [gicf:5.6:14.1] [ec:1.1.1.31] [keggf:5.6] [bsorffc:8.1.1] [db:gtc-bacillus subtilis]
CONTIG5759	24002183_f3_10	2667	16770	1620	540	lyss	604	5.9(10)-59	Bacillus subtilis	[ui:lyss] [pn:lysyl-trna synthetase:lysine--trna ligase:lysr] [gicf:10.6] [ec:6.1.1.6] [keggf:5.8:10.1:10.2] [bsorffc:4.3.1] [db:gtc-bacillus subtilis]
CONTIG5692	172037_c2_13	2668	16771	1863	621	egt	535	1.2(10)-51	Bacillus subtilis	[ui:egt] [pn:gamma-glutamyltranspeptidase:gamma-glutamyltranspeptidase precursor] [gn:pac] [gicf:6.16:6.4:6.5:8.2:10.11] [ec:2.3.2.2] [keggf:6.4:6.5:6.9:8.6] [bsorffc:4.3.4] [db:gtc-bacillus subtilis]
CONTIG2262	12287750_f1_1	2669	16772	1290	430	iolA	666	1.6(10)-65	Bacillus subtilis	[ui:iolA] [pn:methylmalonate-semialdehyde dehydrogenase:probable methylmalonate-semialdehyde dehydrogenase:acylating:mmsdh] [gn:mmsa:xxda:e83a] [gicf:8.2] [ec:1.2.1.27] [keggf:14.1] [bsorffc:7.7.1] [db:gtc-bacillus subtilis]

CONTIG3774	26196900_13_3	2670	16773	2332	784	lonA	534	5.2(10)-85	Bacillus subtilis	[ui:lonA] [pn:class iii heat-shock atp-dependent lon protease:atp- dependent protease la 1] [gn:lon] [gicfc:10.11] [cc:3.4.21.53] [keggfc:14.1] [bsorffc:4.3.4] [db:gic-bacillus subtilis]
CONTIG701	9790932_13_1	2671	16774	606	202	rpsK	116	4.0(10)-7	Bacillus subtilis	[ui:rpsK] [pn:ribosomal protein s18:30s ribosomal protein s18:bs21] [gicfc:10.4] [keggfc:14.2] [bsorffc:4.3.2] [db:gic-bacillus subtilis]
CONTIG3565	20501555_12_4	2672	16775	741	247	yqjZ	100	0.00519	Bacillus subtilis	[ui:yqjZ] [pn:hypothetical protein:probable amino-acid abc transporter atp-binding protein in bmr-u-ansr intergenic region] [gicfc:12.6:14.1] [keggfc:11.1] [bsorffc:8.1.1] [db:gic-bacillus subtilis]
CONTIG5605	579677_13_18	2673	16776	2205	735	dnaJ	148	2.8(10)-7	Bacillus subtilis	[ui:dnaJ] [pn:heat-shock protein:dnaJ protein] [gicfc:12.7] [keggfc:14.2] [bsorffc:6.5.1] [db:gic-bacillus subtilis]
CONTIG4618	14850312_13_1	2674	16777	594	198	cinaA	126	1.8(10)-7	Bacillus subtilis	[ui:cinaA] [pn:competence-damage inducible protein:putative competence-damage protein] [gn:ymfo:yzb] [gicfc:13.2] [keggfc:14.2] [bsorffc:7.1.1] [db:gic-bacillus subtilis]
CONTIG5273	6718755_13_5	2675	16778	558	186	yaaeE	228	4.0(10)-19	Bacillus subtilis	[ui:yaae] [pn:hypothetical protein:hypothetical 21.4 kd protein in dacta-sers intergenic region] [gicfc:14.1] [keggfc:14.2] [bsorffc:8.1.1] [db:gic-bacillus subtilis]

CONTIG1303	11203402_c3_4	2676	16779	1179	393	yaaT	136	6.9(10)-8	Bacillus subtilis	[ui:yaaT] [pn:hypothetical protein:hypothetical 31.2 kd protein in xpac-abrb intergenic region] [gtcf:14.1] [keggfc:14.2] [bsorffc:8.1.1] [db:gtc-bacillus subtilis]
CONTIG1670	4547139_c1_3	2677	16780	1113	371	yacA	171	4.5(10)-10	Bacillus subtilis	[ui:yacA] [pn:hypothetical protein:hypothetical 55.1 kd protein in spoIIE-hpt intergenic region] [gtcf:14.1] [keggfc:14.2] [bsorffc:8.1.1] [db:gtc-bacillus subtilis]
CONTIG5226	19625251_c2_15	2678	16781	993	331	ybgG	430	1.6(10)-40	Bacillus subtilis	[ui:ybgG] [pn:hypothetical protein:similar to hypothetical proteins] [gtcf:14.1] [keggfc:14.2] [bsorffc:8.1.1] [db:gtc-bacillus subtilis]
CONTIG4075	25680130_f1_1	2679	16782	483	161	yceI	99	0.00014	Bacillus subtilis	[ui:yceI] [pn:hypothetical protein:similar to transporter] [gtcf:14.1] [keggfc:14.2] [bsorffc:8.1.1] [db:gtc-bacillus subtilis]
CONTIG4844	16287676_f1_1	2680	16783	294	98	yceI	91	0.0011	Bacillus subtilis	[ui:yceI] [pn:hypothetical protein:similar to transporter] [gtcf:14.1] [keggfc:14.2] [bsorffc:8.1.1] [db:gtc-bacillus subtilis]
CONTIG1646	4688219_c1_4	2681	16784	927	309	yfmT	414	8.0(10)-39	Bacillus subtilis	[ui:yfmT] [pn:hypothetical protein:similar to benzaldehyde dehydrogenase] [gtcf:14.1] [keggfc:14.2] [bsorffc:8.1.1] [db:gtc-bacillus subtilis]

CONTIG5571	25445253_c1_19	2682	16785	975	325	yfmJ	340	5.5(10)-31	Bacillus subtilis	[ui:yfmj] [pn:hypothetical protein:similar to quinone oxidoreductase] [gtcf:9.12] [keggf:14.2] [bsorffc:8.1.1] [db:gtc-bacillus subtilis]
CONTIG2618	23469053_c2_7	2683	16786	597	199	yfG	130	9.0(10)-8	Bacillus subtilis	[ui:yfG] [pn:hypothetical protein:hypothetical metabolic transport protein in glvbc 3' region] [gtcf:14.1] [keggf:14.2] [bsorffc:8.1.1] [db:gtc-bacillus subtilis]
CONTIG2776	25975063_c1_6	2684	16787	621	207	yfbB	158	2.5(10)-11	Bacillus subtilis	[ui:yfbB] [pn:hypothetical protein:similar to hypothetical proteins] [gtcf:14.1] [keggf:14.2] [bsorffc:8.1.1] [db:gtc-bacillus subtilis]
CONTIG3317	25975063_f1_2	2685	16788	699	233	yfbB	157	3.2(10)-11	Bacillus subtilis	[ui:yfbB] [pn:hypothetical protein:similar to hypothetical proteins] [gtcf:14.1] [keggf:14.2] [bsorffc:8.1.1] [db:gtc-bacillus subtilis]
CONTIG3317	6056286_f2_4	2686	16789	426	142	yfbB	116	1.2(10)-6	Bacillus subtilis	[ui:yfbB] [pn:hypothetical protein:similar to hypothetical proteins] [gtcf:14.1] [keggf:14.2] [bsorffc:8.1.1] [db:gtc-bacillus subtilis]
CONTIG2581	5900817_f2_3	2687	16790	531	177	yfbM	122	2.7(10)-6	Bacillus subtilis	[ui:yfbM] [pn:hypothetical protein:similar to epoxide hydrolase] [gtcf:14.1] [keggf:14.2] [bsorffc:8.1.1] [db:gtc-bacillus subtilis]

CONTIG5773	115662_c2_30	2688	16791	513	171	yhK	298	1.6(10)-26	Bacillus subtilis	[ui:yhK] [pn:hypothetical protein:similar to hypothetical proteins] [gtcf:14.1] [keggfc:14.2] [bsorffc:8.1.1] [db:gtc-bacillus subtilis]
CONTIG5761	21687788_c1_21	2689	16792	897	299	yisK	405	7.2(10)-38	Bacillus subtilis	[ui:yisK] [pn:hypothetical protein:similar to 5-oxo-1,2,5-tricarboxylic-3-penten acid decarboxylase] [gtcf:14.1] [keggfc:14.2] [bsorffc:8.1.1] [db:gtc-bacillus subtilis]
CONTIG3702	20392302_f1_2	2690	16793	423	141	ykS	156	7.4(10)-11	Bacillus subtilis	[ui:ykS] [pn:hypothetical protein:similar to initiation factor eif-2b:alpha subunit] [gtcf:14.1] [keggfc:14.2] [bsorffc:8.1.1] [db:gtc-bacillus subtilis]
CONTIG4770	2157713_c2_8	2691	16794	756	252	ykS	230	3.1(10)-19	Bacillus subtilis	[ui:ykS] [pn:hypothetical protein:similar to initiation factor eif-2b:alpha subunit] [gtcf:14.1] [keggfc:14.2] [bsorffc:8.1.1] [db:gtc-bacillus subtilis]
b3x16064.y	26255192_f3_3	2692	16795	495	165	ykvO	118	4.9(10)-7	Bacillus subtilis	[ui:ykvO] [pn:hypothetical protein:similar to glucose 1-dehydrogenase] [gtcf:14.1] [keggfc:14.2] [bsorffc:8.1.1] [db:gtc-bacillus subtilis]
CONTIG432	2385942_f2_1	2693	16796	1251	417	yloO	101	0.00959	Bacillus subtilis	[ui:yloO] [pn:hypothetical protein:similar to hypothetical proteins] [gtcf:14.1] [keggfc:14.2] [bsorffc:8.1.1] [db:gtc-bacillus subtilis]

CONTIG4735	33241263_c1_5	2694	16797	291	97	yJua	101	4.4(10)-5	Bacillus subtilis	[ui:yJua] [pn:hypothetical protein:similar to hypothetical proteins] [gctc:14.1] [keggfc:14.2] [bsorffc:8.1.1] [db:gtc-bacillus subtilis]
CONTIG4811	10970438_c1_9	2695	16798	1551	517	yncC	106	0.00979	Bacillus subtilis	[ui:yncC] [pn:hypothetical protein:similar to metabolic transport protein] [gctc:14.1] [keggfc:14.2] [bsorffc:8.1.1] [db:gtc-bacillus subtilis]
CONTIG1944	14070443_c1_4	2696	16799	1179	393	yodT	409	2.7(10)-38	Bacillus subtilis	[ui:yodT] [pn:hypothetical protein:similar to adenosylmethionine-8-amino-7-oxononanoate aminotransferase] [gctc:14.1] [keggfc:14.2] [bsorffc:8.1.1] [db:gtc-bacillus subtilis]
CONTIG4745	36150003_f3_3	2697	16800	1107	369	yogW	149	5.7(10)-14	Bacillus subtilis	[ui:yogW] [pn:hypothetical protein:similar to hypothetical proteins] [gctc:14.1] [keggfc:14.2] [bsorffc:8.1.1] [db:gtc-bacillus subtilis]
CONTIG5750	14240693_c2_20	2698	16801	2400	800	yprA	336	1.2(10)-49	Bacillus subtilis	[ui:yprA] [pn:hypothetical protein:hypothetical helicase in pona-cold intergenic region] [gctc:14.1] [keggfc:14.2] [bsorffc:8.1.1] [db:gtc-bacillus subtilis]
CONTIG3492	22453202_c2_7	2699	16802	480	160	yqkG	133	4.7(10)-9	Bacillus subtilis	[ui:yqkG] [pn:hypothetical protein:hypothetical 21.0 kd protein in glng-anst intergenic region] [gctc:14.1] [keggfc:14.2] [bsorffc:8.1.1] [db:gtc-bacillus subtilis]

CONTIG4458	21656962_f2_2	2700	16803	1140	380	yqjM	442	8.6(10)-42	Bacillus subtilis	[ui:yqjM] [pn:hypothetical protein:probable nadh-dependent flavin oxidoreductase yqjM] [gtrc:14.1] [cc:1-...-] [keggfc:14.1] [bsorffc:8.1.1] [db:gtrc-bacillus subtilis]
CONTIG5794	629681_c3_39	2701	16804	1293	431	yqjM	334	4.4(10)-53	Bacillus subtilis	[ui:yqjM] [pn:hypothetical protein:probable nadh-dependent flavin oxidoreductase yqjM] [gtrc:14.1] [cc:1-...-] [keggfc:14.1] [bsorffc:8.1.1] [db:gtrc-bacillus subtilis]
CONTIG5616	34178755_c2_26	2702	16805	477	159	yrvI	285	3.7(10)-25	Bacillus subtilis	[ui:yrvI] [pn:hypothetical protein:similar to hypothetical proteins] [gtrc:14.1] [keggfc:14.2] [bsorffc:8.1.1] [db:gtrc-bacillus subtilis]
CONTIG5621	21906280_c2_16	2703	16806	1140	380	ysxC	174	8.6(10)-13	Bacillus subtilis	[ui:ysxC] [pn:hypothetical protein:hypothetical gtp-binding protein in lona-hema intergenic region:orfX] [gtrc:14.1] [keggfc:14.2] [bsorffc:8.1.1] [db:gtrc-bacillus subtilis]
CONTIG5204	3163282_f3_3	2704	16807	732	244	ytag	390	2.7(10)-36	Bacillus subtilis	[ui:ytag] [pn:hypothetical protein:similar to hypothetical proteins] [gtrc:14.1] [keggfc:14.2] [bsorffc:8.1.1] [db:gtrc-bacillus subtilis]
CONTIG3297	4776412_c1_6	2705	16808	1095	365	yulF	268	2.3(10)-23	Bacillus subtilis	[ui:yulF] [pn:hypothetical protein:similar to hypothetical proteins] [gtrc:14.1] [keggfc:14.2] [bsorffc:8.1.1] [db:gtrc-bacillus subtilis]

CONTIG1602	15828510_c3_3	2706	16809	972	324	yutK	401	1.8(10)-37	Bacillus subtilis	[ui:yutK] [pn:hypothetical protein:similar to na ⁺ /nucleoside cotransporter] [gctc:14.1] [keggfc:14.2] [bsorffc:8.1.1] [db:gic-bacillus subtilis]
CONTIG5426	5892951_f1_1	2707	16810	1161	387	yutI	198	1.3(10)-13	Bacillus subtilis	[ui:yutI] [pn:hypothetical protein:similar to nadh dehydrogenase] [gctc:14.1] [keggfc:14.2] [bsorffc:8.1.1] [db:gic-bacillus subtilis]
b3x16037.y	34663505_f1_1	2708	16811	276	92	yusJ	189	5.5(10)-14	Bacillus subtilis	[ui:yusJ] [pn:hypothetical protein:similar to butyryl-coa dehydrogenase] [gctc:14.1] [keggfc:14.2] [bsorffc:8.1.1] [db:gic-bacillus subtilis]
CONTIG3334	34408268_f1_1	2709	16812	1431	477	yusP	293	2.2(10)-25	Bacillus subtilis	[ui:yusP] [pn:hypothetical protein:similar to multidrug-efflux transporter] [gctc:14.1] [keggfc:14.2] [bsorffc:8.1.1] [db:gic-bacillus subtilis]
CONTIG942	291663_f2_1	2710	16813	906	302	yusP	278	1.0(10)-23	Bacillus subtilis	[ui:yusP] [pn:hypothetical protein:similar to multidrug-efflux transporter] [gctc:14.1] [keggfc:14.2] [bsorffc:8.1.1] [db:gic-bacillus subtilis]
b9x10u32.x	36147679_c2_1	2711	16814	663	221	yusP	193	1.8(10)-14	Bacillus subtilis	[ui:yusP] [pn:hypothetical protein:similar to multidrug-efflux transporter] [gctc:14.1] [keggfc:14.2] [bsorffc:8.1.1] [db:gic-bacillus subtilis]
CONTIG5277	5117037_c1_9	2712	16815	681	227	yvgV	99	0.00339	Bacillus subtilis	[ui:yvgV] [pn:hypothetical protein:similar to hypothetical proteins] [gctc:14.1] [keggfc:14.2] [bsorffc:8.1.1] [db:gic-bacillus subtilis]

CONTIG4307	35195927_c3_9	2713	16816	1329	443	yvgX	387	4.9(10)-35	Bacillus subtilis	[ui:yvgX] [pn:hypothetical protein:similar to heavy metal-transporting atpase] [gicf:14.1] [ec:3.6.1.-] [keggf:14.1] [bsorf:8.1.1] [db:gic-bacillus subtilis]
CONTIG4704	14632762_c1_5	2714	16817	393	131	yvcI	120	1.1(10)-7	Bacillus subtilis	[ui:yvcI] [pn:hypothetical protein:similar to mutator mut protein] [gicf:14.1] [keggf:14.2] [bsorf:8.1.1] [db:gic-bacillus subtilis]
CONTIG3934	10189577_c1_5	2715	16818	739	253	yvcE	97	0.03799	Bacillus subtilis	[ui:yvcE] [pn:hypothetical protein:similar to cell wall-binding protein] [gn:yzka] [gicf:14.1] [keggf:14.2] [bsorf:8.1.1] [db:gic-bacillus subtilis]
CONTIG2976	3942506_c1_7	2716	16819	840	280	ywtG	135	1.7(10)-6	Bacillus subtilis	[ui:ywtG] [pn:hypothetical protein:similar to metabolite transport protein] [gicf:14.1] [keggf:14.2] [bsorf:8.1.1] [db:gic-bacillus subtilis]
CONTIG5813	14066375_c1_35	2717	16820	570	190	ywtG	130	8.4(10)-8	Bacillus subtilis	[ui:ywtG] [pn:hypothetical protein:similar to metabolite transport protein] [gicf:14.1] [keggf:14.2] [bsorf:8.1.1] [db:gic-bacillus subtilis]
CONTIG5316	12305293_c3_20	2718	16821	330	110	ywrf	191	3.3(10)-15	Bacillus subtilis	[ui:ywrf] [pn:hypothetical protein] [gicf:14.1] [keggf:14.2] [bsorf:8.1.1] [db:gic-bacillus subtilis]

CONTIG3309	4095375_B_2	2719	16822	1065	355	ywfD	135	1.1(10)-6	Bacillus subtilis	[ui:ywfD] [pn:hypothetical protein:hypothetical oxidoreductase in rocc-pia intergenic region] [gn:ipa-82d] [gtcf:14.1] [ec:1.-.-] [keggfc:14.1] [bsorffc:8.1.1] [db:gtc-bacillus subtilis]
CONTIG5352	14579127_c1_7	2720	16823	930	310	ywfD	248	3.1(10)-21	Bacillus subtilis	[ui:ywfD] [pn:hypothetical protein:hypothetical oxidoreductase in rocc-pia intergenic region] [gn:ipa-82d] [gtcf:14.1] [ec:1.-.-] [keggfc:14.1] [bsorffc:8.1.1] [db:gtc-bacillus subtilis]
CONTIG5647	24648332_c3_20	2721	16824	1509	503	yxio	113	0.0016	Bacillus subtilis	[ui:yxio] [pn:hypothetical protein:hypothetical 47.3 kd protein in wapa-hot intergenic region] [gn:3ar] [gtcf:14.1] [keggfc:14.2] [bsorffc:8.1.1] [db:gtc-bacillus subtilis]
CONTIG5514	1172313_c2_11	2722	16825	456	152	yxek	120	9.5(10)-7	Bacillus subtilis	[ui:yxek] [pn:hypothetical protein:hypothetical 49.3 kd protein in idh-deor intergenic region] [gn:lp9c] [gtcf:14.1] [keggfc:14.2] [bsorffc:8.1.1] [db:gtc-bacillus subtilis]
CONTIG5514	23611307_c1_8	2723	16826	1221	407	yxek	483	3.8(10)-46	Bacillus subtilis	[ui:yxek] [pn:hypothetical protein:hypothetical 49.3 kd protein in idh-deor intergenic region] [gn:lp9c] [gtcf:14.1] [keggfc:14.2] [bsorffc:8.1.1] [db:gtc-bacillus subtilis]

CONTIG5693	23442181_c3_19	2724	16827	1620	540	yyeK	662	4.2(10)-65	Bacillus subtilis	[ui:yyeK] [pn:hyposhethcal 49.3 kd protein in idh-deor intergenic region] [gn:ip9c] [gtcf:14.1] [keggcf:14.2] [bsorffc:8.1.1] [db:gtc-bacillus subtilis]
CONTIG313	10738907_c3_12	2725	16828	1239	413	yyaF	557	5.5(10)-54	Bacillus subtilis	[ui:yyaF] [pn:hyposhethcal 40.1 kd gfp-binding protein in rpsf-spoJ intergenic region] [gtcf:14.1] [keggcf:14.2] [bsorffc:8.1.1] [db:gtc-bacillus subtilis]
b2x10759.x	23478184_c2_2	2726	16829	279	93	b2661	199	3.1(10)-15	Escherichia coli	[ui:b2661] [pn:succinate-semialdehyde dehydrogenase:nadp+:ssdh] [gn:gabd] [gtcf:1.4:1.8] [ec:1.2.1.16] [keggcf:1.1:5.1:5.1:2] [rileyfc:1.3.1] [db:gtc-escherichia coli]
CONTIG661	14072189_c1_3	2727	16830	687	229	b2841	266	1.3(10)-22	Escherichia coli	[ui:b2841] [pn:l-arabinose isomerase:arabinose-proton symport:arabinose transporter] [gn:arae] [gtcf:12.2] [ec:5.3.1.4] [keggcf:1.4] [rileyfc:4.1.3] [db:gtc-escherichia coli]
CONTIG5820	5944017_f3_54	2728	16831	357	119	b2276	97	0.00027	Escherichia coli	[ui:b2276] [pn:nadh dehydrogenase i chain n:nadh-ubiquinone oxidoreductase chain 14:nuo14] [gn:nuon] [gtcf:2.1:2.8:9.12] [ec:1.6.5.3] [keggcf:2.1:9.13] [rileyfc:1.2.6] [db:gtc-escherichia coli]

CONTIG5820	12142885_c3_93	2729	16832	273	91	b2282	143	1.6(10)-9	Escherichia coli	[ui:b2282] [pn:nadh dehydrogenase i chain h:nadh-ubiquinone oxidoreductase chain 8:nuo8] [gn:nuoh] [gicf:2.1:2.8:9.12] [ec:1.6.5.3] [keggf:2.1:9.13] [rileyf:1.2.6] [db:gic-escherichia coli]
CONTIG5694	3938800_c1_17	2730	16833	825	275	b1619	234	9.5(10)-20	Escherichia coli	[ui:b1619] [pn:7-alpha-hydroxysteroid dehydrogenase:7-alpha-hsdh] [gn:hda:hsdh] [gicf:2.3] [ec:1.1.1.159] [keggf:14.1] [rileyf:1.3.1] [db:gic-escherichia coli]
b3x16064.y	33259633_f2_2	2731	16834	324	108	b1619	111	3.2(10)-6	Escherichia coli	[ui:b1619] [pn:7-alpha-hydroxysteroid dehydrogenase:7-alpha-hsdh] [gn:hda:hsdh] [gicf:2.3] [ec:1.1.1.159] [keggf:14.1] [rileyf:1.3.1] [db:gic-escherichia coli]
CONTIG5792	21882777_c3_41	2732	16835	1278	426	b2552	368	6.0(10)-34	Escherichia coli	[ui:b2552] [pn:flavohemoprotein:haemoglobin-like protein:flavohemoglobin:dihydropteridine reductase:ferrisiderophore reductase b] [gn:hmpa:hmp:fsrb] [gicf:2.8:9.6] [ec:1.6.99.7] [keggf:9.7] [rileyf:1.2.6] [db:gic-escherichia coli]
CONTIG1757	31683136_f3_1	2733	16836	879	293	b4051	438	2.2(10)-41	Escherichia coli	[ui:b4051] [pn:quinone oxidoreductase:nadh:quinone reductase:zeta-crystallin homolog protein] [gn:qor:hcz] [gicf:2.8:9.12] [ec:1.6.5.5] [keggf:14.1] [rileyf:1.2.6] [db:gic-escherichia coli]

CONTIG3667	21665635_c3_2	2734	16837	909	303	b0452	216	7.7(10)-18	Escherichia coli	[ui:b0452] [pn:acyl-coa thioesterase ii] [gn:resb] [gcfc:3.1] [ec:3.1.2.-] [keggfc:14.1] [rileyfc:1.8.0] [db:gtc- escherichia coli]
CONTIG5588	3910635_f2_4	2735	16838	1173	391	b0452	114	1.6(10)-7	Escherichia coli	[ui:b0452] [pn:acyl-coa thioesterase ii] [gn:resb] [gcfc:3.1] [ec:3.1.2.-] [keggfc:14.1] [rileyfc:1.8.0] [db:gtc- escherichia coli]
CONTIG5588	4880002_f3_9	2736	16839	1002	334	b0452	108	1.0(10)-9	Escherichia coli	[ui:b0452] [pn:acyl-coa thioesterase ii] [gn:resb] [gcfc:3.1] [ec:3.1.2.-] [keggfc:14.1] [rileyfc:1.8.0] [db:gtc- escherichia coli]
CONTIG5588	21665635_f2_5	2737	16840	291	97	b0452	111	4.2(10)-6	Escherichia coli	[ui:b0452] [pn:acyl-coa thioesterase ii] [gn:resb] [gcfc:3.1] [ec:3.1.2.-] [keggfc:14.1] [rileyfc:1.8.0] [db:gtc- escherichia coli]
CONTIG5669	21756888_c2_24	2738	16841	1143	381	b0452	154	1.2(10)-15	Escherichia coli	[ui:b0452] [pn:acyl-coa thioesterase ii] [gn:resb] [gcfc:3.1] [ec:3.1.2.-] [keggfc:14.1] [rileyfc:1.8.0] [db:gtc- escherichia coli]
CONTIG5059	35806687_c1_8	2739	16842	420	140	b2407	198	6.2(10)-16	Escherichia coli	[ui:b2407] [pn:xanthosine phosphorylase] [gn:xapa.pndal] [gcfc:4.1.5.11] [ec:2.4.2.-] [keggfc:5.11] [rileyfc:1.6.5] [db:gtc- escherichia coli]

CONTIG5560	11955213_c3_15	2744	16847	832	284	b0774	743	1.1(10)-73	Escherichia coli	[ui:b0774] [pn:adenosylmethionine-8-amino-7-oxononanoate aminotransferase:7,8- diamino- pelargonic acid aminotransferase:dapa aminotransferase] [gn:bioa] [gicfc:9.6] [ec:2.6.1.62] [keggfc:9.6] [rileyfc:1.7.1] [db:gtc- escherichia coli]
CONTIG5600	26384652_c1_17	2745	16848	2703	901	b2592	1732	1.7(10)-178	Escherichia coli	[ui:b2592] [pn:clpb protein:heat shock protein 84.1] [gn:clpb:htpm] [gicfc:10.11] [keggfc:14.2] [rileyfc:3.2.3] [db:gtc-escherichia coli]
CONTIG4921	4694052_f3_4	2746	16849	1725	575	b2213	122	1.3(10)-8	Escherichia coli	[ui:b2213] [pn:ada regulatory protein:regulatory protein:regulatory protein of adaptative response:contains:methylated-dna-- protein-cysteine methyltransferase:o-6- methylguanine-dna alkyltransferase] [gn:ada] [gicfc:10.8] [ec:2.1.1.63]
CONTIG5387	20364175_c1_14	2747	16850	561	187	b2213	251	1.5(10)-21	Escherichia coli	[ui:b2213] [pn:ada regulatory protein:regulatory protein:regulatory protein of adaptative response:contains:methylated-dna-- protein-cysteine methyltransferase:o-6- methylguanine-dna alkyltransferase] [gn:ada] [gicfc:10.8] [ec:2.1.1.63]

CONTIG4535	5901965_f1_1	2748	16851	1704	568	b3741	1082	1.3(10)-109	Escherichia coli	[ui:b3741] [pn:glucose inhibited division protein:glucose inhibited division protein a] [gn:gida] [gctc:10.8] [keggfc:14.2] [rileyfc:3.1.7] [db:gtc-escherichia coli]
CONTIG2974	29554062_f2_4	2749	16852	666	222	b2156	259	8.8(10)-22	Escherichia coli	[ui:b2156] [pn:lysine-specific permease] [gn:lysp:cad] [gctc:12.1] [keggfc:14.2] [rileyfc:4.1.1] [db:gtc-escherichia coli]
CONTIG2974	35189040_f3_6	2750	16853	597	199	b2156	254	3.1(10)-21	Escherichia coli	[ui:b2156] [pn:lysine-specific permease] [gn:lysp:cad] [gctc:12.1] [keggfc:14.2] [rileyfc:4.1.1] [db:gtc-escherichia coli]
CONTIG5319	34387_c1_7	2751	16854	243	81	b4031	114	5.0(10)-6	Escherichia coli	[ui:b4031] [pn:xylose-proton symport:xylose transporter] [gn:xyie] [gctc:12.2] [keggfc:14.2] [rileyfc:4.1.3] [db:gtc-escherichia coli]
CONTIG3369	12925062_f1_1	2752	16855	264	88	b3849	91	0.00129	Escherichia coli	[ui:b3849] [pn:trkh] [gctc:12.5] [keggfc:14.2] [rileyfc:4.1.2] [db:gtc-escherichia coli]
b9x1247.y	26284428_c2_9	2753	16856	498	166	b1158	230	2.5(10)-19	Escherichia coli	[ui:b1158] [pn:dna-invertase pin:dna-invertase] [gn:pin] [gctc:13.1] [keggfc:14.2] [rileyfc:5.1.0] [db:gtc-escherichia coli]
CONTIG1700	4328557_f1_1	2754	16857	630	210	b0156	90	0.00017	Escherichia coli	[ui:b0156] [pn:hypothetical 12.1 kd protein in heml-pfs intergenic region] [gn:yadr] [gctc:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gtc-escherichia coli]

CONTIG4907	5371099_c1_7	2755	16858	444	148	b0368	153	8.1(10)-11	Escherichia coli	[ui:b0368] [pn:hypothetical protein:probable taurine catabolism dioxygenase:sulfate starvation-induced protein 3:ssi3] [gn:taud:ssid] [gctc:14.1] [ec:1.-.-] [keggfc:14.1] [rileyfc:5.7.0] [db:gic-escherichia coli]
CONTIG5567	23992328_f2_6	2756	16859	840	280	b0489	251	1.5(10)-21	Escherichia coli	[ui:b0489] [pn:hypothetical protein:hypothetical 33.7 kd protein in usha-tesa intergenic region] [gn:ybbk] [gctc:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gic-escherichia coli]
CONTIG4609	33781579_c2_12	2757	16860	366	122	b0686	99	6.9(10)-5	Escherichia coli	[ui:b0686] [pn:hypothetical protein] [gctc:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gic-escherichia coli]
CONTIG5221	14316656_f3_11	2758	16861	1068	356	b0821	244	5.5(10)-19	Escherichia coli	[ui:b0821] [pn:hypothetical protein] [gctc:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gic-escherichia coli]
CONTIG5221	26197177_f1_2	2759	16862	573	191	b0821	139	1.5(10)-8	Escherichia coli	[ui:b0821] [pn:hypothetical protein] [gctc:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gic-escherichia coli]
CONTIG4368	35445263_c2_6	2760	16863	699	233	b0838	157	1.3(10)-11	Escherichia coli	[ui:b0838] [pn:hypothetical protein] [gctc:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gic-escherichia coli]
CONTIG4011	29475724_c1_3	2761	16864	1503	501	b1045	276	1.3(10)-23	Escherichia coli	[ui:b1045] [pn:hypothetical protein] [gctc:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gic-escherichia coli]

CONTIG3953	22454827_f2_3	2762	16865	921	307	b1120	210	2.0(10)-28	Escherichia coli	[ui:b1120] [pn:hypothetical protein] [gcf:14.1] [keggf:14.2] [rleyf:5.7.0] [db:glc-escherichia coli]
CONTIG5552	2126680_c3_18	2763	16866	1299	433	b1133	633	5.0(10)-62	Escherichia coli	[ui:b1133] [pn:hypothetical protein in purb 5' region:hypothetical 42.6 kd protein in purb-icda intergenic region:orf-15] [gn:yctb] [gcf:14.1] [keggf:14.2] [rleyf:5.7.0] [db:glc-escherichia coli]
CONTIG5552	20320152_f3_10	2764	16867	762	254	b1180	315	2.5(10)-28	Escherichia coli	[ui:b1180] [pn:hypothetical protein] [gcf:14.1] [keggf:14.2] [rleyf:5.7.0] [db:glc-escherichia coli]
CONTIG3219	979812_c3_7	2765	16868	384	128	b1203	252	1.2(10)-21	Escherichia coli	[ui:b1203] [pn:hypothetical gtp-binding protein in pth 3" region:probable gtp-binding protein in urea-pth intergenic region:orf-3] [gn:yctf:gtp1] [gcf:14.1] [keggf:14.2] [rleyf:5.7.0] [db:glc-escherichia coli]
CONTIG5786	24807805_c3_34	2766	16869	1278	426	b1680	149	1.3(10)-7	Escherichia coli	[ui:b1680] [pn:hypothetical protein] [gcf:14.1] [keggf:14.2] [rleyf:5.7.0] [db:glc-escherichia coli]
CONTIG4264	2429075_c1_5	2767	16870	1749	583	b1706	296	5.5(10)-44	Escherichia coli	[ui:b1706] [pn:hypothetical protein] [gcf:14.1] [keggf:14.2] [rleyf:5.7.0] [db:glc-escherichia coli]

CONTIG5307	4804587_c2_9	2768	16871	696	232	b1768	204	2.1(10)-32	Escherichia coli	[ui:b1768] [pn:hypothetical 23.4 kd protein in ansa 3"region] [gn:ydb] [gtcf:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gtc-escherichia coli]
CONTIG4649	4100307_c3_9	2769	16872	729	243	b1802	287	2.2(10)-25	Escherichia coli	[ui:b1802] [pn:hypothetical protein] [gtcf:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gtc-escherichia coli]
CONTIG5804	3912761_c3_62	2770	16873	681	227	b1802	91	0.08899	Escherichia coli	[ui:b1802] [pn:hypothetical protein] [gtcf:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gtc-escherichia coli]
CONTIG2979	10179037_f2_4	2771	16874	561	187	b1864	235	7.5(10)-20	Escherichia coli	[ui:b1864] [pn:hypothetical 26.4 kd protein in ruvc-asps intergenic region] [gn:yebc] [gtcf:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gtc-escherichia coli]
CONTIG5587	20423312_c2_22	2772	16875	600	200	b1970	115	3.8(10)-7	Escherichia coli	[ui:b1970] [pn:hypothetical protein] [gtcf:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gtc-escherichia coli]
CONTIG1954	11172650_f2_2	2773	16876	600	200	b2086	90	0.068	Escherichia coli	[ui:b2086] [pn:hypothetical protein:hypothetical 32.0 kd protein in ogrk-gatr intergenic region] [gn:yegs] [gtcf:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gtc-escherichia coli]
CONTIG5772	31250050_c2_34	2774	16877	954	318	b2165	680	5.2(10)-67	Escherichia coli	[ui:b2165] [pn:hypothetical 32.9 kd protein in nfo-trua intergenic region] [gn:yein] [gtcf:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gtc-escherichia coli]

CONTIG5772	15839713_c3_41	2775	16878	1068	356	b2166	165	4.9(10)-12	Escherichia coli	[ui:b2166] [pn:hypothetical 33.6 kd protein in nfo-frua intergenic region] [gn:yeic] [gctc:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gic-escherichia coli]
CONTIG712	23550942_13_2	2776	16879	558	186	b2302	233	1.2(10)-19	Escherichia coli	[ui:b2302] [pn:hypothetical protein:hypothetical 24.5 kd protein in pla-folx intergenic region] [gn:yfeg] [gctc:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gic-escherichia coli]
CONTIG3649	11929704_c1_5	2777	16880	723	241	b2374	116	0.0002	Escherichia coli	[ui:b2374] [pn:hypothetical protein] [gctc:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gic-escherichia coli]
CONTIG5682	803825_c2_23	2778	16881	1065	355	b2426	224	1.1(10)-18	Escherichia coli	[ui:b2426] [pn:hypothetical protein in cyp 5"region:oxidoreductase ucpa] [gn:yfct:ucpa] [gctc:14.1] [ec:1.-.-.] [keggfc:14.1] [rileyfc:5.7.0] [db:gic-escherichia coli]
b9x12u56.x	29416408_f2_1	2779	16882	564	188	b2430	108	0.00079	Escherichia coli	[ui:b2430] [pn:hypothetical protein] [gctc:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gic-escherichia coli]
CONTIG1270	4770427_c2_8	2780	16883	621	207	b2545	198	1.8(10)-15	Escherichia coli	[ui:b2545] [pn:hypothetical protein] [gctc:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gic-escherichia coli]
b9x11160.x	5447303_f1_1	2781	16884	549	183	b2627	772	9.3(10)-77	Escherichia coli	[ui:b2627] [pn:hypothetical protein:hypothetical 83.1 kd protein in alpa-gabd intergenic region:1729] [gn:yfjk] [gctc:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gic-escherichia coli]

b9x11160.x	14572755_f2_3	2782	16885	399	133	b2627	318	1.1(10)-27	Escherichia coli	[ui:b2627] [pn:hypothetical protein: hypothetical 83.1 kd protein in alpa-gabp intergenic region: f729] [gn:yfk] [gctc:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gic-escherichia coli]
CONTIG4008	21484383_f3_5	2783	16886	639	213	b2660	159	5.7(10)-11	Escherichia coli	[ui:b2660] [pn:hypothetical protein in gapb 3"region: hypothetical 48.6 kd protein in alpa-gabp intergenic region] [gn:yga] [gctc:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gic-escherichia coli]
CONTIG4114	30504076_c2_5	2784	16887	528	176	b2666	98	2.5(10)-5	Escherichia coli	[ui:b2666] [pn:hypothetical protein] [gctc:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gic-escherichia coli]
CONTIG2751	26195262_f2_3	2785	16888	318	106	b2666	125	3.3(10)-8	Escherichia coli	[ui:b2666] [pn:hypothetical protein] [gctc:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gic-escherichia coli]
CONTIG1536	26172806_c1_2	2786	16889	942	314	b2883	178	1.3(10)-21	Escherichia coli	[ui:b2883] [pn:hypothetical protein] [gctc:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gic-escherichia coli]
CONTIG4759	9773275_f3_8	2787	16890	747	249	b2928	197	7.9(10)-16	Escherichia coli	[ui:b2928] [pn:hypothetical 27.1 kd protein in gapb-cmta intergenic region: hypothetical 27.1 kd protein in epd-cmta intergenic region:orf 3: f237] [gn:yggc] [gctc:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gic-escherichia coli]

CONTIG3163	5281562_f1_1	2788	16891	423	141	b3102	255	5.7(10)-22	Escherichia coli	[ui:b3102] [pn:hypothetical 37.4 kd protein in exur-tdec intergenic region:o328] [gn:yqjg] [gicfc:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gic-escherichia coli]
CONTIG3163	32070907_f3_3	2789	16892	636	212	b3102	466	2.5(10)-44	Escherichia coli	[ui:b3102] [pn:hypothetical 37.4 kd protein in exur-tdec intergenic region:o328] [gn:yqjg] [gicfc:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gic-escherichia coli]
CONTIG5427	5194430_c1_18	2790	16893	531	177	b3152	196	1.0(10)-15	Escherichia coli	[ui:b3152] [pn:hypothetical 24.8 kd protein in agai-mtr intergenic region:t226] [gn:yrar] [gicfc:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gic-escherichia coli]
CONTIG4150	1992151_f3_7	2791	16894	363	121	b3190	99	1.8(10)-5	Escherichia coli	[ui:b3190] [pn:hypothetical 9.5 kd protein in murz-rpon intergenic region] [gn:yrba] [gicfc:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gic-escherichia coli]
CONTIG2380	12166461_f2_1	2792	16895	1233	411	b3232	184	1.2(10)-13	Escherichia coli	[ui:b3232] [pn:hypothetical 43.1 kd protein in rplm-rhoa intergenic region:t375] [gn:yhcm] [gicfc:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gic-escherichia coli]
b2x17123.y	3956967_f1_1	2793	16896	513	171	b3232	142	1.5(10)-14	Escherichia coli	[ui:b3232] [pn:hypothetical 43.1 kd protein in rplm-rhoa intergenic region:t375] [gn:yhcm] [gicfc:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gic-escherichia coli]

CONTIG2301	9957660_f2_2	2794	16897	660	220	b3248	172	3.5(10)-13	Escherichia coli	[ui:b3248] [pn:hypothetical 21.5 kd protein in catA-mred intergenic region:orf2] [gn:yhde] [gctc:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gtc-escherichia coli]
b4x10264.y	29474001_f2_1	2795	16898	609	203	b3654	309	1.3(10)-27	Escherichia coli	[ui:b3654] [pn:hypothetical 48.9 kd protein in glis 3"region:hypothetical 48.9 kd protein in glis-selc intergenic region] [gn:yice] [gctc:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gtc-escherichia coli]
CONTIG1347	25588577_f2_1	2796	16899	327	109	b3676	95	5.0(10)-5	Escherichia coli	[ui:b3676] [pn:hypothetical 12.8 kd protein in ivb1-ibpb intergenic region:hypothetical 12.8 kd protein in emrd-glyg intergenic region] [gn:yidh] [gctc:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gtc-escherichia coli]
CONTIG5666	10945130_f3_7	2797	16900	465	155	b4056	329	8.1(10)-30	Escherichia coli	[ui:b4056] [pn:hypothetical 15.7 kd protein in tyrb-uvra intergenic region:hypothetical 15.7 kd protein in alpha-uvra intergenic region:oi38] [gn:yibq] [gctc:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gtc-escherichia coli]
CONTIG5808	14454062_f1_4	2798	16901	1062	354	b0651	373	1.8(10)-34	Escherichia coli	[ui:b0651] [pn:hypothetical 33.8 kd protein in leus-gli intergenic region] [gn:ybek] [gctc:14.2] [keggfc:14.2] [rileyfc:5.9.0] [db:gtc-escherichia coli]

CONTIG2954	4301532_c1_6	2799	16902	708	236	b1539	325	2.2(10)-29	Escherichia coli	[ui:b1539] [pn:hyposhical oxidoreductase in dep-noha intergenic region] [gn:ydfg] [gctc:14.2] [ec:1.-.-.] [keggfc:14.1] [rileyfc:5.9.0] [db:gic-escherichia coli]
CONTIG69	4301532_c3_1	2800	16903	630	210	b1539	284	4.7(10)-25	Escherichia coli	[ui:b1539] [pn:hyposhical oxidoreductase in dep-noha intergenic region] [gn:ydfg] [gctc:14.2] [ec:1.-.-.] [keggfc:14.1] [rileyfc:5.9.0] [db:gic-escherichia coli]
b2x15517.y	33243942_f2_1	2801	16904	540	180	b2184	151	6.7(10)-10	Escherichia coli	[ui:b2184] [pn:hyposhical 66.4 kd protein in rsua-rpy intergenic region] [gn:yeh] [gctc:14.2] [keggfc:14.2] [rileyfc:5.9.0] [db:gic-escherichia coli]
CONTIG5796	10348161_f1_6	2802	16905	1095	365	b3039	130	4.5(10)-6	Escherichia coli	[ui:b3039] [pn:hyposhical 29.9 kd protein in tolc-ribb intergenic region:orf:1271] [gn:ygid] [gctc:14.2] [keggfc:14.2] [rileyfc:5.9.0] [db:gic-escherichia coli]
CONTIG1787	15656875_f1_1	2803	16906	357	119	b0036	112	3.5(10)-6	Escherichia coli	[ui:b0036] [pn:carnitine racemase] [gn:caid] [gctc:9.13] [ec:5.-.-.] [keggfc:14.1] [rileyfc:5.8.0] [db:gic-escherichia coli]
CONTIG2965	7032092_c3_5	2804	16907	699	233	b0256	94	0.04599	Escherichia coli	[ui:b0256] [pn:transposase for insertion sequence element is30] [gn:tra8_1] [gctc:13.5] [keggfc:14.2] [rileyfc:5.8.0] [db:gic-escherichia coli]

CONTIG2046	23457035_f2_2	2805	16908	333	111	b0890	90	0.00619	Escherichia coli	[ui:b0890] [pn:cell division protein ftsk] [gn:ftsks] [gtrfc:12.8] [keggc:14.2] [rileyfc:5.8.0] [db:gtrfc:escherichia coli]
CONTIG5554	12672811_f2_7	2806	16909	888	296	HI0611	191	3.3(10)-15	Haemophilus influenzae	[ui:hi0611] [pn:fuculose-1-phosphate aldolase:l-fuculose phosphate aldolase] [gn:fucal] [gtrfc:1.4:1.8:7.1] [ec:4.1.2.17] [keggc:1.8] [tigrfc:6.12] [db:gtrfc-haemophilus influenzae]
CONTIG5605	19957807_f1_1	2807	16910	684	228	HI0611	152	2.6(10)-10	Haemophilus influenzae	[ui:hi0611] [pn:fuculose-1-phosphate aldolase:l-fuculose phosphate aldolase] [gn:fucal] [gtrfc:1.4:1.8:7.1] [ec:4.1.2.17] [keggc:1.8] [tigrfc:6.12] [db:gtrfc-haemophilus influenzae]
CONTIG5488	1209433_c1_11	2808	16911	1068	356	HI0193	223	4.9(10)-24	Haemophilus influenzae	[ui:hi0193] [pn:dhv-drolipoamide acetyltransferase] [gn:acoc] [gtrfc:1.8] [keggc:14.2] [tigrfc:6.11] [db:gtrfc-haemophilus influenzae]
CONTIG4812	1955078_f3_3	2809	16912	711	237	HI0155	271	1.1(10)-23	Haemophilus influenzae	[ui:hi0155] [pn:3-ketoacyl-acyl carrier protein reductase:3-oxoacyl-acyl-carrier protein reductase] [gn:fabg] [gtrfc:3.1.3.2] [ec:1.1.1.100] [keggc:3.1] [tigrfc:7.1] [db:gtrfc-haemophilus influenzae]
CONTIG5669	4472010_c1_19	2810	16913	909	303	HI0076	187	4.2(10)-13	Haemophilus influenzae	[ui:hi0076] [pn:acyl-coa thioesterase ii] [gn:tesb] [gtrfc:3.1.3.2] [ec:3.1.2.-] [keggc:14.1] [tigrfc:7.1] [db:gtrfc-haemophilus influenzae]

CONTIG4600	29312556_c3_5	2811	16914	1863	621	HI0748	243	4.2(10)-17	Haemophilus influenzae	[ui:hi0748] [pn:glycerol-3-phosphate acyltransferase] [gn:pls] [gic:3.1.3.2.8.1] [ec:2.3.1.15] [kegg:8.1] [tigr:7.1] [db:gc-haemophilus influenzae]
CONTIG5068	23867137_c1_8	2812	16915	270	90	HI1277	173	1.3(10)-12	Haemophilus influenzae	[ui:hi1277] [pn:putative apase:mrp:protein homolog] [gn:mrp] [gic:4.4] [kegg:14.2] [tigr:8.5] [db:gc-haemophilus influenzae]
CONTIG5316	7070278_f1_3	2813	16916	447	149	HI0970	347	1.0(10)-31	Haemophilus influenzae	[ui:hi0970] [pn:3-dehydroquinate dehydratase:3-dehydroquinate] [gn:aroq] [gic:5.15] [ec:4.2.1.10] [kegg:5.15] [tigr:1.1] [db:gc-haemophilus influenzae]
CONTIG4751	1427_f1_1	2814	16917	1335	445	HI0140	373	1.8(10)-34	Haemophilus influenzae	[ui:hi0140] [pn:n-acetylglucosamine-6-phosphate deacetylase] [gn:naga] [gic:7.1] [ec:3.5.1.25] [kegg:4.4] [tigr:5.1] [db:gc-haemophilus influenzae]
CONTIG5682	22851702_c2_24	2815	16918	873	291	HI0645	172	4.7(10)-11	Haemophilus influenzae	[ui:hi0645] [pn:lysophospholipase 12:probable lysophospholipase 12:lecithinase b] [gn:pldb] [gic:8.4:13.10] [ec:3.1.1.5] [kegg:8.4] [tigr:5.3] [db:gc-haemophilus influenzae]

CONTIG3550	6273399_c1_2	2816	16919	642	214	HI1559	122	1.3(10)-5	Haemophilus influenzae	[ui:h1559] [pn:protoporphyrinogen oxidase:possible protoporphyrinogen oxidase] [gn:henk] [gtcf:9.10] [ec:1.3.3.-] [kegfc:14.1] [tigrfc:2.3] [db:gtc- haemophilus influenzae]
CONTIG3548	157305_f2_5	2817	16920	438	146	HI0892	168	5.4(10)-12	Haemophilus influenzae	[ui:h0892] [pn:atp-dependent rna helicase:atp-dependent rna helicase homolog] [gn:rhb] [gtcf:10.2] [kegfc:14.2] [tigrfc:1.2] [db:gtc- haemophilus influenzae]
CONTIG2918	36330092_c2_4	2818	16921	1221	407	HI0588	478	1.3(10)-45	Haemophilus influenzae	[ui:h0588] [pn:n-carbamyl-l-amino acid amidohydrolase] [gtcf:5.16] [kegfc:14.2] [tigrfc:14.7] [db:gtc- haemophilus influenzae]
CONTIG4823	1282542_f3_2	2819	16922	408	136	HI0163	151	5.9(10)-11	Haemophilus influenzae	[ui:h0163] [pn:putative murein gene regulator:protein homolog] [gn:bola] [gtcf:12.13] [kegfc:14.2] [tigrfc:9.1] [db:gtc- haemophilus influenzae]
b2x15627.y	13712825_c3_4	2820	16923	210	70	HI0060	115	5.0(10)-6	Haemophilus influenzae	[ui:h0060] [pn:atp dependent translocator homolog:msba:probable transport atp-binding protein msba] [gn:msba:msb-1] [gtcf:12.6] [kegfc:14.2] [tigrfc:13.6] [db:gtc- haemophilus influenzae]
CONTIG5677	23850785_c1_21	2821	16924	969	323	HI1238	113	0.00059	Haemophilus influenzae	[ui:h1238] [pn:heat shock protein:protein] [gn:dnaj] [gtcf:12.7] [kegfc:14.2] [tigrfc:4.3] [db:gtc-haemophilus influenzae]

CONTIG1252	866433_c3_4	2822	16925	699	233	HI1374	101	0.035	Haemophilus influenzae	[ui:hi1374] [pn:cell division protein:cell division protein homolog] [gn:mukb] [gcf:12.8] [kegfc:14.2] [tigrfc:4.1] [db:gtc-haemophilus influenzae]
CONTIG5771	20755077_c1_27	2823	16926	372	124	HI0798B	115	3.8(10)-7	Haemophilus influenzae	[ui:hi0798b] [pn:50s ribosomal protein 136] [gn:rpni:rp136] [gcf:10.4] [kegfc:14.2] [db:gtc-haemophilus influenzae]
CONTIG3608	4031700_c3_11	2824	16927	609	203	HI0572	211	2.6(10)-17	Haemophilus influenzae	[ui:hi0572] [pn:sp:p37687:hypothetical protein] [gn:hin1693] [gcf:14.1] [kegfc:14.2] [tigrfc:15.1] [db:gtc-haemophilus influenzae]
CONTIG3947	3906303_f2_3	2825	16928	1530	510	HI1298	138	4.5(10)-7	Haemophilus influenzae	[ui:hi1298] [pn:sp:p33373:hypothetical protein] [gcf:14.1] [kegfc:14.2] [tigrfc:15.1] [db:gtc-haemophilus influenzae]
CONTIG1443	14569012_f2_1	2826	16929	912	304	HI1590	308	1.3(10)-27	Haemophilus influenzae	[ui:hi1590] [pn:gb:x75627_4:hypothetical protein] [gcf:14.1] [kegfc:14.2] [tigrfc:15.1] [db:gtc-haemophilus influenzae]
b3x16673.y	25422259_c2_2	2827	16930	384	128	HI1612	116	2.7(10)-6	Haemophilus influenzae	[ui:hi1612] [pn:sp:p37340:hypothetical protein] [gcf:14.1] [kegfc:14.2] [tigrfc:15.1] [db:gtc-haemophilus influenzae]

CONTIG3337	4772216_c3_4	2828	16931	774	258	HP1155	112	0.00022	Helicobacter pylori	[ui:hp1155] [pn:transferase, peptidoglycan synthesis] [gn:murg] [gicf:1.5:7.1:8.5:11.3:11.4] [ec:2.4.1.-] [keggf:1.5:7.2:7.3:8.5] [tigrf:3.2] [db:gic-helicobacter pylori]
CONTIG3492	970305_f2_4	2829	16932	615	205	HP1261	357	8.8(10)-33	Helicobacter pylori	[ui:hp1261] [pn:nadh-ubiquinone oxidoreductase, subunit:nadh-ubiquinone oxidoreductase, ngq6 subunit] [gn:ngq6] [gicf:2.1:9.12] [ec:1.6.5.3] [keggf:2.1:9.13] [tigrf:6.1] [db:gic-helicobacter pylori]
CONTIG5759	4960962_f2_9	2830	16933	450	150	HP1263	173	1.3(10)-12	Helicobacter pylori	[ui:hp1263] [pn:nadh-ubiquinone oxidoreductase, subunit:nadh-ubiquinone oxidoreductase, ngq4 subunit] [gn:ngq4] [gicf:2.1:9.12] [ec:1.6.5.3] [keggf:2.1:9.13] [tigrf:6.1] [db:gic-helicobacter pylori]
CONTIG5820	32064012_f3_59	2831	16934	372	124	HP1272	116	3.2(10)-6	Helicobacter pylori	[ui:hp1272] [pn:nadh-ubiquinone oxidoreductase, subunit:nadh-ubiquinone oxidoreductase, ngq13 subunit] [gn:ngq13] [gicf:2.1:9.12] [ec:1.6.5.3] [keggf:2.1:9.13] [tigrf:6.1] [db:gic-helicobacter pylori]
CONTIG5820	788552_f3_53	2832	16935	291	97	HP1273	91	0.0015	Helicobacter pylori	[ui:hp1273] [pn:nadh-ubiquinone oxidoreductase, subunit:nadh-ubiquinone oxidoreductase, ngq14 subunit] [gn:ngq14] [gicf:2.1:9.12] [ec:1.6.5.3] [keggf:2.1:9.13] [tigrf:6.1] [db:gic-helicobacter pylori]

CONTIG5820	6672680_f3_55	2833	16936	381	127	HP1273	103	7.5(10)-5	Helicobacter pylori	[ui:hp1273] [pn:nadh-ubiquinone oxidoreductase, subunit:nadh-ubiquinone oxidoreductase, nqo14 subunit] [gn:nqo14] [gtcf:2.1.9.12] [ec:1.6.5.3] [keggfc:2.1.9.13] [tigrfc:6.1] [db:gtc-helicobacter pylori]
CONTIG5805	38177_c2_30	2834	16937	1560	520	HP0416	361	3.2(10)-33	Helicobacter pylori	[ui:hp0416] [pn:cyclopropane fatty acid synthase] [gn:cia] [gtcf:3.1.3.2.8.1] [ec:2.1.1.79] [keggfc:14.1] [tigrfc:7.1] [db:gtc-helicobacter pylori]
CONTIG3544	14534556_c2_8	2835	16938	537	179	HP0171	146	1.0(10)-9	Helicobacter pylori	[ui:hp0171] [pn:peptide chain release factor rf-2] [gn:prfb] [gtcf:10.7] [keggfc:14.2] [tigrfc:12.8] [db:gtc-helicobacter pylori]
CONTIG2099	24812790_f2_1	2836	16939	717	239	HP0247	142	2.2(10)-7	Helicobacter pylori	[ui:hp0247] [pn:atp-dependent rna helicase, dead-box family] [gn:dead] [gtcf:10.7] [keggfc:14.2] [tigrfc:12.8] [db:gtc-helicobacter pylori]
CONTIG5594	23525277_f1_3	2837	16940	726	242	HP0701	108	0.0035	Helicobacter pylori	[ui:hp0701] [pn:dna gyrase, sub a gyra:dna gyrase subunit a] [gn:gyra] [gtcf:10.8] [ec:5.99.1.3] [keggfc:14.1] [tigrfc:10.2] [db:gtc-helicobacter pylori]
CONTIG1082	234436_c3_3	2838	16941	1113	371	HP1403	91	0.48999	Helicobacter pylori	[ui:hp1403] [pn:tyrosine restriction enzyme m protein] [gn:hndm] [gtcf:10.8] [keggfc:14.2] [tigrfc:10.2] [db:gtc-helicobacter pylori]

CONTIG3810	21515925_f1_2	2839	16942	1026	342	HP1429	253	9.1(10)-22	Helicobacter pylori	[ui:hp1429] [pn:polysialic acid capsule expression protein] [gn:kpsf] [gncf:11.3] [keggcf:14.2] [tigrfc:3.3] [db:gtc-helicobacter pylori]
CONTIG4735	24015962_f3_3	2840	16943	756	252	HP0244	100	0.01299	Helicobacter pylori	[ui:hp0244] [pn:signal-transducing protein, histidine kinase] [gn:atos] [gncf:12.13] [keggcf:14.2] [tigrfc:9.1] [db:gtc-helicobacter pylori]
CONTIG5519	14547217_c3_9	2841	16944	1908	636	HP0600	92	0.4	Helicobacter pylori	[ui:hp0600] [pn:multidrug resistance protein] [gn:spab] [gncf:12.6] [keggcf:14.2] [tigrfc:13.1] [db:gtc-helicobacter pylori]
CONTIG5406	10007752_f3_5	2842	16945	1101	367	HP0082	91	0.37	Helicobacter pylori	[ui:hp0082] [pn:methyl-accepting chemotaxis transducer] [gn:tlpc] [gncf:12.9] [keggcf:14.2] [tigrfc:4.1] [db:gtc-helicobacter pylori]
CONTIG5096	4381577_c2_10	2843	16946	849	283	HP0392	101	0.012	Helicobacter pylori	[ui:hp0392] [pn:histidine kinase chea:histidine kinase] [gn:chea] [gncf:12.9] [cc:2.7.3.-] [keggcf:14.1] [tigrfc:4.1] [db:gtc-helicobacter pylori]
CONTIG726	4978942_f1_1	2844	16947	642	214	HP0059	100	0.00519	Helicobacter pylori	[ui:hp0059] [pn:h] [gncf:14.1:14.2] [keggcf:14.2] [db:gtc-helicobacter pylori]
CONTIG3233	22343915_c1_4	2845	16948	432	144	HP0207	208	2.1(10)-16	Helicobacter pylori	[ui:hp0207] [pn:atp-binding protein:mpf] [gncf:14.1:14.2] [keggcf:14.2] [db:gtc-helicobacter pylori]
CONTIG4026	10048388_f1_1	2846	16949	1125	375	HP0479	91	0.13	Helicobacter pylori	[ui:hp0479] [pn:h] [gncf:14.1:14.2] [keggcf:14.2] [db:gtc-helicobacter pylori]

CONTIG2852	19720063_c1_3	2847	16950	1569	523	HP0880	98	0.0014	Helicobacter pylori	[ui:hp0880] [pn:h] [gctc:14.1:14.2] [keggfc:14.2] [db-gtc-helicobacter pylori]
CONTIG1918	31281693_c3_4	2848	16951	981	327	HP1142	92	0.22	Helicobacter pylori	[ui:hp1142] [pn:h] [gctc:14.1:14.2] [keggfc:14.2] [db-gtc-helicobacter pylori]
CONTIG2319	2741577_f3_1	2849	16952	417	139	HP1142	90	0.0033	Helicobacter pylori	[ui:hp1142] [pn:h] [gctc:14.1:14.2] [keggfc:14.2] [db-gtc-helicobacter pylori]
CONTIG3408	22725327_f2_5	2850	16953	597	199	HP1117	127	5.7(10)-7	Helicobacter pylori	[ui:hp1117] [pn:conserved hypothetical secreted protein] [gctc:14.1] [keggfc:14.2] [tigrfc:15.1] [db-gtc-helicobacter pylori]
CONTIG3192	24649077_f1_1	2851	16954	1191	397	HP1117	145	5.5(10)-8	Helicobacter pylori	[ui:hp1117] [pn:conserved hypothetical secreted protein] [gctc:14.1] [keggfc:14.2] [tigrfc:15.1] [db-gtc-helicobacter pylori]
CONTIG5491	25579711_f2_1	2852	16955	594	198	MG355	95	0.05999	Mycoplasma genitalium	[ui:mg355] [pn:atp-dependent protease binding subunit:protein] [gn:clpb] [gctc:10.11] [keggfc:14.2] [tigrfc:12.3] [db-gtc-mycoplasma genitalium]
CONTIG5294	14664026_f1_1	2853	16956	807	269	MG435	182	3.1(10)-14	Mycoplasma genitalium	[ui:mg435] [pn:ribosome recycling factor:ribosome releasing factor:rtf] [gn:frt] [gctc:10.7] [keggfc:14.2] [tigrfc:12.4] [db-gtc-mycoplasma genitalium]
CONTIG4749	6337916_c1_6	2854	16957	906	302	MG386	109	0.008	Mycoplasma genitalium	[ui:mg386] [pn:cytadherence-accessory protein:hmw1] [gctc:11.3] [keggfc:14.2] [tigrfc:3.4] [db-gtc-mycoplasma genitalium]

CONTIG4889	33320277_f1_1	2855	16958	936	312	MG002	142	1.8(10)-7	Mycoplasma genitalium	[ui:mg002] [pn:heat shock protein:dna:dna]-like protein mg002] [gtcf:12.7] [kegfc:14.2] [tigrfc:4.3] [db:gtc-mycoplasma genitalium]
CONTIG5280	4197137_f1_2	2856	16959	597	199	MG019	144	1.8(10)-9	Mycoplasma genitalium	[ui:mg019] [pn:heat shock protein:protein] [gn:dna] [gtcf:12.7] [kegfc:14.2] [tigrfc:4.3] [db:gtc-mycoplasma genitalium]
CONTIG4205	581252_c2_6	2857	16960	981	327	MG218	130	7.2(10)-5	Mycoplasma genitalium	[ui:mg218] [pn:hyposhethical protein mg218] [gtcf:14.1:14.2] [kegfc:14.2] [db:gtc-mycoplasma genitalium]
b2x17609.y	2773313_c2_2	2858	16961	861	287	MG397	95	0.099	Mycoplasma genitalium	[ui:mg397] [pn:hyposhethical protein mg397] [gtcf:14.1:14.2] [kegfc:14.2] [db:gtc-mycoplasma genitalium]
CONTIG5283	24486437_f2_1	2859	16962	615	205	MG148	95	0.01499	Mycoplasma genitalium	[ui:mg148] [pn:hyposhethical protein:gb:118965_6:hyposhethical protein mg148] [gtcf:14.1] [kegfc:14.2] [tigrfc:15.1] [db:gtc-mycoplasma genitalium]
CONTIG5678	10728160_c1_11	2860	16963	975	325	MG280	95	0.02999	Mycoplasma genitalium	[ui:mg280] [pn:sensory rhodopsin ii transducer:htr:hyposhethical protein mg280] [gtcf:14.3] [kegfc:14.2] [tigrfc:14.2] [db:gtc-mycoplasma genitalium]
CONTIG5801	6923161_c1_34	2861	16964	672	224	MG328	102	0.014	Mycoplasma genitalium	[ui:mg328] [pn:protein v] [gn:fcv] [gtcf:14.3] [kegfc:14.2] [tigrfc:14.2] [db:gtc-mycoplasma genitalium]

CONTIG4858	23832787_f2_1	2862	16965	624	208	MJ10001	193	7.0(10)-15	Methanococcus jannaschii	[ui:mj0001] [pn:aspartate amino transferase:aspl:probable aspartate amino transferase:transaminase a:aspl] [gicf:2.4:5.1:5.10:5.15:5.2:5.5] [ec:2.6.1.1] [keggf:2.3:5.1:5.2:5.5:5.10:5.15] [tigrf:1.3] [db:gic-methanococcus jannaschii]
CONTIG5062	9775636_f1_3	2863	16966	867	289	MJ1575	97	0.0063	Methanococcus jannaschii	[ui:mj1575] [pn:gmp synthase:guaa:gmp synthetase] [gicf:4.1:5.1] [ec:6.3.5.2] [keggf:4.1:5.1] [tigrf:8.3] [db:gic- methanococcus jannaschii]
CONTIG2795	4473261_c1_6	2864	16967	615	205	MJ0174	187	2.5(10)-14	Methanococcus jannaschii	[ui:mj0174] [pn:cell division protein pelota:pela:cell division protein] [gicf:12.8] [keggf:14.2] [tigrf:4.2] [db:gic-methanococcus jannaschii]
CONTIG5295	34064518_c3_12	2865	16968	2103	701	MJ1156	1346	1.3(10)-137	Methanococcus jannaschii	[ui:mj1156] [pn:cell division control protein 48:cdc48, aaa family:cell division cycle protein 48 homolog] [gicf:12.8] [keggf:14.2] [tigrf:4.2] [db:gic-methanococcus jannaschii]
CONTIG903	9798252_f1_1	2866	16969	882	294	MJ1156	652	4.7(10)-64	Methanococcus jannaschii	[ui:mj1156] [pn:cell division control protein 48:cdc48, aaa family:cell division cycle protein 48 homolog] [gicf:12.8] [keggf:14.2] [tigrf:4.2] [db:gic-methanococcus jannaschii]

CONTIG2194	22437812_c3_5	2867	16970	549	183	MJ1643	102	0.01299	Methanococcus jannaschii	[ui:mj1643] [pn:chromosome segregation protein:smc1.p115 protein] [gicfc:12.8] [kegfc:14.2] [tigrfc:4.2] [db:gic-methanococcus jannaschii]
CONTIG4182	11132965_c1_5	2868	16971	1176	392	MJ1643	145	1.3(10)-6	Methanococcus jannaschii	[ui:mj1643] [pn:chromosome segregation protein:smc1.p115 protein] [gicfc:12.8] [kegfc:14.2] [tigrfc:4.2] [db:gic-methanococcus jannaschii]
CONTIG5059	10962750_c1_11	2869	16972	822	274	MJ1643	115	0.0011	Methanococcus jannaschii	[ui:mj1643] [pn:chromosome segregation protein:smc1.p115 protein] [gicfc:12.8] [kegfc:14.2] [tigrfc:4.2] [db:gic-methanococcus jannaschii]
CONTIG5636	10641386_f1_1	2870	16973	3027	1009	MJ0063	97	0.035	Methanococcus jannaschii	[ui:mj0063] [pn:hypothetical protein] [gicfc:14.1] [kegfc:14.2] [tigrfc:15.1] [db:gic-methanococcus jannaschii]
CONTIG1386	29723450_f3_1	2871	16974	948	316	MJ0064	90	0.047	Methanococcus jannaschii	[ui:mj0064] [pn:hypothetical protein] [gicfc:14.1] [kegfc:14.2] [tigrfc:15.1] [db:gic-methanococcus jannaschii]
CONTIG3038	35581503_c2_3	2872	16975	1302	434	MJ0147	95	0.1	Methanococcus jannaschii	[ui:mj0147] [pn:hypothetical protein:hypothetical atp-binding protein] [gicfc:14.1] [kegfc:14.2] [tigrfc:15.1] [db:gic-methanococcus jannaschii]
CONTIG2069	473160_c1_4	2873	16976	450	150	MJ0691	135	2.8(10)-9	Methanococcus jannaschii	[ui:mj0691] [pn:conserved hypothetical protein:m] [gicfc:14.1] [kegfc:14.2] [tigrfc:15.1] [db:gic- methanococcus jannaschii]

CONTIG5738	24656658_c3_16	2874	16977	2091	697	MJ10895	97	0.098	Methanococcus jannaschii	[ui:mj10895] [pn:hypothetical protein:mj] [gtrfc:14.1] [kegtrfc:14.2] [tigrfc:15.1] [db:gtc-methanococcus.jannaschii]
CONTIG132	36072535_c2_4	2875	16978	240	80	MJ1073	108	7.9(10)-6	Methanococcus jannaschii	[ui:mj1073] [pn:conserved hypothetical protein:mj] [gtrfc:14.1] [kegtrfc:14.2] [tigrfc:15.1] [db:gtc-methanococcus.jannaschii]
b2x12825.y	24022655_f2_1	2876	16979	294	98	MJ1136	211	2.0(10)-16	Methanococcus jannaschii	[ui:mj1136] [pn:conserved hypothetical protein:hypothetical protein] [gtrfc:14.1] [kegtrfc:14.2] [tigrfc:15.1] [db:gtc-methanococcus.jannaschii]
CONTIG4469	33438217_c2_8	2877	16980	720	240	MJ1326	461	8.4(10)-44	Methanococcus jannaschii	[ui:mj1326] [pn:gtp-binding protein] [gtrfc:14.1] [kegtrfc:14.2] [tigrfc:15.1] [db:gtc-methanococcus.jannaschii]
CONTIG5130	20117131_f2_5	2878	16981	759	253	MJ1332	512	3.2(10)-49	Methanococcus jannaschii	[ui:mj1332] [pn:gtp-binding protein] [gtrfc:14.1] [kegtrfc:14.2] [tigrfc:15.1] [db:gtc-methanococcus.jannaschii]
CONTIG1055	6339517_f3_2	2879	16982	471	157	MJ1372	144	8.3(10)-10	Methanococcus jannaschii	[ui:mj1372] [pn:conserved hypothetical protein:hypothetical protein] [gtrfc:14.1] [kegtrfc:14.2] [tigrfc:15.1] [db:gtc-methanococcus.jannaschii]
CONTIG4735	6843878_c3_10	2880	16983	705	235	MJ1372	278	2.1(10)-24	Methanococcus jannaschii	[ui:mj1372] [pn:conserved hypothetical protein:hypothetical protein] [gtrfc:14.1] [kegtrfc:14.2] [tigrfc:15.1] [db:gtc-methanococcus.jannaschii]

CONTIG3725	30174007_f3_3	2881	16984	198	66	MJ1432	114	5.0(10)-7	Methanococcus jannaschii	[ui:mj1432] [pn:conserved hypothetical protein] [glcfc:14.1] [keggfc:14.2] [tigrfc:15.1] [db:glc-methanococcus jannaschii]
CONTIG4562	3914062_f2_2	2882	16985	978	326	MJ1674	94	0.14999	Methanococcus jannaschii	[ui:mj1674] [pn:hypothetical protein] [glcfc:14.1] [keggfc:14.2] [tigrfc:15.1] [db:glc-methanococcus jannaschii]
CONTIG1865	32428125_f2_1	2883	16986	1296	432	MJ1322	93	0.40999	Methanococcus jannaschii	[ui:mj1322] [pn:purine ntpase:m] [glcfc:14.3] [keggfc:14.2] [tigrfc:4.1] [db:glc-methanococcus jannaschii]
b2x11334.y	33234637_c3_3	2884	16987	564	188	MJ1322	100	0.00038	Methanococcus jannaschii	[ui:mj1322] [pn:purine ntpase:m] [glcfc:14.3] [keggfc:14.2] [tigrfc:4.1] [db:glc-methanococcus jannaschii]
CONTIG1904	36367206_f1_1	2885	16988	954	318	R02_orf648	95	0.12	Mycoplasma pneumoniae	[ui:R02_orf648] [pn:transketolase-1:transketolase:tk] [gn:tkb:tkl:tkta] [glcfc:1.3:2.4] [ec:2.2.1.1] [keggfc:1.3:2.3] [zmbhfc:5.6] [db:glc-mycoplasma pneumoniae]
CONTIG5346	3960933_c1_16	2886	16989	1281	427	F11_orf479	122	0.00014	Mycoplasma pneumoniae	[ui:F11_orf479] [pn:nadh oxidase:probable nadh oxidase:nnoxase] [gn:nnox] [glcfc:2.1] [ec:1.6.-.-] [keggfc:1.1.1] [zmbhfc:5.1] [db:glc-mycoplasma pneumoniae]
CONTIG2582	31444037_f2_1	2887	16990	939	313	P02_orf793	95	0.17	Mycoplasma pneumoniae	[ui:P02_orf793] [pn:putative lipoprotein,mg260 homolog:hypothetical protein] [glcfc:1.1.1] [keggfc:1.1.2] [zmbhfc:2.1] [db:glc-mycoplasma pneumoniae]

CONTIG541	12595056_c2_18	2888	16991	648	216	H08_orf101 8	148	9.0(10)-9	Mycoplasma pneumoniae	[ui:h08_orf101.8] [pn:cytadherence accessory protein:cytadherence high molecular weight protein 1:cytadherence accessory protein 1] [gn:hmw1] [gicf:1.3] [keggf:1.1.2] [zmbhfc:2.2] [db:gic- mycoplasma pneumoniae]
CONTIG4543	36339188_f3_4	2889	16992	861	287	D12_orf390 0	174	1.0(10)-12	Mycoplasma pneumoniae	[ui:d12_orf390] [pn:heat shock protein dnaJ:protein] [gn:dnaJ] [gicf:12.7] [keggf:1.1.2] [zmbhfc:3.3] [db:gic-mycoplasma pneumoniae]
CONTIG2428	14179051_f1_1	2890	16993	267	89	G12_orf168	93	0.0001	Mycoplasma pneumoniae	[ui:g12_orf168] [pn:hypothetical protein] [gicf:14.1] [keggf:1.1.2] [zmbhfc:14.0] [db:gic-mycoplasma pneumoniae]
CONTIG5039	30526503_c1_5	2891	16994	1122	374	MTH1789	619	1.5(10)-60	Methanobacteriu m thermoautotroph icum	[ui:mth1789] [pn:ddp-glucose 4,6- dehydratase] [gicf:1.5.4.3] [ec:4.2.1.46] [keggf:1.5.4.3] [genomf:1.5] [db:gic- methanobacterium thermoautotrophicum]
CONTIG5202	20114002_f2_3	2892	16995	585	195	MTH1582	195	1.3(10)-15	Methanobacteriu m thermoautotroph icum	[ui:mth1582] [pn:carbonic anhydrase] [gicf:2.6] [ec:4.2.1.1] [keggf:2.5] [genomf:2.6] [db:gic- methanobacterium thermoautotrophicum]
CONTIG4609	14850055_f3_8	2893	16996	354	118	MTH1811	95	0.00022	Methanobacteriu m thermoautotroph icum	[ui:mth1811] [pn:n-carbamoyl-d- amino acid amidohydrolase] [gicf:5.16.6.6] [ec:3.5.1.77] [keggf:14.1] [genomf:6.6] [db:gic-methanobacterium thermoautotrophicum]

CONTIG4609	13863762_r3_9	2894	16997	588	196	MTH1811	382	2.0(10)-35	Methanobacterium thermoautotrophicum	[ui:rnth1811] [pn:n-carbamoyl-d-amino acid amidohydrolase] [gicfc:5.16:6.6] [ec:3.5.1.77] [keggfc:14.1] [genomfc:6.6] [db:gic-methanobacterium thermoautotrophicum]
b2x16028.y	2042153_c3_4	2895	16998	576	192	MTH1811	289	1.3(10)-25	Methanobacterium thermoautotrophicum	[ui:rnth1811] [pn:n-carbamoyl-d-amino acid amidohydrolase] [gicfc:5.16:6.6] [ec:3.5.1.77] [keggfc:14.1] [genomfc:6.6] [db:gic-methanobacterium thermoautotrophicum]
CONTIG1619	13065655_f2_1	2896	16999	1215	405	MTH1516	430	1.6(10)-39	Methanobacterium thermoautotrophicum	[ui:rnth1516] [pn:cation-transporting p-atpase pac] [gicfc:9.6:12.5] [ec:3.6.1.-] [keggfc:9.7] [genomfc:12.5] [db:gic-methanobacterium thermoautotrophicum]
CONTIG5242	20725138_f1_3	2897	17000	1878	626	MTH1893	174	1.3(10)-10	Methanobacterium thermoautotrophicum	[ui:rnth1893] [pn:cation efflux system protein:zinc/cadmium] [gicfc:9.6:12.12] [ec:3.6.1.-] [keggfc:9.7] [genomfc:12.11] [db:gic-methanobacterium thermoautotrophicum]
b9x13u44.y	26600942_c1_3	2898	17001	315	105	MTH72	92	0.00088	Methanobacterium thermoautotrophicum	[ui:rnth72] [pn:o-linked glucan transferase] [gicfc:10.2:14.1:14.2] [keggfc:14.2] [genomfc:10.2] [db:gic-methanobacterium thermoautotrophicum]
CONTIG2169	1221001_c2_4	2899	17002	648	216	MTH250	96	0.0032	Methanobacterium thermoautotrophicum	[ui:rnth250] [pn:rna intron endonuclease] [gicfc:10.6:14.1:14.2] [keggfc:14.2] [genomfc:10.6] [db:gic-methanobacterium thermoautotrophicum]

CONTIG1943	24328182_B_2	2900	17003	588	196	MTTH535	367	7.7(10)-34	Methanobacterium m thermoautotroph icum	[ui:mtth535] [pn:peptide methionine sulfoxide reductase] [gicfc:10.7:14.1:14.2] [keggfc:14.2] [genomfc:10.7] [db:gic- methanobacterium thermoautotrophicum]
CONTIG3927	34431287_B_3	2901	17004	1386	462	MTTH1633	154	2.5(10)-8	Methanobacterium m thermoautotroph icum	[ui:mtth1633] [pn:dna repair protein rad2] [gicfc:10.8:14.1:14.2] [keggfc:14.2] [genomfc:10.8] [db:gic-methanobacterium thermoautotrophicum]
CONTIG3832	36331311_F1_1	2902	17005	477	159	MTTH1780	141	2.1(10)-9	Methanobacterium m thermoautotroph icum	[ui:mtth1780] [pn:stomatin-like protein] [gicfc:11.1:14.1:14.2] [keggfc:14.2] [genomfc:11.1] [db:gic-methanobacterium thermoautotrophicum]
CONTIG1207	26853825_c1_4	2903	17006	852	284	MTTH104	1093	9.0(10)-111	Methanobacterium m thermoautotroph icum	[ui:mtth104] [pn:multidrug transporter homolog] [gicfc:12.12:14.1:14.2] [keggfc:14.2] [genomfc:12.11] [db:gic-methanobacterium thermoautotrophicum]
CONTIG5273	14720037_c2_9	2904	17007	891	297	MTTH666	889	3.7(10)-89	Methanobacterium m thermoautotroph icum	[ui:mtth666] [pn:ethylene-inducible protein] [gicfc:13.2:14.1:14.2] [keggfc:14.2] [genomfc:13.2] [db:gic-methanobacterium thermoautotrophicum]

CONTIG5796	11844077_c3_22	2905	17008	1143	381	MTH875	146	1.2(10)-10	Methanobacterium thermoautotrophicum	[ui:mh875] [pn:3-chlorobenzoate-3,4-dioxygenase dyhydrogenase related protein] [gicfc:14.1:14.3] [ec:1.1.1.18] [keggfc:14.1] [genomfc:13.7] [db:gic-methanobacterium thermoautotrophicum]
CONTIG2686	195312_c1_7	2906	17009	762	254	MTH1005	295	3.2(10)-26	Methanobacterium thermoautotrophicum	[ui:mh1005] [pn:conserved protein] [gicfc:14.1:14.2] [keggfc:14.2] [genomfc:14.2] [db:gic-methanobacterium thermoautotrophicum]
b3x13349.y	15023312_c3_5	2907	17010	747	249	MTH1280	225	3.7(10)-18	Methanobacterium thermoautotrophicum	[ui:mh1280] [pn:pet112-like protein] [gicfc:14.1:14.2:14.3] [keggfc:14.2] [genomfc:13.7] [db:gic-methanobacterium thermoautotrophicum]
CONTIG3655	24329683_c1_5	2908	17011	1185	395	MTH1621	836	1.5(10)-83	Methanobacterium thermoautotrophicum	[ui:mh1621] [pn:gip-binding protein, gip1/obg family] [gicfc:14.1:14.2:14.3] [keggfc:14.2] [genomfc:13.7] [db:gic-methanobacterium thermoautotrophicum]
CONTIG3976	6765885_c2_6	2909	17012	477	159	MTH232	220	2.8(10)-18	Methanobacterium thermoautotrophicum	[ui:mh232] [pn:conserved protein] [gicfc:14.1:14.2] [keggfc:14.2] [genomfc:14.2] [db:gic-methanobacterium thermoautotrophicum]
CONTIG1704	31330317_c1_4	2910	17013	396	132	MTH649	108	2.1(10)-6	Methanobacterium thermoautotrophicum	[ui:mh649] [pn:conserved protein] [gicfc:14.1:14.2] [keggfc:14.2] [genomfc:14.2] [db:gic-methanobacterium thermoautotrophicum]

CONTIG799	4317062_fl_2	2911	17014	300	100	MTH649	123	5.5(10)-8	Methanobacterium thermoautotrophicum	[ui:mtmh649] [pn:conserved protein] [gicf:14.1:14.2] [keggf:14.2] [genomf:14.2] [db:gtc-methanobacterium thermoautotrophicum]
CONTIG567	19548176_fl_5	2912	17015	1050	350	MTH682	238	3.6(10)-20	Methanobacterium thermoautotrophicum	[ui:mtmh682] [pn:conserved protein] [gicf:14.1:14.2] [keggf:14.2] [genomf:14.2] [db:gtc-methanobacterium thermoautotrophicum]
CONTIG5455	17067162_fl_2	2913	17016	942	314	YAL054C	1159	9.0(10)-118	Saccharomyces cerevisiae	[ui:yal054c] [pn:acetyl-coa synthetase:acetyl-coenzyme a synthetase 1:acetate--coa ligase 1:acyl-activating enzyme 1] [gn:acs1:fun44] [gicf:1.10:1.1:1.8:2.5:2.8:12.6] [ec:6.2.1.1] [keggf:1.8:1.10:2.4] [sgdfc:1.5:1.9:7.0:9:8.0] [db:g
CONTIG5455	24486326_fl_5	2914	17017	210	70	YAL054C	211	3.2(10)-16	Saccharomyces cerevisiae	[ui:yal054c] [pn:acetyl-coa synthetase:acetyl-coenzyme a synthetase 1:acetate--coa ligase 1:acyl-activating enzyme 1] [gn:acs1:fun44] [gicf:1.10:1.1:1.8:2.5:2.8:12.6] [ec:6.2.1.1] [keggf:1.8:1.10:2.4] [sgdfc:1.5:1.9:7.0:9:8.0] [db:g
CONTIG252	24896937_c2_2	2915	17018	795	265	YER073W	597	3.2(10)-58	Saccharomyces cerevisiae	[ui:yer073w] [pn:aldehyde dehydrogenase:nad+ aldehyde dehydrogenase, mitochondrial 3 precursor] [gn:ald3] [gicf:1.8:2.5:3.2:3.5:8.1] [ec:1.2.1.3] [keggf:1.7:1.8:1.10:1.11:3.2:3.5:6:5:9:5:10:5:11:5:12:5:14:6:1:8.1] [sgdfc:2.6:0:9:7

CONTIG3474	7035662_ft_1	2916	17019	1149	383	YER073W	1317	1.6(10)-134	Saccharomyces cerevisiae	[ui:yer073w] [pn:aldehyde dehydrogenase:nad+ aldehyde dehydrogenase, mitochondrial 3 precursor] [gn:ald3] [gcfc:1.8:2.5:3.2:3.5:8.1] [ec:1.2.1.3] [keggfc:1.7:1.8:1.10:1.11:3.2:3.5:5.6:5.9:5.10:5.11:5.12:5.14:6.1:8.1] [sgdfc:2.6:0:9.7]
b2x11307.x	19688251_c2_1	2917	17020	201	67	YER073W	102	0.00011	Saccharomyces cerevisiae	[ui:yer073w] [pn:aldehyde dehydrogenase:nad+ aldehyde dehydrogenase, mitochondrial 3 precursor] [gn:ald3] [gcfc:1.8:2.5:3.2:3.5:8.1] [ec:1.2.1.3] [keggfc:1.7:1.8:1.10:1.11:3.2:3.5:5.6:5.9:5.10:5.11:5.12:5.14:6.1:8.1] [sgdfc:2.6:0:9.7]
CONTIG2610	11801563_c3_3	2918	17021	669	223	YGR019W	626	2.7(10)-61	Saccharomyces cerevisiae	[ui:ygr019w] [pn:4-aminobutyrate aminotransferase:gamma-amino-n-butyrate transaminase:gaba transaminase:gaba aminotransferase] [gn:uga1] [gcfc:1.10:1.11:2.6:2.7:5.1:5.2:6.1:6.6:10.2] [ec:2.6.1.19] [keggfc:1.10:1.11:5.1:5.2:6.1] [sgdf

CONTIG3637	33628160_f3_5	2919	17022	1308	436	YGR019W	1419	2,6(10)-145	Saccharomyces cerevisiae	[ui:yg019w] [pn:4-aminobutyrate aminotransferase:gamma-amino-n-butyrate transaminase:gaba transaminase:gaba aminotransferase] [gn:uga1] [glcfc:1.10:1.11:2.6:2.7:5.1:5.2:6.1:6.6:10.2] [ec:2.6.1.19] [keggfc:1.10:1.11:5.1:5.2:6.1] [sgdf
CONTIG5510	34189425_f1_7	2920	17023	1008	336	YGR019W	657	1,3(10)-64	Saccharomyces cerevisiae	[ui:yg019w] [pn:4-aminobutyrate aminotransferase:gamma-amino-n-butyrate transaminase:gaba transaminase:gaba aminotransferase] [gn:uga1] [glcfc:1.10:1.11:2.6:2.7:5.1:5.2:6.1:6.6:10.2] [ec:2.6.1.19] [keggfc:1.10:1.11:5.1:5.2:6.1] [sgdf
CONTIG355	25392812_c3_4	2921	17024	273	91	YGR244C	249	6,5(10)-21	Saccharomyces cerevisiae	[ui:yg244c] [pn:strong similarity to rumen fungus beta-succinyl coa synthetase:probable succinyl-coa ligase:gdp-forming, beta-chain precursor:succinyl-coa synthetase, beta chain:scs-beta] [glcfc:1.10:1.11:2] [ec:6.2.1.4] [keggfc:1.2
CONTIG1081	2445338_c2_2	2922	17025	726	242	YLR153C	799	1,3(10)-79	Saccharomyces cerevisiae	[ui:ylr153c] [pn:acetyl-coenzyme a synthetase:acetyl-coenzyme a synthetase 2:acetate--coa ligase 2:acyl-activating enzyme 2] [gn:acs2:19634] [glcfc:1.10:1.11:8:2:5] [ec:6.2.1.1] [keggfc:1.8:1.10:2.4] [sgdf:1.5.1] [db:glc-saccharomyc

CONTIG4927	24339162_f2_2	2923	17026	2046	682	YLR153C	2212	2.3(10)-229	Saccharomyces cerevisiae	[ui:yr153c] [pn:acetyl-coenzyme a synthetase:acetyl-coenzyme a synthetase 2:acetate--coa ligase 2:acetyl-activating enzyme 2] [gn:acs2:19634] [gicf:1.10:1.1:1.8:2.5] [ec:6.2.1.1] [keggf:1.8:1.10:2.4] [sgdfc:1.5.1] [db:gic-saccharomyc]
CONTIG3915	3314002_c3_3	2924	17027	1326	442	YNR016C	1776	3.7(10)-183	Saccharomyces cerevisiae	[ui:ynr016c] [pn:acetyl-coa carboxylase:acc:contains:biotin carboxylase] [gn:fas3:accl:n3175] [gicf:1.10:1.8:3.1:3.4:8.1:8.2] [keggf:1.8:1.10:3.1] [sgdfc:1.6:1:9.2.0] [db:gic-saccharomyc cerevisiae]
CONTIG4685	24409557_f3_3	2925	17028	531	177	YNR016C	314	1.7(10)-26	Saccharomyces cerevisiae	[ui:ynr016c] [pn:acetyl-coa carboxylase:acc:contains:biotin carboxylase] [gn:fas3:accl:n3175] [gicf:1.10:1.8:3.1:3.4:8.1:8.2] [keggf:1.8:1.10:3.1] [sgdfc:1.6:1:9.2.0] [db:gic-saccharomyc cerevisiae]
CONTIG5087	34189752_f2_2	2926	17029	3069	1023	YNR016C	3168	0	Saccharomyces cerevisiae	[ui:ynr016c] [pn:acetyl-coa carboxylase:acc:contains:biotin carboxylase] [gn:fas3:accl:n3175] [gicf:1.10:1.8:3.1:3.4:8.1:8.2] [keggf:1.8:1.10:3.1] [sgdfc:1.6:1:9.2.0] [db:gic-saccharomyc cerevisiae]

CONTIG5557	21619200_c3_18	2927	17030	1833	611	YNR016C	2162	4.7(10)-224	Saccharomyces cerevisiae	[ui:ynr016c] [pn:acetyl-coa carboxylase:acc:contains:biotin carboxylase] [gn:fas3:acc:1:n3175] [glcfc:1.10:1.8:3.1:3.4:8.1:8.2] [keggfc:1.8:1.10:3.1] [sgdfe:1.6:1:9:2.0] [db:glc-saccharomyces cerevisiae]
CONTIG4347	2848338_ft_2	2928	17031	1284	428	YOR142W	769	1.8(10)-76	Saccharomyces cerevisiae	[ui:yor142w] [pn:strong similarity to succinate-coa ligase alpha subunit:probable succinyl-coa ligase:gdp-forming, alpha-chain precursor:succinyl-coa synthetase, alpha chain:scs-alpha] [gn:yor3352w] [glcfc:1.10:1.2] [ec:6.2.1.4] [keg
CONTIG1267	9815702_ft_1	2929	17032	429	143	YPL028W	393	1.3(10)-36	Saccharomyces cerevisiae	[ui:ypi028w] [pn:acetyl-coa c-acetyltransferase, cytosolic:acetyl-coa acetyltransferase:acetoacetyl-coa thiolase] [gn:erg10:pb3] [glcfc:1.10:1.11:1.8:3.1:3.2:3.3:4:5.14:5.9:8.1:8.2] [ec:2.3.1.9] [keggfc:1.8:1.10:1.11:3.1:3.2:3.3:5.
b3x11289.y	29376500_c2_2	2930	17033	378	126	YPL028W	300	9.6(10)-27	Saccharomyces cerevisiae	[ui:ypi028w] [pn:acetyl-coa c-acetyltransferase, cytosolic:acetyl-coa acetyltransferase:acetoacetyl-coa thiolase] [gn:erg10:pb3] [glcfc:1.10:1.11:1.8:3.1:3.2:3.3:4:5.14:5.9:8.1:8.2] [ec:2.3.1.9] [keggfc:1.8:1.10:1.11:3.1:3.2:3.3:5.
CONTIG1300	5125166_ft_1	2931	17034	1062	354	YAL038W	1395	8.9(10)-143	Saccharomyces cerevisiae	[ui:yal038w] [pn:pyruvate kinase] [gn:pyk1:cdc19] [glcfc:1.1:1.8:2.4] [ec:2.7.1.40] [keggfc:1.1:1.8:2.3] [sgdfe:1.5:1:2.1:0.9:2.0] [db:glc-saccharomyces cerevisiae]

CONTIG2666	957500_c2_5	2932	17035	225	75	YBR019C	217	7.2(10)-17	Saccharomyces cerevisiae	[ui:ybr019c] [pn:udp-glucose 4-epimerase:galactowaldenase / aldose 1-epimerase:mutarotase] [gn:gal10:ybr0301] [gicf:1.1:1.6:4.3] [keggfc:1.1:1.6:4.3] [sgdfc:1.5:1.9:2.0] [db:glc-saccharomyces cerevisiae]
CONTIG4753	15058513_f1_1	2933	17036	1833	611	YBR019C	1475	3.0(10)-151	Saccharomyces cerevisiae	[ui:ybr019c] [pn:udp-glucose 4-epimerase:galactowaldenase / aldose 1-epimerase:mutarotase] [gn:gal10:ybr0301] [gicf:1.1:1.6:4.3] [keggfc:1.1:1.6:4.3] [sgdfc:1.5:1.9:2.0] [db:glc-saccharomyces cerevisiae]
CONTIG5365	21135176_f3_12	2934	17037	1635	545	YBR196C	2153	4.2(10)-223	Saccharomyces cerevisiae	[ui:ybr196c] [pn:glucose-6-phosphate isomerase:gpi-phosphoglucose isomerase:pgi:phosphohexose isomerase:phi] [gn:pgi1:ybr1406] [gicf:1.1:1.3:7.2] [ec:5.3.1.9] [keggfc:1.1:1.3:7.1] [sgdfc:1.5:1.2:1.0:2.2:0.9:2.0] [db:glc-saccharomyces]
CONTIG5785	1382806_c3_33	2935	17038	1164	388	YBR221C	1287	2.5(10)-131	Saccharomyces cerevisiae	[ui:ybr221c] [pn:pyruvate dehydrogenase:liponamide beta chain precursor:pyruvate dehydrogenase e1 component, beta subunit precursor:pdh-e1-b] [gn:pdh1:ybr1511] [gicf:1.1:1.1:1.8:2.8:5.7] [ec:1.2.4.1] [keggfc:1.1:1.8:1.1:5:7] [sgdfc:1

CONTIG2247	2386458_12_2	2936	17039	693	231	YCL040W	523	2.2(10)-50	Saccharomyces cerevisiae	[ui:ycl040w] [pn:aldohexose specific glucokinase:glucokinase:glucose kinase:glk] [gn:glk1:hor3:ycl40w:ycl312] [glcfc:1.1:1.3:1.5:1.6:7.2:12.2:12.6] [ec:2.7.1.2] [keggfc:1.1:1.3:1.5:1.6:7.1] [sgdfe:1.5:1.1:5.3:8.7:0:9:2.0] [db:glc-sacc
CONTIG4802	162635_cl_8	2937	17040	1440	480	YCL040W	1059	3.6(10)-107	Saccharomyces cerevisiae	[ui:ycl040w] [pn:aldohexose specific glucokinase:glucokinase:glucose kinase:glk] [gn:glk1:hor3:ycl40w:ycl312] [glcfc:1.1:1.3:1.5:1.6:7.2:12.2:12.6] [ec:2.7.1.2] [keggfc:1.1:1.3:1.5:1.6:7.1] [sgdfe:1.5:1.1:5.3:8.7:0:9:2.0] [db:glc-sacc
CONTIG5783	162635_13_15	2938	17041	1440	480	YCL040W	1056	7.5(10)-107	Saccharomyces cerevisiae	[ui:ycl040w] [pn:aldohexose specific glucokinase:glucokinase:glucose kinase:glk] [gn:glk1:hor3:ycl40w:ycl312] [glcfc:1.1:1.3:1.5:1.6:7.2:12.2:12.6] [ec:2.7.1.2] [keggfc:1.1:1.3:1.5:1.6:7.1] [sgdfe:1.5:1.1:5.3:8.7:0:9:2.0] [db:glc-sacc

CONTIG4104	2_c1_8	2939	17042	1434	478	YCR012W	1450	1.3(10)-148	Saccharomyces cerevisiae	[ui:ycr012w] [pn:phosphoglycerate kinase] [gn:pgk1:ycr12w] [gicfc:1.1:2.4] [ec:2.7.2.3] [keggfc:1.1:2.3] [sgdffc:1.5.1:2.1:0:2.2:0:9.2:0] [db:glc-saccharomyces cerevisiae]
CONTIG5310	4189443_c1_7	2940	17043	621	207	YDL168W	715	1.0(10)-70	Saccharomyces cerevisiae	[ui:ydl168w] [pn:long-chain alcohol dehydrogenase:glutathione-dependent formaldehyde dehydrogenase:fdh:aldh:alcohol dehydrogenase sfa] [gn:sfa1:sfa] [gicfc:1.1:1.8:2.2:3.2:3.5:5.12:8.1:12.12] [keggfc:1.1:1.8:2.2:3.2:3.5:5.12:8.1] [sg
CONTIG1950	13828410_c3_3	2941	17044	408	136	YDR050C	393	1.3(10)-36	Saccharomyces cerevisiae	[ui:ydr050c] [pn:ribose-phosphate isomerase:ribosephosphate isomerase:tim] [gn:tpi1:ydr9609] [gicfc:1.1:1.5:2.4:8.1] [ec:5.3.1.1] [keggfc:1.1:1.5:2.3:8.1] [sgdffc:1.5.1:2.1:0:2.2:0:9.2:0] [db:glc-saccharomyces cerevisiae]
CONTIG2445	16146893_f3_1	2942	17045	231	77	YDR050C	270	1.5(10)-23	Saccharomyces cerevisiae	[ui:ydr050c] [pn:ribose-phosphate isomerase:tim] [gn:tpi1:ydr9609] [gicfc:1.1:1.5:2.4:8.1] [ec:5.3.1.1] [keggfc:1.1:1.5:2.3:8.1] [sgdffc:1.5.1:2.1:0:2.2:0:9.2:0] [db:glc-saccharomyces cerevisiae]

CONTIG5651	78258_f1_2	2943	17046	1260	420	YER178W	1514	2.2(10)-155	Saccharomyces cerevisiae	[ui:yer178w] [pn:pyruvate dehydrogenase:lipamide alpha chain precursor:pyruvate dehydrogenase e1 component, alpha subunit precursor:pdhel-a] [gn:pda1] [glcfc:1.1:1.11:1.8:2.8:5.7] [ec:1.2.4.1] [keggfc:1.1:1.8:1.11:5.7] [sgdfc:1.5.1:2]
CONTIG5801	1956302_c2_37	2944	17047	1518	506	YFL018C	1527	9.1(10)-157	Saccharomyces cerevisiae	[ui:yf018c] [pn:dihydroliipoamide dehydrogenase precursor] [gn:ipd1:dhlp1] [glcfc:1.1:1.2:1.8:2.8:5.3:6.6] [ec:1.8.1.4] [keggfc:1.1:1.2:1.8:5.3] [sgdfc:1.1:1.2:4.0:9.7.0] [db:glc-saccharomyces cerevisiae]
CONTIG4065	29774166_f2_2	2945	17048	1371	457	YFR053C	230	1.6(10)-16	Saccharomyces cerevisiae	[ui:yfr053c] [pn:hexokinase ii:hexokinase a:hexokinase pi] [gn:hkk1:hka] [glcfc:1.1:1.5:1.6:7.1:7.2] [ec:2.7.1.1] [keggfc:1.1:1.5:1.6:4.4:7.1] [sgdfc:1.5:1.2:1.0:9.2.0] [db:glc-saccharomyces cerevisiae]
CONTIG5810	3907775_c1_25	2946	17049	1476	492	YGL253W	1631	8.6(10)-168	Saccharomyces cerevisiae	[ui:ygl253w] [pn:hexokinase ii:hexokinase b:hexokinase pi] [gn:hkk2:hkb:hex1:nrb486] [glcfc:1.1:1.5:1.6:7.1:7.2:12.13] [ec:2.7.1.1] [keggfc:1.1:1.5:1.6:4.4:7.1] [sgdfc:1.5:1.1:5.2:2.1:0:9.2.0] [db:glc-saccharomyces cerevisiae]

CONTIG5145	29321963_c2_9	2947	17050	954	318	YGR192C	1094	7.0(10)-111	Saccharomyces cerevisiae	[ui:gr192c] [pn:glyceraldehyde-3-phosphate dehydrogenase 3:glyceraldehyde 3-phosphate dehydrogenase 3] [gn:ldh3:gpdc3:g7576] [gicf:1.1:6.14:6.8] [ec:1.2.1.12] [keggfc:1.1:6.7] [sgdfe:1.5.1:2.1:0:9:2.0] [db:gtc-saccharomyces cerevisia
CONTIG5528	24484691_c1_12	2948	17051	1023	341	YGR240C	400	3.2(10)-36	Saccharomyces cerevisiae	[ui:gr240c] [pn:6-phosphofructokinase, alpha subunit:6-phosphofructokinase alpha subunit:phosphofructokinase 1:phosphohexokinase] [gn:pk1:g8599] [gicf:1.1:1.3:1.5:1.6:12.13] [ec:2.7.1.11] [keggfc:1.1:1.3:1.5:1.6] [sgdfe:1.5.1:1.5.2
b9x12e78.x	10646902_c3_5	2949	17052	711	237	YGR240C	604	3.0(10)-58	Saccharomyces cerevisiae	[ui:gr240c] [pn:6-phosphofructokinase, alpha subunit:6-phosphofructokinase alpha subunit:phosphofructokinase 1:phosphohexokinase] [gn:pk1:g8599] [gicf:1.1:1.3:1.5:1.6:12.13] [ec:2.7.1.11] [keggfc:1.1:1.3:1.5:1.6] [sgdfe:1.5.1:1.5.2

CONTIG3948	4105275_12_2	2950	17053	903	301	YGR254W	1069	3,1(10)-108	Saccharomyces cerevisiae	[ui:yg254w] [pn:enolase i:enolase 1,2-phosphoglycerate dehydratase:2-phospho-d-glycerate hydro-lyase] [gn:enoi:enoahsp48:g9160] [gctc:1.1] [ec:4.2.1.11] [keggfc:1.1] [sgdfc:1.5.1.2.1.0.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2892	9812809_c2_4	2951	17054	447	149	YGR254W	601	1,2(10)-58	Saccharomyces cerevisiae	[ui:yg254w] [pn:enolase i:enolase 1,2-phosphoglycerate dehydratase:2-phospho-d-glycerate hydro-lyase] [gn:enoi:enoahsp48:g9160] [gctc:1.1] [ec:4.2.1.11] [keggfc:1.1] [sgdfc:1.5.1.2.1.0.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5145	16835300_c1_8	2952	17055	255	85	YJR009C	310	8,4(10)-28	Saccharomyces cerevisiae	[ui:yj009c] [pn:glyceraldehyde-3-phosphate dehydrogenase 2-glyceraldehyde 3-phosphate dehydrogenase 2] [gn:rdh2:gpdc2:j1433] [gctc:1.1.6.14.6.8] [ec:1.2.1.12] [keggfc:1.1.6.7] [sgdfc:1.5.1.2.1.0.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1975	4801385_c2_7	2953	17056	414	138	YKL152C	525	1,3(10)-50	Saccharomyces cerevisiae	[ui:ykl152c] [pn:phosphoglycerate mutase:phosphoglyceromutase:pga m:mpgm:bpge-dependent pgam] [gn:gpm1:gpm:ykl607] [gctc:1.1] [ec:5.4.2.1] [keggfc:1.1] [sgdfc:1.5.1.2.1.0.9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2345	1284500_f2_1	2954	17057	372	124	YKL152C	412	1.3(10)-38	Saccharomyces cerevisiae	[ui:ykl152c] [pn:phosphoglycerate mutase:phosphoglyceromutase:pgam:m:mpgm:bpg-dependent pgam] [gn:gpm1:gpm:ykl607] [glcfc:1.1] [ec:5.4.2.1] [keggfc:1.1] [sgdfe:1.5.1:2.1.0:9.2.0] [db:glc-saccharomyces cerevisiae]
CONTIG4584	21640652_f2_2	2955	17058	807	269	YKL152C	585	6.0(10)-57	Saccharomyces cerevisiae	[ui:ykl152c] [pn:phosphoglycerate mutase:phosphoglyceromutase:pgam:m:mpgm:bpg-dependent pgam] [gn:gpm1:gpm:ykl607] [glcfc:1.1] [ec:5.4.2.1] [keggfc:1.1] [sgdfe:1.5.1:2.1.0:9.2.0] [db:glc-saccharomyces cerevisiae]
CONTIG3611	4094055_c2_7	2956	17059	1101	367	YKL060C	1339	7.7(10)-137	Saccharomyces cerevisiae	[ui:ykl060c] [pn:fructose-bisphosphate aldolase] [gn:fbal:ykl320] [glcfc:1.1:1.3:1.5:2.4] [ec:4.1.2.13] [keggfc:1.1:1.3:1.5:2.3] [sgdfe:1.5.1:2.1.0:9.2.0] [db:glc-saccharomyces cerevisiae]
CONTIG2376	10829012_f1_1	2957	17060	1323	441	YLR044C	865	2.1(10)-113	Saccharomyces cerevisiae	[ui:ylr044c] [pn:pyruvate decarboxylase, isozyme 1] [gn:pdcl] [glcfc:1.1:2.2:2.8] [ec:4.1.1.1] [keggfc:1.1] [sgdfe:1.5.1:2.5.0:2.6.0:9.2.0] [db:glc-saccharomyces cerevisiae]

CONTIG5280	2932825_c2_14	2958	17061	960	320	YLR044C	1083	1.0(10)-109	Saccharomyces cerevisiae	[ui:y t044c] [pn:pyruvate decarboxylase, isozyme 1:pyruvate decarboxylase isozyme 1] [gn:pdcl] [gctc:1.1:2.2:2.8] [ec:4.1.1.1] [keggfc:1.1] [sgdfc:1.5.1:2.5.0:2.6.0:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG5280	4866287_c1_11	2959	17062	777	259	YLR044C	893	1.3(10)-89	Saccharomyces cerevisiae	[ui:y t044c] [pn:pyruvate decarboxylase, isozyme 1:pyruvate decarboxylase isozyme 1] [gn:pdcl] [gctc:1.1:2.2:2.8] [ec:4.1.1.1] [keggfc:1.1] [sgdfc:1.5.1:2.5.0:2.6.0:9.2.0] [db:gic-saccharomyces cerevisiae]
b2x18774.y	9788376_f2_2	2960	17063	234	78	YLR044C	210	2.7(10)-16	Saccharomyces cerevisiae	[ui:y t044c] [pn:pyruvate decarboxylase, isozyme 1:pyruvate decarboxylase isozyme 1] [gn:pdcl] [gctc:1.1:2.2:2.8] [ec:4.1.1.1] [keggfc:1.1] [sgdfc:1.5.1:2.5.0:2.6.0:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG5432	14547013_c2_22	2961	17064	711	237	YLR377C	740	2.2(10)-73	Saccharomyces cerevisiae	[ui:y t377c] [pn:fructose-1,6-bisphosphatase:d-fructose-1,6-bisphosphate 1-phosphohydrolyase:fbpase] [gn:fbp1:18039] [gctc:1.1:1.3:1.5:2.4] [ec:3.1.3.11] [keggfc:1.1:1.3:1.5:2.3] [sgdfc:1.5.1:2.2.0:9.2.0] [db:gic-saccharomyces cerevi

CONTIG2467	24307150_c1_3	2962	17065	942	314	YMR083W	1139	1.2(10)-115	Saccharomyces cerevisiae	[ui:ymr083w] [pn:alcohol dehydrogenase iii:alcohol dehydrogenase iii precursor] [gn:adh3:ym9582] [glcfc:1.1.2.8.3.2.3.5.5.12.8.1] [ec:1.1.1.1] [keggfc:1.1.3.2.3.5.5.12.8.1] [sgdfc:1.5.1.9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5698	14220276_f2_14	2963	17066	1059	353	YMR083W	1207	7.4(10)-123	Saccharomyces cerevisiae	[ui:ymr083w] [pn:alcohol dehydrogenase iii:alcohol dehydrogenase iii precursor] [gn:adh3:ym9582] [glcfc:1.1.2.8.3.2.3.5.5.12.8.1] [ec:1.1.1.1] [keggfc:1.1.3.2.3.5.5.12.8.1] [sgdfc:1.5.1.9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5021	1175126_f2_3	2964	17067	1308	436	YMR105C	1585	6.5(10)-163	Saccharomyces cerevisiae	[ui:ymr105c] [pn:phosphoglucumutase, major isoform:phosphoglucumutase 2:glucose phosphomutase 2:pgm 2] [gn:pgm2:gal5:ym9718] [glcfc:1.1.1.6.7.1.7.2] [ec:5.4.2.2] [keggfc:1.1.1.6.7.1] [sgdfc:1.5.1.2.7.0.9.2.0] [db:gtc-saccharomyces cer

CONTIG5021	24298762_11_1	2965	17068	447	149	YMR105C	318	4.9(10)-28	Saccharomyces cerevisiae	[ui:ymr105c] [pn:phosphoglucumutase, major isoform:phosphoglucumutase 2:glucose phosphomutase 2:pgm 2] [gn:pgm2:gal5:ym9718] [gicf:1.1:1.6:7.1:7.2] [ec:5.4.2.2] [kegfc:1.1:1.6:7.1] [sgdfc:1.5.1:2.7:0:9:2.0] [db:gic-saccharomyces cer
CONTIG5634	22379531_c3_27	2966	17069	297	99	YMR205C	117	5.7(10)-6	Saccharomyces cerevisiae	[ui:ymr205c] [pn:6-phosphofructokinase, beta subunit:6-phosphofructokinase beta subunit:phosphofructokinase 1:phosphohexokinase] [gn:pk2:ym8325] [gicf:1.1:1.3:1.5:1.6:12.13] [ec:2.7.1.11] [kegfc:1.1:1.3:1.5:1.6] [sgdfc:1.5.1:1.5.2:
CONTIG5634	6834712_c2_24	2967	17070	1632	544	YMR205C	1854	2.0(10)-191	Saccharomyces cerevisiae	[ui:ymr205c] [pn:6-phosphofructokinase, beta subunit:6-phosphofructokinase beta subunit:phosphofructokinase 1:phosphohexokinase] [gn:pk2:ym8325] [gicf:1.1:1.3:1.5:1.6:12.13] [ec:2.7.1.11] [kegfc:1.1:1.3:1.5:1.6] [sgdfc:1.5.1:1.5.2:

CONTIG5634	4892193_c1_15	2968	17071	300	100	YMR205C	341	6.5(10)-30	Saccharomyces cerevisiae	[ui:ymr205c] [pn:6-phosphofructokinase, beta subunit:6-phosphofructokinase beta subunit:phosphofructokinase 1:phosphohexokinase] [gn:pk2:ym8325] [gncf:1.1:1.3:1.5:1.6:12.13] [ec:2.7.1.11] [keggfc:1.1:1.3:1.5:1.6] [sgdfc:1.5:1:1.5:2]
CONTIG5634	14570316_c2_23	2969	17072	816	272	YMR205C	309	1.7(10)-26	Saccharomyces cerevisiae	[ui:ymr205c] [pn:6-phosphofructokinase, beta subunit:6-phosphofructokinase beta subunit:phosphofructokinase 1:phosphohexokinase] [gn:pk2:ym8325] [gncf:1.1:1.3:1.5:1.6:12.13] [ec:2.7.1.11] [keggfc:1.1:1.3:1.5:1.6] [sgdfc:1.5:1:1.5:2]
b3x15367.x	20525058_c3_2	2970	17073	396	132	YMR303C	121	4.9(10)-7	Saccharomyces cerevisiae	[ui:ymr303c] [pn:alcohol dehydrogenase ii] [gn:adh2:adr2:ym9952] [gncf:1.1:2.2:3.2:3.5:5.12:8.1] [ec:1.1.1.1] [keggfc:1.1:3.2:3.5:5.12:8.1] [sgdfc:1.5:1.2:6:0:9:2.0] [db:gnc-saccharomyces cerevisiae]

CONTIG4969	10975252_f2_3	2971	17074	528	176	YNL071W	361	3.2(10)-33	Saccharomyces cerevisiae	[ui:ynl071w] [pn:dihydroliipoamide S-acyltransferase:dihydroliipoamide acetyltransferase component:c2 of pyruvate dehydrogenase complex precursor:pdh-c2] [gn:pdh2:lat1:n2374] [gdcf:1.1:1.8:2.8] [ec:2.3.1.12] [kegfc:1.1:1.8] [sgdc:1]
CONTIG4969	24665786_f3_5	2972	17075	1215	405	YNL071W	701	3.1(10)-69	Saccharomyces cerevisiae	[ui:ynl071w] [pn:dihydroliipoamide S-acyltransferase:dihydroliipoamide acetyltransferase component:c2 of pyruvate dehydrogenase complex precursor:pdh-c2] [gn:pdh2:lat1:n2374] [gdcf:1.1:1.8:2.8] [ec:2.3.1.12] [kegfc:1.1:1.8] [sgdc:1]
CONTIG4567	36000_c3_8	2973	17076	669	223	YGR193C	314	3.2(10)-28	Saccharomyces cerevisiae	[ui:ygr193c] [pn:pyruvate dehydrogenase complex protein x:pyruvate dehydrogenase protein x component precursor] [gn:pdh1:g7579] [gdcf:1.1:2.8] [kegfc:14.2] [sgdc:1.5.1:2.1.0.9.7.0] [db:gdc-saccharomyces cerevisiae]
CONTIG4920	35344675_f2_3	2974	17077	1143	381	YIL107C	309	1.3(10)-26	Saccharomyces cerevisiae	[ui:yil107c] [pn:6-phosphofructose-2-kinase, isozyme 1:6-phosphofructose-2-kinase:phosphofructokinase 2] [gn:pfk26] [gdcf:1.1:1.5:12.13] [ec:2.7.1.105] [kegfc:1.5] [sgdc:1.5.1:1.5.2.2.1.0.9.2.0] [db:gdc-saccharomyces cerevisiae]

CONTIG5066	20319181_c3_18	2975	17078	1365	455	YIL107C	810	8.6(10)-81	Saccharomyces cerevisiae	[ui:yil107c] [pn:6-phosphofructose-2-kinase, isozyme 1:6-phosphofructo-2-kinase:phosphofructokinase 2] [gn:pk26] [gtcf:1.1:1.5:12.13] [ec:2.7.1.105] [kegfc:1.5] [sgdfc:1.5:1.1:5.2:2.1:0.9:2.0] [db:glc-saccharomyces cerevisiae]
CONTIG5066	30273463_c2_17	2976	17079	183	61	YIL107C	165	3.5(10)-11	Saccharomyces cerevisiae	[ui:yil107c] [pn:6-phosphofructose-2-kinase, isozyme 1:6-phosphofructo-2-kinase:phosphofructokinase 2] [gn:pk26] [gtcf:1.1:1.5:12.13] [ec:2.7.1.105] [kegfc:1.5] [sgdfc:1.5:1.1:5.2:2.1:0.9:2.0] [db:glc-saccharomyces cerevisiae]
CONTIG5066	14553952_c1_12	2977	17080	1986	662	YIL107C	261	2.2(10)-19	Saccharomyces cerevisiae	[ui:yil107c] [pn:6-phosphofructose-2-kinase, isozyme 1:6-phosphofructo-2-kinase:phosphofructokinase 2] [gn:pk26] [gtcf:1.1:1.5:12.13] [ec:2.7.1.105] [kegfc:1.5] [sgdfc:1.5:1.1:5.2:2.1:0.9:2.0] [db:glc-saccharomyces cerevisiae]
CONTIG3176	893802_f3_2	2978	17081	279	93	YKL029C	115	6.0(10)-6	Saccharomyces cerevisiae	[ui:ykl029c] [pn:strong similarity to s.pombe malate oxidoreductase:probable malate oxidoreductase:nad malic enzyme:me] [gtcf:1.1:1.8] [ec:1.1.1.38] [kegfc:1.8] [sgdfc:1.5:1.2:1.0] [db:glc-saccharomyces cerevisiae]

CONTIG3176	20444443_f3_3	2979	17082	855	285	YKL029C	1096	4.2(10)-111	Saccharomyces cerevisiae	[ui:yk1029c] [pn:strong similarity to s.pombe malate oxidoreductase:probable malate oxidoreductase:nad malic enzyme:me] [gtcf:1.1:1.8] [ec:1.1.1.38] [kegfc:1.8] [sgdfe:1.5.1:2.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5433	172156_f1_1	2980	17083	801	267	YKL029C	875	1.1(10)-87	Saccharomyces cerevisiae	[ui:yk1029c] [pn:strong similarity to s.pombe malate oxidoreductase:probable malate oxidoreductase:nad malic enzyme:me] [gtcf:1.1:1.8] [ec:1.1.1.38] [kegfc:1.8] [sgdfe:1.5.1:2.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG147	32553308_f2_1	2981	17084	285	95	YKR043C	125	3.7(10)-12	Saccharomyces cerevisiae	[ui:ykr043c] [pn:weak similarity to phosphoglycerate mutase:hypothetical 31.0 kd protein in gap1-nap1 intergenic region] [gtcf:1.1] [kegfc:14.2] [sgdfe:1.5.1:2.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG495	4410010_f1_1	2982	17085	474	158	YKR043C	323	3.5(10)-29	Saccharomyces cerevisiae	[ui:ykr043c] [pn:weak similarity to phosphoglycerate mutase:hypothetical 31.0 kd protein in gap1-nap1 intergenic region] [gtcf:1.1] [kegfc:14.2] [sgdfe:1.5.1:2.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5808	14531880_c1_22	2983	17086	831	277	YKR043C	455	1.0(10)-57	Saccharomyces cerevisiae	[ui:ykr043c] [pn:weak similarity to phosphoglycerate mutase:hypothetical 31.0 kd protein in gap1-nap1 intergenic region] [gtfc:1.1] [keggfc:14.2] [sgdgc:1.5.1:2.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3889	25681252_c3_10	2984	17087	738	246	YLR345W	530	4.0(10)-51	Saccharomyces cerevisiae	[ui:ylr345w] [pn:similarity to pfk26p and other 6-phosphofructo-2-kinases] [gtfc:1.1:12.13] [keggfc:14.2] [sgdgc:1.5.2:2.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3889	10750702_c1_7	2985	17088	861	287	YLR345W	376	8.5(10)-35	Saccharomyces cerevisiae	[ui:ylr345w] [pn:similarity to pfk26p and other 6-phosphofructo-2-kinases] [gtfc:1.1:12.13] [keggfc:14.2] [sgdgc:1.5.2:2.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5226	26289018_f2_4	2986	17089	2454	818	YMR125W	840	5.7(10)-84	Saccharomyces cerevisiae	[ui:ymr125w] [pn:transcription factor for glycolytic genes:ger3 protein:sto1 protein:sut1 protein] [gn:ger3:sto1:sut1:ymr5564] [gtfc:1.1:10.2] [keggfc:14.2] [sgdgc:1.5.2:2.1.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4859	14882635_f1_1	2987	17090	675	225	YOR283W	433	7.7(10)-41	Saccharomyces cerevisiae	[ui:yor283w] [pn:weak similarity to phosphoglycerate mutases] [gtfc:1.1] [keggfc:14.2] [sgdgc:1.5.1:2.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG532	24650192_f3_1	2988	17091	666	222	YBR218C	845	1.7(10)-84	Saccharomyces cerevisiae	[ui:ybr218c] [pn:pyruvate carboxylase 2:pyruvic carboxylase 2:pcb 2] [gn:pyc2:ybr1507] [gtcf:1.1:1.2:1.8:5.2] [ec:6.4.1.1] [keggfc:1.2:1.8:5.2] [sgdfe:1.5:1.2:2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1968	34409567_c3_4	2989	17092	501	167	YER065C	637	1.8(10)-62	Saccharomyces cerevisiae	[ui:yer065c] [pn:isocitrate lyase:isocitrate:isocitrate:ic] [gn:ic1] [gtcf:1.1:1.8:1.9:12.6] [ec:4.1.3.1] [keggfc:1.9] [sgdfe:1.5:1.2:2.0:2.8:0:9.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4616	34566587_c3_9	2990	17093	1074	358	YER065C	1126	2.8(10)-114	Saccharomyces cerevisiae	[ui:yer065c] [pn:isocitrate lyase:isocitrate:isocitrate:ic] [gn:ic1] [gtcf:1.1:1.8:1.9:12.6] [ec:4.1.3.1] [keggfc:1.9] [sgdfe:1.5:1.2:2.0:2.8:0:9.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2543	4085906_c3_5	2991	17094	1428	476	YGL062W	1795	3.7(10)-185	Saccharomyces cerevisiae	[ui:ygl062w] [pn:pyruvate carboxylase 1:pyruvic carboxylase 1:pcb 1] [gn:pyc1:pyv] [gtcf:1.1:1.2:1.8:5.2] [ec:6.4.1.1] [keggfc:1.2:1.8:5.2] [sgdfe:1.5:1.2:2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1319	16411385_f1_1	2992	17095	351	117	YIL167W	126	3.1(10)-8	Saccharomyces cerevisiae	[ui:yil167w] [pn:serine dehydratase:putative l-serine dehydratase c-terminal section] [gn:sd1] [gtcf:1.1:5.3:5.5] [ec:4.2.1.13] [keggfc:5.3:5.5] [sgdfe:1.1:4:2.2:0:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5766	4335050_c1_22	2993	17096	1671	557	YKR097W	2129	1.5(10)-220	Saccharomyces cerevisiae	[ui:ykr097w] [pn:phosphoenolpyruvate carboxykinase:arp] [gn:pck1:ppc1:pepc] [gicfc:1.1:1.2:1.8:2.4] [ec:4.1.1.49] [keggfc:1.2:1.8:2.3] [sgdfe:1.5:1.2:2.0:9.2.0] [db:gic- saccharomyces cerevisiae]
CONTIG169	10833262_f3_2	2994	17097	738	246	YMR280C	152	1.7(10)-9	Saccharomyces cerevisiae	[ui:ymr280c] [pn:transcription factor involved in gluconeogenesis:regulatory protein cat8] [gn:cat8:msp8:ym8021] [gicfc:1.1:10.2] [keggfc:14.2] [sgdfe:1.5:2.2:0.4:8.2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG2265	182030_f3_2	2995	17098	1377	459	YMR280C	159	7.2(10)-12	Saccharomyces cerevisiae	[ui:ymr280c] [pn:transcription factor involved in gluconeogenesis:regulatory protein cat8] [gn:cat8:msp8:ym8021] [gicfc:1.1:10.2] [keggfc:14.2] [sgdfe:1.5:2.2:0.4:8.2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG3354	4398317_c3_9	2996	17099	1008	336	YMR280C	171	1.3(10)-9	Saccharomyces cerevisiae	[ui:ymr280c] [pn:transcription factor involved in gluconeogenesis:regulatory protein cat8] [gn:cat8:msp8:ym8021] [gicfc:1.1:10.2] [keggfc:14.2] [sgdfe:1.5:2.2:0.4:8.2:9.5.0] [db:gic-saccharomyces cerevisiae]

CONTIG5285	2812758_c1_9	2997	17100	975	325	YAL061W	598	2.5(10)-58	Saccharomyces cerevisiae	[ui:yal061w] [pn:similarity to alcohol/sorbitol dehydrogenase:hyphothetical zinc-type alcohol dehydrogenase-like protein in gdh3-cne1 intergenic region] [gn:fun50] [gtcf:1.1:2.2] [kegfc:1.4.2] [sgdfc:1.5.1:2.6.0] [db:gtc-saccharomyces]
CONTIG4523	10048408_f3_2	2998	17101	849	283	YAL060W	551	2.3(10)-53	Saccharomyces cerevisiae	[ui:yal060w] [pn:similarity to alcohol/sorbitol dehydrogenase:hyphothetical zinc-type alcohol dehydrogenase-like protein in gdh3-cne1 intergenic region] [gn:fun49] [gtcf:1.1:2.2] [kegfc:1.4.2] [sgdfc:1.5.1:2.6.0] [db:gtc-saccharomyces]
CONTIG5145	24492160_c2_10	2999	17102	2109	703	YAL023C	2237	5.2(10)-232	Saccharomyces cerevisiae	[ui:yal023c] [pn:mannosyltransferase:dolichyl-phosphate-mannose--protein mannosyltransferase 2] [gn:pmf2.fun25] [gtcf:1.1:7.1:10.7:11.3:12.16] [ec:2.4.1.109] [kegfc:7.2] [sgdfc:1.5.1:6.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4677	4484501_c2_8	3000	17103	843	281	YBL082C	380	3.2(10)-35	Saccharomyces cerevisiae	[ui:ybl082c] [pn:mannosyltransferase:hm-1 killer toxin resistance protein] [gn:rhk1:alg3:ybl0720] [gtcf:1.1:10.7:12.16] [kegfc:14.2] [sgdfc:1.5.1:6.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]

CONTIG755	12673375_c2_2	3001	17104	771	257	YBL082C	198	6.7(10)-24	Saccharomyces cerevisiae	[ui:ybl082c] [pn:mannosyltransferase:hm-1 killer toxin resistance protein] [gn:rhk1:alg3:ybl0720] [gicfc:1.1:10.7:12.16] [keggfc:14.2] [sgdfe:1.5.1:6.3:0.9:4.0] [db:gic-saccharomyces cerevisiae]
CONTIG5425	23939752_f3_6	3002	17105	294	98	YBL001C	280	1.3(10)-24	Saccharomyces cerevisiae	[ui:ybl001c] [pn:strong similarity to s.xylosus glucose kinase:hypothetical 11.5 kd protein in htb2-nth2 intergenic region] [gn:ybl0105] [gicfc:1.1] [keggfc:14.2] [sgdfe:1.5.1] [db:gic-saccharomyces cerevisiae]
CONTIG487	12277313_c2_3	3003	17106	540	180	YBR018C	505	1.8(10)-48	Saccharomyces cerevisiae	[ui:ybr018c] [pn:udp-glucose--hexose-1-phosphate uridylyltransferase:galactose-1-phosphate uridylyltransferase] [gn:gal7:ybr0226] [gicfc:1.1:1.6:4.3] [ec:2.7.7.10] [keggfc:1.6:4.3] [sgdfe:1.5.1:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG5039	10601413_f1_3	3004	17107	495	165	YBR018C	477	1.7(10)-45	Saccharomyces cerevisiae	[ui:ybr018c] [pn:udp-glucose--hexose-1-phosphate uridylyltransferase:galactose-1-phosphate uridylyltransferase] [gn:gal7:ybr0226] [gicfc:1.1:1.6:4.3] [ec:2.7.7.10] [keggfc:1.6:4.3] [sgdfe:1.5.1:9.2.0] [db:gic-saccharomyces cerevisiae]

CONTIG5709	32244212_f1_3	3005	17108	3282	1094	YBR023C	3197	0	Saccharomyces cerevisiae	[ui:ybr023c] [pn:chitin synthase iii:chitin synthase 3:chitin-udp acetyl-glucosaminyl transferase 3] [gn:chs3:cal1:csd2:dit101:ki12:ybr0305] [gicf:1.1.4.7.2] [ec:2.4.1.16] [keggfc:4.4] [sgdfc:1.5.1.3.2.0.3.3.0.3.4.0.9.1.0.9.9.0] [db:g
CONTIG5407	4378465_f3_8	3006	17109	2238	746	YBR038W	1545	1.1(10)-158	Saccharomyces cerevisiae	[ui:ybr038w] [pn:chitin synthase ii:chitin synthase 2:chitin-udp acetyl-glucosaminyl transferase 2] [gn:chs2:ybr0407] [gicf:1.1.4.7.2] [ec:2.4.1.16] [keggfc:4.4] [sgdfc:1.5.1.3.2.0.9.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG5750	16587807_f3_12	3007	17110	1512	504	YBR056W	763	8.3(10)-76	Saccharomyces cerevisiae	[ui:ybr056w] [pn:similarity to glucan 1,3-beta-glucosidase:hyphothetical 57.8 kd protein in prp6-ubp14 intergenic region] [gn:ybr0510] [gicf:1.1] [keggfc:1.4.2] [sgdfc:1.5.1] [db:gic-saccharomyces cerevisiae]
CONTIG4111	22401037_f1_1	3008	17111	534	178	YBR084W	497	1.2(10)-46	Saccharomyces cerevisiae	[ui:ybr084w] [pn:c1-tetrahydrofolate synthase precursor, mitochondrial c-1-tetrahydrofolate synthase mitochondrial precursor:c1-thf synthase:methylenetetrahydrofolate dehydrogenase / methenyltetrahydrofolate cyclohydrolase / formyltetra

CONTIG4111	5173563_f2_2	3009	17112	279	93	YBR084W	198	1.3(10)-14	Saccharomyces cerevisiae	[ui:ybr084w] [pn:c]-tetrahydrofolate synthase precursor, mitochondrial:c-1-tetrahydrofolate synthase mitochondrial precursor:c1-thf synthase:methylenetetrahydrofolate dehydrogenase / methenyltetrahydrofolate cyclohydrolase / formyltetra
CONTIG4111	1228412_f3_4	3010	17113	243	81	YBR084W	124	1.0(10)-6	Saccharomyces cerevisiae	[ui:ybr084w] [pn:c]-tetrahydrofolate synthase precursor, mitochondrial:c-1-tetrahydrofolate synthase mitochondrial precursor:c1-thf synthase:methylenetetrahydrofolate dehydrogenase / methenyltetrahydrofolate cyclohydrolase / formyltetra
CONTIG4111	972662_f2_3	3011	17114	1536	512	YBR084W	1725	9.5(10)-178	Saccharomyces cerevisiae	[ui:ybr084w] [pn:c]-tetrahydrofolate synthase precursor, mitochondrial:c-1-tetrahydrofolate synthase mitochondrial precursor:c1-thf synthase:methylenetetrahydrofolate dehydrogenase / methenyltetrahydrofolate cyclohydrolase / formyltetra

CONTIG5680	31422827_c3_47	3012	17115	3063	1021	YBR084W	2843	3.2(10)-296	Saccharomyces cerevisiae	[ui:ybr084w] [pn:cl-tetrahydrofolate synthase precursor, mitochondrial:c-1-tetrahydrofolate synthase mitochondrial precursor:c1-thf synthase:methylenetetrahydrofolate dehydrogenase / methenyltetrahydrofolate cyclohydrolase / formyltr
CONTIG4603	5087562_c2_10	3013	17116	267	89	YBR110W	134	3.0(10)-8	Saccharomyces cerevisiae	[ui:ybr110w] [pn:beta-mannosyltransferase] [gn:alg1:ybr0906] [gicf:1.1:1.5:7.1:8.5:10.7:11.3:11.4:12.16] [ec:2.4.1.-] [keggfc:1.5:7.2:7.3:8.5] [sgdfc:1.5:1:6.3:0:9:4.0] [db:gic-saccharomyces cerevisiae]
CONTIG4603	33317155_c1_8	3014	17117	1194	398	YBR110W	773	7.2(10)-77	Saccharomyces cerevisiae	[ui:ybr110w] [pn:beta-mannosyltransferase] [gn:alg1:ybr0906] [gicf:1.1:1.5:7.1:8.5:10.7:11.3:11.4:12.16] [ec:2.4.1.-] [keggfc:1.5:7.2:7.3:8.5] [sgdfc:1.5:1:6.3:0:9:4.0] [db:gic-saccharomyces cerevisiae]
CONTIG5444	4772937_c3_14	3015	17118	1446	482	YBR126C	1855	1.6(10)-191	Saccharomyces cerevisiae	[ui:ybr126c] [pn:alpha,alpha-trehalose-phosphate synthase, 56 kd subunit:alpha,alpha-trehalose-phosphate synthase:udp-forming 56 kd subunit:trehalose-6-phosphate synthase:udp-glucose-glucosephosphate glucosyltransferase:general gluco

CONTIG1352	9767807_c1_3	3016	17119	624	208	YBR149W	446	3.2(10)-42	Saccharomyces cerevisiae	[ui:ybr149w] [pn:similarity to gcy1 p and aldose reductases:hypothetical 38.9 kd protein in ysw1-rib7 intergenic region] [gn:ybr1127] [gctc:1.1] [keggfc:14.2] [sgdfc:1.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4959	21656687_c3_9	3017	17120	1347	449	YBR199W	868	6.2(10)-87	Saccharomyces cerevisiae	[ui:ybr199w] [pn:strong similarity to alpha-1,2-mannosyltransferase:probable mannosyltransferase ktr4] [gn:ktr4:ybr1411] [gctc:1.1.7.1:10.7:11.3] [ec:2.4.1.131] [keggfc:7.2] [sgdfc:1.5.1:6.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5462	25567318_f1_1	3018	17121	2190	730	YBR229C	1929	2.2(10)-199	Saccharomyces cerevisiae	[ui:ybr229c] [pn:glucosidase ii, catalytic subunit:putative family 31 glucosidase in pcs60-abd1 intergenic region] [gn:rot2:ybr1526] [gctc:1.1.4.3:7.1:7.2] [ec:3.2.1.-] [keggfc:4.3.4.4] [sgdfc:1.5.1:2.7.0] [db:gtc-saccharomyces cerev]
CONTIG5761	4377176_f3_15	3019	17122	1494	498	YBR243C	789	4.5(10)-109	Saccharomyces cerevisiae	[ui:ybr243c] [pn:udp-n-acetylglucosamine-1-phosphate transferase:udp-n-acetylglucosamine--dolichyl-phosphate n-acetylglucosaminophosphotransferase:gpi:pt:n-acetylglucosamine-1-phosphate transferase:glcnac-1-p transferase:tunicamyci

CONTIG1695	4063925_c2_4	3020	17123	612	204	YCR034W	624	4.5(10)-61	Saccharomyces cerevisiae	[ui:ycr034w] [pn:probable beta-1,3-glucan synthase subunit:gns1 protein] [gn:gns1:ycr34w:ycr521] [gfc:1.3.4.8.1.8.2.1.1.12.15.12.8.12.9] [kegfc:14.2] [sgdfe:1.5.1.1.6.1.3.1.0.3.2.0.3.3.0.3.4.0.9.1.0] [db:glc-saccharomyces cerevi
CONTIG1695	2_cl_1	3021	17124	384	128	YCR034W	270	1.5(10)-23	Saccharomyces cerevisiae	[ui:ycr034w] [pn:probable beta-1,3-glucan synthase subunit:gns1 protein] [gn:gns1:ycr34w:ycr521] [gfc:1.3.4.8.1.8.2.1.1.12.15.12.8.12.9] [kegfc:14.2] [sgdfe:1.5.1.1.6.1.3.1.0.3.2.0.3.3.0.3.4.0.9.1.0] [db:glc-saccharomyces cerevi
CONTIG3665	4493931_f3_3	3022	17125	888	296	YCR034W	760	1.7(10)-75	Saccharomyces cerevisiae	[ui:ycr034w] [pn:probable beta-1,3-glucan synthase subunit:gns1 protein] [gn:gns1:ycr34w:ycr521] [gfc:1.3.4.8.1.8.2.1.1.12.15.12.8.12.9] [kegfc:14.2] [sgdfe:1.5.1.1.6.1.3.1.0.3.2.0.3.3.0.3.4.0.9.1.0] [db:glc-saccharomyces cerevi
CONTIG5358	4493931_cl_9	3023	17126	429	143	YCR034W	270	1.5(10)-23	Saccharomyces cerevisiae	[ui:ycr034w] [pn:probable beta-1,3-glucan synthase subunit:gns1 protein] [gn:gns1:ycr34w:ycr521] [gfc:1.3.4.8.1.8.2.1.1.12.15.12.8.12.9] [kegfc:14.2] [sgdfe:1.5.1.1.6.1.3.1.0.3.2.0.3.3.0.3.4.0.9.1.0] [db:glc-saccharomyces cerevi

CONTIG1596	29722631_c3_3	3024	17127	687	229	YCR036W	150	2.8(10)-10	Saccharomyces cerevisiae	[ui:ycr036w] [pn:ribokinase:probable ribokinase] [gn:rbk1:ycr36w:ycr523] [gfc:1.1:1.3] [ec:2.7.1.15] [kegfc:1.3] [sgdfe:1.5.1] [db:glc-saccharomyces cerevisiae]
CONTIG2716	6281562_c2_5	3025	17128	309	103	YCR036W	179	1.7(10)-13	Saccharomyces cerevisiae	[ui:ycr036w] [pn:ribokinase:probable ribokinase] [gn:rbk1:ycr36w:ycr523] [gfc:1.1:1.3] [ec:2.7.1.15] [kegfc:1.3] [sgdfe:1.5.1] [db:glc-saccharomyces cerevisiae]
CONTIG5447	15645177_f2_6	3026	17129	534	178	YDL246C	306	2.2(10)-27	Saccharomyces cerevisiae	[ui:ydl246c] [pn:strong similarity to sor1p] [gfc:1.1] [kegfc:14.2] [sgdfe:1.5.1] [db:glc-saccharomyces cerevisiae]
CONTIG5447	11964657_f1_2	3027	17130	816	272	YDL246C	564	1.0(10)-54	Saccharomyces cerevisiae	[ui:ydl246c] [pn:strong similarity to sor1p] [gfc:1.1] [kegfc:14.2] [sgdfe:1.5.1] [db:glc-saccharomyces cerevisiae]
CONTIG1067	4807887_c2_4	3028	17131	726	242	YDL174C	442	8.6(10)-42	Saccharomyces cerevisiae	[ui:ydl174c] [pn:d-lactate ferriochrom c oxidoreductase:d-lactate dehydrogenase:cytochrome precursor:d-lactate ferriochrom c oxidoreductase:d-lcr] [gn:ddl:ddl] [gfc:1.1:1.8:2.2:2.8] [ec:1.1.2.4] [kegfc:1.8] [sgdfe:1.5.1:2]

CONTIG4144	10162766_f2_2	3029	17132	1140	380	YDL174C	789	1.5(10)-78	Saccharomyces cerevisiae	[jui:ydl174c] [pn:d-lactate ferricytochrome c oxidoreductase:d- lactate dehydrogenase:cytochrome precursor:d-lactate ferricytochrome c oxidoreductase:d-lcr] [gn:ddl:ddl] [glcfc:1.1:1.8:2.2:2.8] [ec:1.1.2.4] [keggfc:1.8] [sgdfe:1.5.1:2]
CONTIG5161	1173275_c2_9	3030	17133	570	190	YDL174C	163	3.5(10)-11	Saccharomyces cerevisiae	[jui:ydl174c] [pn:d-lactate ferricytochrome c oxidoreductase:d- lactate dehydrogenase:cytochrome precursor:d-lactate ferricytochrome c oxidoreductase:d-lcr] [gn:ddl:ddl] [glcfc:1.1:1.8:2.2:2.8] [ec:1.1.2.4] [keggfc:1.8] [sgdfe:1.5.1:2]
CONTIG3136	22667053_f2_3	3031	17134	429	143	YDL174C	113	8.1(10)-6	Saccharomyces cerevisiae	[jui:ydl174c] [pn:d-lactate ferricytochrome c oxidoreductase:d- lactate dehydrogenase:cytochrome precursor:d-lactate ferricytochrome c oxidoreductase:d-lcr] [gn:ddl:ddl] [glcfc:1.1:1.8:2.2:2.8] [ec:1.1.2.4] [keggfc:1.8] [sgdfe:1.5.1:2]

CONTIG4904	15709552_fl_1	3032	17135	1092	364	YDL174C	825	2.2(10)-82	Saccharomyces cerevisiae	[ui:ydl174c] [pn:d-lactate ferricytochrome c oxidoreductase:d-lactate dehydrogenase:cytochrome precursor:d-lactate ferricytochrome c oxidoreductase:d-lcr] [gn:ddl:ddl] [gicfc:1.1:1.8:2.2:2.8] [ec:1.1.2.4] [keggfc:1.8] [sgdfe:1.5.1:2]
CONTIG4967	33254813_c1_8	3033	17136	402	134	YDL174C	375	2.5(10)-34	Saccharomyces cerevisiae	[ui:ydl174c] [pn:d-lactate ferricytochrome c oxidoreductase:d-lactate dehydrogenase:cytochrome precursor:d-lactate ferricytochrome c oxidoreductase:d-lcr] [gn:ddl:ddl] [gicfc:1.1:1.8:2.2:2.8] [ec:1.1.2.4] [keggfc:1.8] [sgdfe:1.5.1:2]
CONTIG2952	33400443_c2_2	3034	17137	732	244	YDL131W	1075	7.2(10)-109	Saccharomyces cerevisiae	[ui:ydl131w] [pn:similarity to homocitrate synthases and isopropylmalate synthases] [gicfc:1.1:6.6] [keggfc:14.2] [sgdfe:1.1:1.1.5.1] [db:gic-saccharomyces cerevisiae]
CONTIG5285	4718875_fl_2	3035	17138	1446	482	YDL131W	1832	4.4(10)-189	Saccharomyces cerevisiae	[ui:ydl131w] [pn:similarity to homocitrate synthases and isopropylmalate synthases] [gicfc:1.1:6.6] [keggfc:14.2] [sgdfe:1.1:1.1.5.1] [db:gic-saccharomyces cerevisiae]
CONTIG5022	29557677_B3_5	3036	17139	522	174	YDL124W	278	2.1(10)-24	Saccharomyces cerevisiae	[ui:ydl124w] [pn:similarity to aldose reductases] [gicfc:1.1] [keggfc:14.2] [sgdfe:1.5.1] [db:gic-saccharomyces cerevisiae]

CONTIG5207	22453383_f3_4	3037	17140	432	144	YDL124W	270	1.5(10)-23	Saccharomyces cerevisiae	[ui:ydl124w] [pn:similarity to aldose reductases] [gicf:1.1] [keggf:14.2] [sgdfc:1.5.1] [db:gic-saccharomyces cerevisiae]
CONTIG3542	2554692_f1_1	3038	17141	888	296	YDL124W	349	6.2(10)-32	Saccharomyces cerevisiae	[ui:ydl124w] [pn:similarity to aldose reductases] [gicf:1.1] [keggf:14.2] [sgdfc:1.5.1] [db:gic-saccharomyces cerevisiae]
CONTIG2193	4569503_f1_1	3039	17142	930	310	YDL095W	294	5.2(10)-25	Saccharomyces cerevisiae	[ui:ydl095w] [pn:mannosyltransferase:dolichyl-phosphate-mannose--protein mannosyltransferase 1] [gn:pmt1:d2390] [gicf:1.1:7.1:10.7:11.3:12.16] [ec:2.4.1.109] [keggf:7.2] [sgdfc:1.5.1:6.3:0.9:4.0] [db:gic-saccharomyces cerevisiae]
CONTIG3599	12509450_c3_3	3040	17143	834	278	YDL095W	383	1.3(10)-34	Saccharomyces cerevisiae	[ui:ydl095w] [pn:mannosyltransferase:dolichyl-phosphate-mannose--protein mannosyltransferase 1] [gn:pmt1:d2390] [gicf:1.1:7.1:10.7:11.3:12.16] [ec:2.4.1.109] [keggf:7.2] [sgdfc:1.5.1:6.3:0.9:4.0] [db:gic-saccharomyces cerevisiae]
CONTIG4614	4104500_f3_4	3041	17144	1383	461	YDL095W	631	8.0(10)-62	Saccharomyces cerevisiae	[ui:ydl095w] [pn:mannosyltransferase:dolichyl-phosphate-mannose--protein mannosyltransferase 1] [gn:pmt1:d2390] [gicf:1.1:7.1:10.7:11.3:12.16] [ec:2.4.1.109] [keggf:7.2] [sgdfc:1.5.1:6.3:0.9:4.0] [db:gic-saccharomyces cerevisiae]

CONTIG5222	7787_c1_8	3042	17145	1776	592	YDL095W	1545	1.1(10)-158	Saccharomyces cerevisiae	[ui:ydl095w] [pn:mannosyltransferase:dolichyl-phosphate-mannose--protein mannosyltransferase 1] [gn:pm11:d2390] [glcfc:1.1:7.1:10.7:11.3:12.16] [ec:2.4.1.109] [keggfc:7.2] [sgdfc:1.5:1.6:3.0:9.4.0] [db:glc-saccharomyces cerevisiae]
CONTIG4498	26362557_f3_2	3043	17146	1323	441	YDL066W	1467	2.1(10)-150	Saccharomyces cerevisiae	[ui:ydl066w] [pn:nadp+, mitochondrial isocitrate dehydrogenase:nadp, mitochondrial precursor:oxalosuccinate decarboxylase:adh:nadp+-specific icdh:icdp] [gn:icdp1] [glcfc:1.1:1.2:1.8:2.5:2.8:6.16] [ec:1.1.1.42] [keggfc:1.2:2.4:6.9] [sgdf]
CONTIG5772	31328125_f2_13	3044	17147	219	73	YDL055C	91	0.00096	Saccharomyces cerevisiae	[ui:ydl055c] [pn:mannose-1-phosphate guanylyltransferase:atp-mannose-1-phosphate guanylyltransferase:ndp-hexose pyrophosphorylase] [gn:mpg1:psa1] [glcfc:1.1:1.5:9.12] [keggfc:1.5:9.13] [sgdfc:1.5.1] [db:glc-saccharomyces cerevisiae]

CONTIG5772	25820161_f2_14	3045	17148	984	328	YDL055C	1374	1.5(10)-140	Saccharomyces cerevisiae	[ui:ydl055c] [pn:mannose-1-phosphate guanyltrifosphate:atp-mannose-1-phosphate guanyltrifosphate:ndp-hexose pyrophosphorylase] [gn:mpg1:psa1] [gctc:1.1:1.5:9.12] [kegfc:1.5:9.13] [sgdfe:1.5.1] [db:glc-saccharomyces cerevisiae]
CONTIG5779	6647157_c1_15	3046	17149	1389	463	YDL055C	173	4.4(10)-24	Saccharomyces cerevisiae	[ui:ydl055c] [pn:mannose-1-phosphate guanyltrifosphate:atp-mannose-1-phosphate guanyltrifosphate:ndp-hexose pyrophosphorylase] [gn:mpg1:psa1] [gctc:1.1:1.5:9.12] [kegfc:1.5:9.13] [sgdfe:1.5.1] [db:glc-saccharomyces cerevisiae]
CONTIG4188	31808333_f3_2	3047	17150	1332	444	YDL022W	1253	9.9(10)-128	Saccharomyces cerevisiae	[ui:ydl022w] [pn:nad+, cytoplasmic:glycerol-3-phosphate dehydrogenase:nad+ 1] [gn:gpdl:osg1:dar1:hor1:d2830] [gctc:1.1:8.1:12.11] [ec:1.1.1.8] [kegfc:8.1] [sgdfe:1.5.1:9.2:0.10.3.5] [db:glc-saccharomyces cerevisiae]
CONTIG5474	4867002_f3_7	3048	17151	1143	381	YDL022W	1039	4.7(10)-105	Saccharomyces cerevisiae	[ui:ydl022w] [pn:nad+, cytoplasmic:glycerol-3-phosphate dehydrogenase:nad+ 1] [gn:gpdl:osg1:dar1:hor1:d2830] [gctc:1.1:8.1:12.11] [ec:1.1.1.8] [kegfc:8.1] [sgdfe:1.5.1:9.2:0.10.3.5] [db:glc-saccharomyces cerevisiae]

CONTIG5613	16804668_c1_17	3052	17155	1398	466	YDR074W	1257	3.7(10)-128	Saccharomyces cerevisiae	[ui:Ydr074w] [pn:catalyzes the hydrolysis of trehalose 6-phosphate to trehalose:trehalose-6-phosphate phosphatase:ipp] [gn:tps2:pk3:yd8554] [gclfc:1.7.1:7.2:13.2] [ec:3.1.3.12] [kegfc:7.1] [sgdfe:1.5.1:2.7.0]
CONTIG1934	4409650_c1_4	3053	17156	972	324	YDR148C	388	6.2(10)-62	Saccharomyces cerevisiae	[ui:Ydr148c] [pn:2-oxoglutarate dehydrogenase complex c2 component:diacylipoamide succinyltransferase component:c2 of 2-oxoglutarate dehydrogenase complex precursor] [gn:kgd2:yd8358] [gclfc:1.1:1.2:2.8] [ec:2.3.1.61] [kegfc:1.2] [s]
CONTIG2364	11042506_f1_1	3054	17157	264	88	YDR148C	373	1.8(10)-34	Saccharomyces cerevisiae	[ui:Ydr148c] [pn:2-oxoglutarate dehydrogenase complex c2 component:diacylipoamide succinyltransferase component:c2 of 2-oxoglutarate dehydrogenase complex precursor] [gn:kgd2:yd8358] [gclfc:1.1:1.2:2.8] [ec:2.3.1.61] [kegfc:1.2] [s]

CONTIG5523	988557_f1_4	3055	17158	600	200	YDR178W	305	2.8(10)-27	Saccharomyces cerevisiae	[ui:ydr178w] [pn:succinate dehydrogenase membrane anchor subunit for sdh2p:succinate dehydrogenase membrane anchor subunit precursor] [gn:sdh4.yd9395] [gicf:1.1:1.2:2.8] [kegfc:14.2] [sgdfc:1.5:1:2.4:0.2:5.0:9.7:0] [db:gic-saccharom]
CONTIG866	14900381_f2_1	3056	17159	435	145	YDR178W	355	1.3(10)-32	Saccharomyces cerevisiae	[ui:ydr178w] [pn:succinate dehydrogenase membrane anchor subunit for sdh2p:succinate dehydrogenase membrane anchor subunit precursor] [gn:sdh4.yd9395] [gicf:1.1:1.2:2.8] [kegfc:14.2] [sgdfc:1.5:1:2.4:0.2:5.0:9.7:0] [db:gic-saccharom]
CONTIG3342	267212_f1_3	3057	17160	831	277	YDR245W	365	1.2(10)-33	Saccharomyces cerevisiae	[ui:ydr245w] [pn:similarity to s.pombe galactosyltransferase:galactosyltransferase mnn10:bud emergence delay protein 1] [gn:mnn10:bed1.yd8419] [gicf:1.1:1.5:7.1:8.5:10.7:11.3:11.4:12.16:12.8] [ec:2.4.1.-] [kegfc:1.5:7.2:7.3:8.5] [sg

CONTIG3345	31287567_c1_6	3058	17161	360	120	YDR245W	461	8.4(10)-44	Saccharomyces cerevisiae	[ui:y/d245w] [pn:similarity to s.pombe galactosyltransferase:galactosyltransferase mnn10:bud emergence delay protein 1] [gn:mnn10:bed1:y/d8419] [glcfc:1.1:1.5:7.1:8.5:10.7:11.3:11.4:12.16:12.8] [ec:2.4.1.-] [keggfc:1.5:7.2:7.3:8.5] [sg
CONTIG4410	14882157_c3_9	3059	17162	582	194	YDR248C	352	3.0(10)-32	Saccharomyces cerevisiae	[ui:y/d248c] [pn:similarity to e.coli thermoresistant gluconokinase] [glcfc:1.1] [keggfc:14.2] [sgdffc:1.5.1] [db:gic-saccharomyces cerevisiae]
b9x13d94.y	22864593_f1_1	3060	17163	702	234	YDR261C	258	1.7(10)-21	Saccharomyces cerevisiae	[ui:y/d261c] [pn:exo-beta-1,3-glucanase minor isoform:glucan 1,3-beta-glucosidase 2 precursor:exo-1,3-beta-glucanase 2] [gn:exg2:y/d9320a] [glcfc:1.1:1.1:1.12:15:12.8:12.9] [ec:3.2.1.58] [keggfc:14.1] [sgdffc:1.5:1.3:1.0:3.3:0.3:4.0:9.1
CONTIG2277	25969375_f3_2	3061	17164	336	112	YDR371W	140	8.4(10)-9	Saccharomyces cerevisiae	[ui:y/d371w] [pn:similarity to chitinases] [glcfc:11.4:7.2] [keggfc:14.2] [sgdffc:1.5.1] [db:gic-saccharomyces cerevisiae]
CONTIG4409	819407_f2_3	3062	17165	564	188	YDR380W	317	9.4(10)-28	Saccharomyces cerevisiae	[ui:y/d380w] [pn:similarity to pdc6p, thi3p and to pyruvate decarboxylases] [glcfc:1.1:2.2] [keggfc:14.2] [sgdffc:1.5:1:2.6:0] [db:gic-saccharomyces cerevisiae]

CONTIG5019	4869458_f2_2	3063	17166	1351	517	YDR380W	555	9.1(10)-54	Saccharomyces cerevisiae	[ui:ydr380w] [pn:similarity to pdc6p, thi3p and to pyruvate decarboxylases] [gtcf:1.1:2.2] [keggfc:14.2] [sgdfc:1.5.1:2.6.0] [db:gic-saccharomyces cerevisiae]
CONTIG5449	22665811_c1_6	3064	17167	1443	481	YDR483W	1019	6.2(10)-103	Saccharomyces cerevisiae	[ui:ydr483w] [pn:glycolipid 2-alpha-mannosyltransferase] [gn:kre2:mnt1:d8035] [gtcf:1.1:7.1:10.7:11.3:12.16] [ec:2.4.1.131] [keggfc:7.2] [sgdfc:1.5.1:6.3.0:9.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG1247	11954562_f3_2	3065	17168	300	100	YEL058W	312	2.1(10)-27	Saccharomyces cerevisiae	[ui:yel058w] [pn:phosphoacetylglucosamine mutase:acetylglucosamine phosphomutase:n-acetylglucosamine-phosphate mutase] [gn:pcml:agm1] [gtcf:1.1:7.1] [ec:5.4.2.3] [keggfc:4.4] [sgdfc:1.5.1] [db:gic-saccharomyces cerevisiae]
CONTIG4592	4775257_f3_4	3066	17169	1005	335	YEL058W	589	2.2(10)-57	Saccharomyces cerevisiae	[ui:yel058w] [pn:phosphoacetylglucosamine mutase:acetylglucosamine phosphomutase:n-acetylglucosamine-phosphate mutase] [gn:pcml:agm1] [gtcf:1.1:7.1] [ec:5.4.2.3] [keggfc:4.4] [sgdfc:1.5.1] [db:gic-saccharomyces cerevisiae]

CONTIG2326	16808312_c1_2	3067	17170	639	213	YEL011W	663	3.2(10)-65	Saccharomyces cerevisiae	[ui:ye011w] [pn:1,4-glucan branching enzyme:1,4-alpha-glucan branching enzyme:glycogen branching enzyme] [gn:glc3] [gctc:1.1:7.1:7.2] [ec:2.4.1.18] [keggfc:7.1] [sgdfc:1.5.1:2.7.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG639	13875325_f3_1	3068	17171	525	175	YEL011W	590	1.8(10)-57	Saccharomyces cerevisiae	[ui:ye011w] [pn:1,4-glucan branching enzyme:1,4-alpha-glucan branching enzyme:glycogen branching enzyme] [gn:glc3] [gctc:1.1:7.1:7.2] [ec:2.4.1.18] [keggfc:7.1] [sgdfc:1.5.1:2.7.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5305	2937780_f2_5	3069	17172	780	260	YEL002C	215	4.0(10)-17	Saccharomyces cerevisiae	[ui:ye002c] [pn:oligosaccharyl transferase beta subunit precursor:dolichyl-diphosphooligosaccharide--protein glycosyltransferase beta subunit precursor:oligosaccharyl transferase beta subunit] [gn:wbp1] [gctc:1.1:7.1:10.7:11.3:12.16]
CONTIG2053	4960878_f3_1	3070	17173	729	243	YER001W	104	0.00689	Saccharomyces cerevisiae	[ui:yer001w] [pn:alpha-1,3-mannosyltransferase] [gn:mmn1] [gctc:1.1:1.5:7.1:8.5:10.7:11.3:11.4:12.16] [ec:2.4.1.-] [keggfc:1.5:7.2:7.3:8.5] [sgdfc:1.5.1:6.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4094	29391927_f1_1	3071	17174	1479	493	YER001W	415	3.7(10)-38	Saccharomyces cerevisiae	[ui:yer001w] [pn:alpha-1,3-mannosyltransferase] [gn:mn1] [glcfc:1.1:1.5:7.1:8.5:10.7:11.3:11.4:12.16] [ec:2.4.1.-] [keggfc:1.5:7.2:7.3:8.5] [sgdfe:1.5:1:6.3:0.9:4.0] [db:glc-saccharomyces cerevisiae]
CONTIG5102	4719577_c2_4	3072	17175	1065	355	YER001W	251	1.8(10)-20	Saccharomyces cerevisiae	[ui:yer001w] [pn:alpha-1,3-mannosyltransferase] [gn:mn1] [glcfc:1.1:1.5:7.1:8.5:10.7:11.3:11.4:12.16] [ec:2.4.1.-] [keggfc:1.5:7.2:7.3:8.5] [sgdfe:1.5:1:6.3:0.9:4.0] [db:glc-saccharomyces cerevisiae]
CONTIG2078	2070212_f1_1	3073	17176	654	218	YER003C	657	1.3(10)-64	Saccharomyces cerevisiae	[ui:yer003c] [pn:mannose-6-phosphate isomerase:phosphomannose isomerase:pmi:phosphohexomutase] [gn:pmi40] [glcfc:1.1:1.5] [ec:5.3.1.8] [keggfc:1.5] [sgdfe:1.5:1:9.2:0] [db:glc-saccharomyces cerevisiae]
CONTIG2078	197825_f2_2	3074	17177	630	210	YER003C	617	2.5(10)-60	Saccharomyces cerevisiae	[ui:yer003c] [pn:mannose-6-phosphate isomerase:phosphomannose isomerase:pmi:phosphohexomutase] [gn:pmi40] [glcfc:1.1:1.5] [ec:5.3.1.8] [keggfc:1.5] [sgdfe:1.5:1:9.2:0] [db:glc-saccharomyces cerevisiae]

CONTIG5632	22459692_c3_14	3075	17178	1812	604	YFL053W	1131	8.4(10)-115	Saccharomyces cerevisiae	[ui:yf003w] [pn:similarity to c.freundii dihydroxyacetone kinase:putative dihydroxyacetone kinase:glycerone kinase] [gtcf:1.1:8.1] [ec:2.7.1.29] [keggfc:8.1] [sgdfc:1.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2334	21494050_f2_2	3076	17179	369	123	YFL045C	446	3.2(10)-42	Saccharomyces cerevisiae	[ui:yf0045c] [pn:phosphomannomutase:pmm] [gn:sec53:alg4] [gtcf:1.1:1.5:10.7] [ec:5.4.2.8] [keggfc:1.5] [sgdfc:1.5.1:6.3:0.9:2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4663	87782_f2_3	3077	17180	450	150	YFL045C	579	2.6(10)-56	Saccharomyces cerevisiae	[ui:yf0045c] [pn:phosphomannomutase:pmm] [gn:sec53:alg4] [gtcf:1.1:1.5:10.7] [ec:5.4.2.8] [keggfc:1.5] [sgdfc:1.5.1:6.3:0.9:2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5374	12345302_f3_3	3078	17181	546	182	YFL014W	194	1.6(10)-15	Saccharomyces cerevisiae	[ui:yf014w] [pn:heat shock protein:12 kd heat shock protein:glucose and lipid regulated protein] [gn:hsp12:gpl:hor5] [gtcf:12.7.1:1.3:1:12.11:13.2] [keggfc:14.2] [sgdfc:1.5.1:1.6.3:10.3:5.1:1.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5290	14727125_c1_10	3079	17182	1998	666	YFR015C	2352	2.0(10)-254	Saccharomyces cerevisiae	[ui:yf015c] [pn:udp glucose--starch glucosyltransferase, isoform 1:glycogen:starch synthase, isoform 1] [gn:gsy1] [gtcf:1.1:7.1:7.2] [ec:2.4.1.11] [keggfc:7.1] [sgdfc:1.5.1:2.7:0.9:2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3286	1376512_f1_1	3080	17183	768	256	YGL257C	184	1.7(10)-13	Saccharomyces cerevisiae	[ui:ygl257c] [pn:similarity to mmi1p:hypothetical 64.9 kd protein in adh4 5"region] [gn:rd558] [glcfc:1.1:1.5:7.1:8.5:10.7:11.3:11.4] [ec:2.4.1.-1] [keggfc:1.5:7.2:7.3:8.5] [sgdfe:1.5:1:6.3:0] [db:glc-saccharomyces cerevisiae]
CONTIG5102	21900180_c1_2	3081	17184	234	78	YGL257C	94	0.00084	Saccharomyces cerevisiae	[ui:ygl257c] [pn:similarity to mmi1p:hypothetical 64.9 kd protein in adh4 5"region] [gn:rd558] [glcfc:1.1:1.5:7.1:8.5:10.7:11.3:11.4] [ec:2.4.1.-1] [keggfc:1.5:7.2:7.3:8.5] [sgdfe:1.5:1:6.3:0] [db:glc-saccharomyces cerevisiae]
CONTIG455	3941563_c1_1	3082	17185	618	206	YGL156W	384	2.0(10)-34	Saccharomyces cerevisiae	[ui:ygl156w] [pn:alpha-mannosidase:alpha-d-mannoside mannohydrolase] [gn:ams1:g1861] [glcfc:1.1:12.16] [ec:3.2.1.24] [keggfc:14.1] [sgdfe:1.5:1:9.10.0] [db:glc-saccharomyces cerevisiae]
CONTIG5170	13938551_f2_2	3083	17186	1704	568	YGL156W	1543	1.8(10)-158	Saccharomyces cerevisiae	[ui:ygl156w] [pn:alpha-mannosidase:alpha-d-mannoside mannohydrolase] [gn:ams1:g1861] [glcfc:1.1:12.16] [ec:3.2.1.24] [keggfc:14.1] [sgdfe:1.5:1:9.10.0] [db:glc-saccharomyces cerevisiae]

CONTIG57	35647067_f2_1	3084	17187	714	238	YGL156W	167	3.5(10)-22	Saccharomyces cerevisiae	[ui:ygl156w] [pn:alpha-mannosidase:alpha-d-mannoside mannohydrolase] [gn:ams1:g1861] [glcfc:1.1:12.16] [ec:3.2.1.24] [keggfc:14.1] [sgdfc:1.5.1:9.10.0] [db:glc-saccharomyces cerevisiae]
CONTIG5180	20523263_f1_1	3085	17188	1338	446	YGL065C	1055	9.5(10)-107	Saccharomyces cerevisiae	[ui:ygl065c] [pn:mannosyltransferase:glycosyltransferase] [gn:alg2] [glcfc:1.1:1.5:7.1:8.5:10.7:11.3:11.4] [ec:2.4.1.-] [keggfc:1.5:7.2:7.3:8.5] [sgdfc:1.5.1:6.3.0] [db:glc-saccharomyces cerevisiae]
CONTIG5618	189436_c1_20	3086	17189	264	88	YGL038C	190	2.8(10)-14	Saccharomyces cerevisiae	[ui:ygl038c] [pn:alpha-1,6-mannosyltransferase] [gn:och1] [glcfc:1.1:1.5:7.1:8.5:10.7:11.3:11.4] [ec:2.4.1.-] [keggfc:1.5:7.2:7.3:8.5] [sgdfc:1.5.1:6.3.0:9.4.0] [db:glc-saccharomyces cerevisiae]
CONTIG5618	234410_c1_19	3087	17190	495	165	YGL038C	194	1.1(10)-14	Saccharomyces cerevisiae	[ui:ygl038c] [pn:alpha-1,6-mannosyltransferase] [gn:och1] [glcfc:1.1:1.5:7.1:8.5:10.7:11.3:11.4] [ec:2.4.1.-] [keggfc:1.5:7.2:7.3:8.5] [sgdfc:1.5.1:6.3.0:9.4.0] [db:glc-saccharomyces cerevisiae]
CONTIG5088	25664200_c3_10	3088	17191	1995	665	YGL027C	1063	1.3(10)-107	Saccharomyces cerevisiae	[ui:ygl027c] [pn:beta-1,6-glucan assembly protein:protein] [gn:cwn41] [glcfc:1.1:12.16] [keggfc:14.2] [sgdfc:1.5.1:9.4.0] [db:glc-saccharomyces cerevisiae]

CONTIG1629	31454501_c3_3	3089	17192	867	289	YGL022W	919	2.5(10)-92	Saccharomyces cerevisiae	[ui:yg022w] [pn:oligosaccharyl transferase subunit] [gn:stt3] [gctc:1.1:10.7:12.16] [keggfc:14.2] [sgdfe:1.5.1:6.3:0:9:4:0] [db:gtc-saccharomyces cerevisiae]
CONTIG2349	20492336_f2_2	3090	17193	594	198	YGL022W	658	1.1(10)-64	Saccharomyces cerevisiae	[ui:yg022w] [pn:oligosaccharyl transferase subunit] [gn:stt3] [gctc:1.1:10.7:12.16] [keggfc:14.2] [sgdfe:1.5.1:6.3:0:9:4:0] [db:gtc-saccharomyces cerevisiae]
CONTIG1430	22152312_c3_2	3091	17194	1233	411	YGR032W	1388	4.9(10)-142	Saccharomyces cerevisiae	[ui:yg032w] [pn:1,3-beta-d-glucan synthase subunit:1,3-beta-glucan synthase component gls2:1,3-beta-d-glucan-udp glucosyltransferase] [gn:gls2:fls2:gs2] [gctc:1.1:7.2:1.1:12.15] [ec:2.4.1.34] [keggfc:7.1] [sgdfe:1.5.1:3.4:0:9:1.0]
CONTIG2205	33464218_f2_1	3092	17195	807	269	YGR032W	679	1.8(10)-65	Saccharomyces cerevisiae	[ui:yg032w] [pn:1,3-beta-d-glucan synthase subunit:1,3-beta-glucan synthase component gls2:1,3-beta-d-glucan-udp glucosyltransferase] [gn:gls2:fls2:gs2] [gctc:1.1:7.2:1.1:12.15] [ec:2.4.1.34] [keggfc:7.1] [sgdfe:1.5.1:3.4:0:9:1.0]

CONTIG4132	I6054160_c3_5	3093	17196	2424	808	YGR032W	1970	4.7(10)-222	Saccharomyces cerevisiae	[ui:ygr032w] [pn:1,3-beta-d-glucan synthase subunit:1,3-beta-glucan synthase component gls2:1,3-beta-d-glucan-udp glucosyltransferase] [gn:gls2:Rks2:gsc2] [gicfc:1.1:7.2:1.1:12.15] [ec:2.4.1.34] [keggfc:7.1] [sgdfe:1.5:1.3:4.0:9.1.0]
CONTIG293	I0016706_f3_1	3094	17197	681	227	YGR032W	547	2.2(10)-51	Saccharomyces cerevisiae	[ui:ygr032w] [pn:1,3-beta-d-glucan synthase subunit:1,3-beta-glucan synthase component gls2:1,3-beta-d-glucan-udp glucosyltransferase] [gn:gls2:Rks2:gsc2] [gicfc:1.1:7.2:1.1:12.15] [ec:2.4.1.34] [keggfc:7.1] [sgdfe:1.5:1.3:4.0:9.1.0]
b2x17884.x	26368942_f1_1	3095	17198	465	155	YGR032W	674	6.5(10)-65	Saccharomyces cerevisiae	[ui:ygr032w] [pn:1,3-beta-d-glucan synthase subunit:1,3-beta-glucan synthase component gls2:1,3-beta-d-glucan-udp glucosyltransferase] [gn:gls2:Rks2:gsc2] [gicfc:1.1:7.2:1.1:12.15] [ec:2.4.1.34] [keggfc:7.1] [sgdfe:1.5:1.3:4.0:9.1.0]
CONTIG2901	2921875_f3_2	3096	17199	1059	353	YGR282C	914	8.3(10)-92	Saccharomyces cerevisiae	[ui:ygr282c] [pn:endo-beta-1,3-glucanase of the cell wall:glucan 1,3-beta-glucosidase precursor:exo-1,3-beta-glucanase-gp29] [gn:bg12] [gicfc:1.1:1.1.1] [ec:3.2.1.58] [keggfc:14.1] [sgdfe:1.5:1.9.1.0] [db:glc-saccharomyces cerevisiae]

CONTIG5189	22472006_c2_19	3097	17200	954	318	YGR282C	187	1.0(10)-12	Saccharomyces cerevisiae	[ui:yg282c] [pn:endo-beta-1,3-glucanase of the cell wall:glucan 1,3-beta-glucosidase precursor:exo-1,3-beta-glucanase:gp29] [gn:bg12] [gctc:1.1:1.1] [ec:3.2.1.58] [keggfc:14.1] [sgdfc:1.5.1:9.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG5723	14538403_c2_23	3098	17201	1029	343	YGR282C	1004	2.3(10)-101	Saccharomyces cerevisiae	[ui:yg282c] [pn:endo-beta-1,3-glucanase of the cell wall:glucan 1,3-beta-glucosidase precursor:exo-1,3-beta-glucanase:gp29] [gn:bg12] [gctc:1.1:1.1] [ec:3.2.1.58] [keggfc:14.1] [sgdfc:1.5.1:9.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG3749	5104186_c1_4	3099	17202	1533	511	YGR287C	1219	4.0(10)-124	Saccharomyces cerevisiae	[ui:yg287c] [pn:strong similarity to maltase:probable alpha-glucosidase:maltase:flocculent specific protein 2] [gn:fsp2] [gctc:1.1:1.6:7.2] [ec:3.2.1.20] [keggfc:1.6:7.1] [sgdfc:1.5.1] [db:gic-saccharomyces cerevisiae]
CONTIG2949	13834406_c3_6	3100	17203	1284	428	YHL032C	1243	1.1(10)-126	Saccharomyces cerevisiae	[ui:yhl032c] [pn:glycerol kinase:atp:glycerol 3-phosphotransferase:glycerokinase:gk] [gn:gut1] [gctc:1.1:8.1] [ec:2.7.1.30] [keggfc:8.1] [sgdfc:1.5.1] [db:gic-saccharomyces cerevisiae]

CONTIG2949	13163142_c2_5	3101	17204	234	78	YHL032C	123	9.0(10)-7	Saccharomyces cerevisiae	[ui:yhr032c] [pn:glycerol kinase:atp:glycerol 3-phosphotransferase:glycerokinase:glc] [gn:gut1] [gtcf:1.1:8.1] [ec:2.7.1.30] [kegfc:8.1] [sgdfe:1.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5707	9769766_f3_10	3102	17205	780	260	YHR043C	407	4.4(10)-38	Saccharomyces cerevisiae	[ui:yhr043c] [pn:2-deoxyglucose-6-phosphate phosphatase:2-deoxyglucose-6-phosphate phosphatase 2:2-dog-6-p-2] [gn:dog2] [gtcf:1.1:7.1:9.1:9.3:9.4:13.10] [ec:3.1.3.-] [kegfc:4.9:1.9:3:9.4] [sgdfe:1.4.1:1.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3875	34414013_f3_1	3103	17206	777	259	YHR101C	233	1.2(10)-19	Saccharomyces cerevisiae	[ui:yhr101c] [pn:big cells phenotype:hyprothetical 39.1 kd protein in hxt5-nrk1 intergenic region precursor] [gn:big1] [gtcf:1.1:12.8] [kegfc:14.2] [sgdfe:1.5.1:3.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4454	23437500_f1_1	3104	17207	1233	411	YHR104W	925	5.7(10)-93	Saccharomyces cerevisiae	[ui:yhr104w] [pn:strong similarity to d-xylose 1-dehydrogenase:hyprothetical 37.1 kd protein in nrk1-cdc12 intergenic region] [gtcf:1.1] [kegfc:14.2] [sgdfe:1.5.1] [db:gtc-saccharomyces cerevisiae]

CONTIG818	25978312_13_3	3105	17208	453	151	YHR183W	542	2.2(10)-52	Saccharomyces cerevisiae	[ui:y:hr183w] [pn:6-phosphogluconate dehydrogenase:6-phosphogluconate dehydrogenase, decarboxylating] [gn:gnd1] [gicf:1.1:1.3] [ec:1.1.1.44] [keggfc:1.3] [sgdfc:1.5:1.2:3:0:9:2:0] [db:gic-saccharomyces cerevisiae]
blx12596.y	26359680_c2_5	3106	17209	777	259	YHR183W	898	4.0(10)-90	Saccharomyces cerevisiae	[ui:y:hr183w] [pn:6-phosphogluconate dehydrogenase:6-phosphogluconate dehydrogenase, decarboxylating] [gn:gnd1] [gicf:1.1:1.3] [ec:1.1.1.44] [keggfc:1.3] [sgdfc:1.5:1.2:3:0:9:2:0] [db:gic-saccharomyces cerevisiae]
CONTIG5119	9630_c3_6	3107	17210	2532	844	YHR204W	917	4.0(10)-92	Saccharomyces cerevisiae	[ui:y:hr204w] [pn:similarity to alpha-mannosidases:hypothetical 91.2 kd protein in rps7a-sch9 intergenic region] [gicf:1.1] [keggfc:1.4:2] [sgdfc:1.5:1] [db:gic-saccharomyces cerevisiae]
CONTIG1374	21914692_c3_2	3108	17211	621	207	YIL155C	443	9.8(10)-42	Saccharomyces cerevisiae	[ui:y:il155c] [pn:glycerol-3-phosphate dehydrogenase, mitochondrial:glycerol-3-phosphate dehydrogenase mitochondrial precursor:gp-d-m:gp-dh-m] [gn:gu2] [gicf:1.1:2:8:8:1] [ec:1.1.99.5] [keggfc:8.1] [sgdfc:1.5:1:9:7:0] [db:gic-saccharom]

CONTIG1666	14531286_12_3	3109	17212	303	101	YIL155C	107	4.0(10)-5	Saccharomyces cerevisiae	[ui:yil155c] [pn:glycerol-3-phosphate dehydrogenase, mitochondrial:glycerol-3-phosphate dehydrogenase mitochondrial precursor:gpd-m:gpdh-m] [gn:gu2] [gicf:1.1:2.8:8.1] [ec:1.1.99.5] [keggfc:8.1] [sgdfc:1.5.1:9.7.0] [db:gic-saccharom
CONTIG5150	13682650_c3_14	3110	17213	390	130	YIL155C	239	2.7(10)-19	Saccharomyces cerevisiae	[ui:yil155c] [pn:glycerol-3-phosphate dehydrogenase, mitochondrial:glycerol-3-phosphate dehydrogenase mitochondrial precursor:gpd-m:gpdh-m] [gn:gu2] [gicf:1.1:2.8:8.1] [ec:1.1.99.5] [keggfc:8.1] [sgdfc:1.5.1:9.7.0] [db:gic-saccharom
CONTIG5150	4798162_c2_12	3111	17214	597	199	YIL155C	433	1.3(10)-40	Saccharomyces cerevisiae	[ui:yil155c] [pn:glycerol-3-phosphate dehydrogenase, mitochondrial:glycerol-3-phosphate dehydrogenase mitochondrial precursor:gpd-m:gpdh-m] [gn:gu2] [gicf:1.1:2.8:8.1] [ec:1.1.99.5] [keggfc:8.1] [sgdfc:1.5.1:9.7.0] [db:gic-saccharom

CONTIG5555	33228437_f1_2	3112	17215	2313	771	YIL125W	2906	0	Saccharomyces cerevisiae	[ui:yil125w] [pn:2-oxoglutarate dehydrogenase complex e1 component:2-oxoglutarate dehydrogenase e1 component precursor:alpha- ketoglutarate dehydrogenase] [gn:kgd1] [gctfc:1.1:2.2:8.5:14:5:9] [ec:1.2.4.2] [keggfc:1.2:5:9:5:14] [sgdf]
CONTIG5555	10628761_f1_3	3113	17216	681	227	YIL125W	833	3.2(10)-83	Saccharomyces cerevisiae	[ui:yil125w] [pn:2-oxoglutarate dehydrogenase complex e1 component:2-oxoglutarate dehydrogenase e1 component precursor:alpha- ketoglutarate dehydrogenase] [gn:kgd1] [gctfc:1.1:1.2:2:8.5:14:5:9] [ec:1.2.4.2] [keggfc:1.2:5:9:5:14] [sgdf]
CONTIG5034	14532806_c1_9	3114	17217	930	310	YIL124W	448	2.0(10)-42	Saccharomyces cerevisiae	[ui:yil124w] [pn:similarity to c.pertingens nanh protein:hypothetical oxidoreductase in kgd1-sim1 intergenic region] [gctfc:1.1] [ec:1.-.-.] [keggfc:14.1] [sgdfc:1.5:1] [db:gtc-saccharomyces cerevisiae]
CONTIG5649	12691892_f1_1	3115	17218	978	326	YIL124W	411	1.7(10)-38	Saccharomyces cerevisiae	[ui:yil124w] [pn:similarity to c.pertingens nanh protein:hypothetical oxidoreductase in kgd1-sim1 intergenic region] [gctfc:1.1] [ec:1.-.-.] [keggfc:14.1] [sgdfc:1.5:1] [db:gtc-saccharomyces cerevisiae]

CONTIG5652	954401_c3_31	3116	17219	909	303	YIL124W	695	1.3(10)-68	Saccharomyces cerevisiae	[ui:yil124w] [pn:similarity to c.perfringens nanh protein:hypothetical oxidoreductase in kgd1-sim1 intergenic region] [gtcf:1.1] [ec:1.-.-] [keggfc:14.1] [sgdfc:1.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG838	4069012_c2_1	3117	17220	378	126	YIL124W	135	1.0(10)-8	Saccharomyces cerevisiae	[ui:yil124w] [pn:similarity to c.perfringens nanh protein:hypothetical oxidoreductase in kgd1-sim1 intergenic region] [gtcf:1.1] [ec:1.-.-] [keggfc:14.1] [sgdfc:1.5.1] [db:gtc-saccharomyces cerevisiae]
b9x12k34.x	214513_f3_1	3118	17221	612	204	YIL099W	203	1.5(10)-15	Saccharomyces cerevisiae	[ui:yil099w] [pn:sporulation specific glucan 1,4-alpha-glucosidase:glucoamylase, intracellular sporulation-specific glucan 1,4-alpha-glucosidase:1,4-alpha-d-glucan glucosyltransferase] [gn:sgal:sga] [gtcf:1.1:7.2:12.15:12.16] [ec:3.2.1.3]
CONTIG4840	23673437_f3_7	3119	17222	843	281	YIL053W	605	4.5(10)-59	Saccharomyces cerevisiae	[ui:yil053w] [pn:di-glycerol phosphatase:glycerol-3-phosphatase 1] [gn:gppi:thr2] [gtcf:1.1:7.1:9.1:9.3:9.4] [ec:3.1.3.-] [keggfc:4.9.1:9.3:9.4] [sgdfc:1.5.1] [db:gtc-saccharomyces cerevisiae]

CONTIG3128	31649166_c3_2	3120	17223	684	228	YIL014W	103	0.00749	Saccharomyces cerevisiae	[ui:yil014w] [pn:similarity to mnn1p:hypothetical 72.4 kd protein in bar1-pdr1 intergenic region] [gctfc:1.1:1.5:7.1:8.5:10.7:11.3:11.4] [ec:2.4.1.-] [keggtc:1.5:7.2:7.3:8.5] [sgdfe:1.5:1:6.3:0] [db:gtc-saccharomyces cerevisiae]
CONTIG3805	36142267_f1_1	3121	17224	405	135	YIL014W	126	3.6(10)-7	Saccharomyces cerevisiae	[ui:yil014w] [pn:similarity to mnn1p:hypothetical 72.4 kd protein in bar1-pdr1 intergenic region] [gctfc:1.1:1.5:7.1:8.5:10.7:11.3:11.4] [ec:2.4.1.-] [keggtc:1.5:7.2:7.3:8.5] [sgdfe:1.5:1:6.3:0] [db:gtc-saccharomyces cerevisiae]

CONTIG2354	10042502_cl_4	3123	17226	576	192	YIR019C	99	0.04	Saccharomyces cerevisiae	[ui:yir019c] [pn:extracellular alpha-1,4-glucan glucosidase:glucoamylase s1/s2 precursor:glucan 1,4-alpha-glucosidase:1,4-alpha-d-glucan glucohydrolase] [gn:sta1:sta2:ma15] [gdcf:1.1:7.2] [ec:3.2.1.3] [keggf:7.1] [sgdf:1.5.1] [db:
CONTIG2436	19615942_f3_2	3124	17227	1386	462	YIR019C	191	1.0(10)-11	Saccharomyces cerevisiae	[ui:yir019c] [pn:extracellular alpha-1,4-glucan glucosidase:glucoamylase s1/s2 precursor:glucan 1,4-alpha-glucosidase:1,4-alpha-d-glucan glucohydrolase] [gn:sta1:sta2:ma15] [gdcf:1.1:7.2] [ec:3.2.1.3] [keggf:7.1] [sgdf:1.5.1] [db:
CONTIG3786	4688136_f1_1	3125	17228	1665	555	YIR019C	124	0.00055	Saccharomyces cerevisiae	[ui:yir019c] [pn:extracellular alpha-1,4-glucan glucosidase:glucoamylase s1/s2 precursor:glucan 1,4-alpha-glucosidase:1,4-alpha-d-glucan glucohydrolase] [gn:sta1:sta2:ma15] [gdcf:1.1:7.2] [ec:3.2.1.3] [keggf:7.1] [sgdf:1.5.1] [db:

CONTIG5196	24328150_f1_3	3126	17229	966	322	YIR019C	103	0.02999	Saccharomyces cerevisiae	[ui:yir019c] [pn:extracellular alpha-1,4-glucan glucosidase:glucoamylase s1/s2 precursor:glucan 1,4-alpha-glucosidase:1,4-alpha-d-glucan glucohydrolase] [gn:sta1:sta2:ma15] [gicfc:1.1:7.2] [ec:3.2.1.3] [keggfc:7.1] [sgdfe:1.5.1] [db:
CONTIG5526	35604642_f2_3	3127	17230	1800	600	YIR019C	117	0.00289	Saccharomyces cerevisiae	[ui:yir019c] [pn:extracellular alpha-1,4-glucan glucosidase:glucoamylase s1/s2 precursor:glucan 1,4-alpha-glucosidase:1,4-alpha-d-glucan glucohydrolase] [gn:sta1:sta2:ma15] [gicfc:1.1:7.2] [ec:3.2.1.3] [keggfc:7.1] [sgdfe:1.5.1] [db:
CONTIG2924	26688474_c1_6	3128	17231	2460	820	YIR019C	134	4.9(10)-5	Saccharomyces cerevisiae	[ui:yir019c] [pn:extracellular alpha-1,4-glucan glucosidase:glucoamylase s1/s2 precursor:glucan 1,4-alpha-glucosidase:1,4-alpha-d-glucan glucohydrolase] [gn:sta1:sta2:ma15] [gicfc:1.1:7.2] [ec:3.2.1.3] [keggfc:7.1] [sgdfe:1.5.1] [db:
CONTIG145	13866412_c1_3	3129	17232	444	148	YJL216C	221	1.8(10)-17	Saccharomyces cerevisiae	[ui:yjl216c] [pn:strong similarity to mal62p:probable alpha-glucosidase yjl216c:maltase] [gn:j0228:hrf581] [gicfc:1.1:1.6:7.1:7.2] [ec:3.2.1.20] [keggfc:1.6:7.1] [sgdfe:1.5.1:2.7.0] [db:glc-saccharomyces cerevisiae]

CONTIG5760	11724137_c1_27	3130	17233	945	315	YJL155C	859	5.5(10)-86	Saccharomyces cerevisiae	[ui:yj1155c] [pn:fructose-2,6-bisphosphatase] [gn:fbp26.j0575] [gctc:1.1:1.5:12.13] [ec:3.1.3.46] [keggfc:1.5] [sgdfc:1.5:1.1:5:2:9:2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5812	550051_f2_10	3131	17234	1578	526	YJL153C	1722	2.0(10)-177	Saccharomyces cerevisiae	[ui:yj1153c] [pn:myo-inositol-1-phosphate synthase:ips] [gn:inol.j0610] [gctc:1.1:8.2] [ec:5.5.1.4] [keggfc:8.2] [sgdfc:1.5:1:9:2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4143	14453192_c1_3	3132	17235	1170	390	YJL137C	316	1.8(10)-28	Saccharomyces cerevisiae	[ui:yj1137c] [pn:self-glucosylating initiator of glycogen synthesis:glycogen synthetase initiator protein glg2] [gn:glg2.j0663] [gctc:1.1:7.1:7.2] [keggfc:14.2] [sgdfc:1.5:1:2:7.0] [db:gtc-saccharomyces cerevisiae]
b9x10p49.y	14851563_c3_2	3133	17236	630	210	YJL137C	251	1.8(10)-21	Saccharomyces cerevisiae	[ui:yj1137c] [pn:self-glucosylating initiator of glycogen synthesis:glycogen synthetase initiator protein glg2] [gn:glg2.j0663] [gctc:1.1:7.1:7.2] [keggfc:14.2] [sgdfc:1.5:1:2:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4913	31515787_c3_10	3134	17237	795	265	YJL121C	780	1.3(10)-77	Saccharomyces cerevisiae	[ui:yj1121c] [pn:d-ribulose-5-phosphate 3-epimerase:ribulose-phosphate 3-epimerase:ppe:rpc] [gn:pos18.rpel.j0731] [gctc:1.1:1.3:1.4:2.4] [ec:5.1.3.1] [keggfc:1.3:1.4:2.3] [sgdfc:1.5:1:2:3.0] [db:gtc-s

b1x19409.y	1431686_ft_1	3135	17238	648	216	YJL099W	151	9.5(10)-10	Saccharomyces cerevisiae	[ui:yj1099w] [pn:chitin biosynthesis protein:chitin biosynthesis protein chs6:csd3 protein] [gn:chs6:csd3:j0838] [gtcf:1.4:7.2] [keggfc:14.2] [sgdfc:1.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG593	553442_cl_1	3136	17239	828	276	YJL002C	404	9.1(10)-38	Saccharomyces cerevisiae	[ui:yj1002c] [pn:oligosaccharyltransferase, alpha subunit:dolichyl-diphosphooligosaccharide--protein glycosyltransferase alpha subunit precursor:oligosaccharyl transferase alpha subunit:oligosaccharyl transferase 64 kd subunit] [gn:ost
CONTIG1556	25593818_ft_1	3137	17240	732	244	YJL075W	644	3.3(10)-63	Saccharomyces cerevisiae	[ui:yj1075w] [pn:suppressor of pkc1:hyposynthetic 46.3 kd protein in pem2-cdc11 intergenic region precursor] [gn:hoc1:j1830] [gtcf:1.1:10.7:12.8] [keggfc:14.2] [sgdfc:1.5.1:3.1:0.3:2.0:6.3:0] [db:gtc-saccharomyces cerevisiae]
CONTIG1933	10972806_c2_3	3138	17241	774	258	YJL096W	514	2.0(10)-49	Saccharomyces cerevisiae	[ui:yj1096w] [pn:similarity to corynebacterium 2,5-diketo-d-gluconic acid reductase and aldehyde reductases:hyposynthetic 32.3 kd protein in acr1-yuh1 intergenic region] [gn:j1926] [gtcf:1.1] [keggfc:14.2] [sgdfc:1.5.1] [db:gtc-saccha

CONTIG3185	24846062_f2_1	3139	17242	474	158	YJR096W	490	7.0(10)-47	Saccharomyces cerevisiae	[ui:yjr096w] [pn:similarity to corynebacterium 2,5-diketo-d-gluconic acid reductase and aldehyde reductases:hypothetical 32.3 kd protein in acr1-yuh1 intergenic region] [gn:j1926] [gicf:1.1] [keggfc:14.2] [sgdfc:1.5.1] [db:gic-saccha
CONTIG3374	4188388_c2_6	3140	17243	789	263	YJR131W	419	2.3(10)-39	Saccharomyces cerevisiae	[ui:yjr131w] [pn:alpha1,2-mannosidase:mannosyl-oligosaccharide alpha-1,2-mannosidase:man-9-alpha-mannosidase] [gn:mns1;j2110] [gicf:1.14.3:7.1:10.7:11.3:12.16] [keggfc:4.3:4.4:7.2] [sgdfc:1.5.1:6.3:0:9.4.0] [db:gic-saccharomyces cer
CONTIG3374	24039035_c2_5	3141	17244	972	324	YJR131W	634	3.8(10)-62	Saccharomyces cerevisiae	[ui:yjr131w] [pn:alpha1,2-mannosidase:mannosyl-oligosaccharide alpha-1,2-mannosidase:man-9-alpha-mannosidase] [gn:mns1;j2110] [gicf:1.14.3:7.1:10.7:11.3:12.16] [keggfc:4.3:4.4:7.2] [sgdfc:1.5.1:6.3:0:9.4.0] [db:gic-saccharomyces cer
CONTIG1648	25672158_c3_3	3142	17245	1005	335	YJR143C	909	2.7(10)-91	Saccharomyces cerevisiae	[ui:yjr143c] [pn:dolichyl-phosphate-mannose--protein o-mannosyl transferase:dolichyl-phosphate-mannose--protein mannosyltransferase 4] [gn:pmt4;j2176] [gicf:1.17.1:10.7:11.3:12.16] [ec:2.4.1.109] [keggfc:7.2] [sgdfc:1.5.1:6.3:0:9.4.

CONTIG899	22265693_c1_3	3143	17246	840	280	YIRL143C	594	6,7(10)-58	Saccharomyces cerevisiae	[ui:yjrl143c] [pn:dolichyl-phosphate-mannose--protein o-mannosyl transferase:dolichyl-phosphate-mannose--protein mannosyltransferase 4] [gn:pmit4:j2176] [gicfc:1.1:7.1:10.7:11.3:12.16] [ec:2.4.1.109] [kegfc:7.2] [sgdfe:1.5.1:6.3.0:9.4.]
CONTIG1855	30111090_c2_6	3144	17247	1056	352	YKL148C	1183	2,6(10)-120	Saccharomyces cerevisiae	[ui:ykl148c] [pn:succinate dehydrogenase flavoprotein precursor:succinate dehydrogenase:ubiquinone flavoprotein subunit precursor:fp:flavoprotein subunit of complex ii] [gn:sdh1:sdha:ykl602] [gicfc:1.1:1.2:9.12] [kegfc:1.5.2.1:5.3.5.]
CONTIG4678	4335002_c1_7	3145	17248	1239	413	YKL148C	1629	1,3(10)-167	Saccharomyces cerevisiae	[ui:ykl148c] [pn:succinate dehydrogenase flavoprotein precursor:succinate dehydrogenase:ubiquinone flavoprotein subunit precursor:fp:flavoprotein subunit of complex ii] [gn:sdh1:sdha:ykl602] [gicfc:1.1:1.2:9.12] [kegfc:1.5.2.1:5.3.5.]

CONTIG4990	14072152_c1_10	3146	17249	744	248	YKL148C	901	2.0(10)-90	Saccharomyces cerevisiae	[ui:ykl148c] [pn:succinate dehydrogenase flavoprotein precursor:succinate dehydrogenase:ubiquinone flavoprotein subunit precursor:fp:flavoprotein subunit of complex ii] [gn:sdh1:sdha:ykl602] [gcfc:1.1:1.2:9.12] [kegfc:1.5.2.1:5.3.5.]
CONTIG3744	1448762_c2_6	3147	17250	1464	488	YKL104C	1631	8.6(10)-168	Saccharomyces cerevisiae	[ui:ykl104c] [pn:glucosamine--fructose-6-phosphate transaminase:glucosamine--fructose-6-phosphate aminotransferase:isomerizing:hexose phosphate aminotransferase:d-fructose-6- phosphate amidotransferase:gfa1] [gn:gfa1:ykl457] [gcfc:1.1:]
CONTIG2790	35400277_c2_8	3148	17251	207	69	YKL104C	196	1.3(10)-14	Saccharomyces cerevisiae	[ui:ykl104c] [pn:glucosamine--fructose-6-phosphate transaminase:glucosamine--fructose-6-phosphate aminotransferase:isomerizing:hexose phosphate aminotransferase:d-fructose-6- phosphate amidotransferase:gfa1] [gn:gfa1:ykl457] [gcfc:1.1:]

CONTIG3300	7070312_f3_5	3149	17252	1029	343	YKL085W	768	2.5(10)-76	Saccharomyces cerevisiae	[ui:ykl085w] [pn:malate dehydrogenase precursor, mitochondrial:malate dehydrogenase, mitochondrial precursor] [gn:mdh1] [gdc:1.1.1.2:1.8:1.9:2.4:2.5:2.8] [ec:1.1.1.37] [keggdc:1.2:1.8:1.9:2.3:2.4] [sgdgc:1.5:1.2:8.0:9:7.0] [db:gtc-s
CONTIG4726	156500_c3_7	3150	17253	1077	359	YKL085W	764	6.5(10)-76	Saccharomyces cerevisiae	[ui:ykl085w] [pn:malate dehydrogenase precursor, mitochondrial:malate dehydrogenase, mitochondrial precursor] [gn:mdh1] [gdc:1.1.1.2:1.8:1.9:2.4:2.5:2.8] [ec:1.1.1.37] [keggdc:1.2:1.8:1.9:2.3:2.4] [sgdgc:1.5:1.2:8.0:9:7.0] [db:gtc-s
CONTIG5378	9775312_c2_13	3151	17254	1002	334	YKL085W	1007	1.2(10)-101	Saccharomyces cerevisiae	[ui:ykl085w] [pn:malate dehydrogenase precursor, mitochondrial:malate dehydrogenase, mitochondrial precursor] [gn:mdh1] [gdc:1.1.1.2:1.8:1.9:2.4:2.5:2.8] [ec:1.1.1.37] [keggdc:1.2:1.8:1.9:2.3:2.4] [sgdgc:1.5:1.2:8.0:9:7.0] [db:gtc-s

CONTIG1698	16804630_f3_1	3152	17255	507	169	YKL035W	747	4.0(10)-74	Saccharomyces cerevisiae	[ui:yk1035w] [pn:utp--glucose-1-phosphate uridylyltransferase:probable utp--glucose-1-phosphate uridylyltransferase:udp-glucose pyrophosphorylase:udpgp] [gn:ugp1.yk1248] [gicfc:1.1:1.4:1.6:4.3:7.1:7.2:10.7] [ec:2.7.7.9] [keggfc:1.4:1.]
CONTIG3835	24031308_c1_4	3153	17256	255	85	YKL035W	228	2.2(10)-18	Saccharomyces cerevisiae	[ui:yk1035w] [pn:utp--glucose-1-phosphate uridylyltransferase:probable utp--glucose-1-phosphate uridylyltransferase:udp-glucose pyrophosphorylase:udpgp] [gn:ugp1.yk1248] [gicfc:1.1:1.4:1.6:4.3:7.1:7.2:10.7] [ec:2.7.7.9] [keggfc:1.4:1.]
b2x18129.x	2110413_f1_1	3154	17257	510	170	YKL035W	660	6.9(10)-65	Saccharomyces cerevisiae	[ui:yk1035w] [pn:utp--glucose-1-phosphate uridylyltransferase:probable utp--glucose-1-phosphate uridylyltransferase:udp-glucose pyrophosphorylase:udpgp] [gn:ugp1.yk1248] [gicfc:1.1:1.4:1.6:4.3:7.1:7.2:10.7] [ec:2.7.7.9] [keggfc:1.4:1.]
CONTIG114	589582_f2_2	3155	17258	615	205	YKR096W	110	4.0(10)-5	Saccharomyces cerevisiae	[ui:ykr096w] [pn:similarity to mitochondrial aldehyde dehydrogenase ald1p:hyposethical 137.5 kd protein in mp1-ppcl intergenic region] [gicfc:1.1:2.2] [keggfc:14.2] [sgdfe:1.5:1.2:6.0] [db:gic-saccharomyces cerevisiae]

CONTIG2645	34062765_c1_3	3156	17259	477	159	YKR096W	167	4.5(10)-14	Saccharomyces cerevisiae	[ui:ykr096w] [pn:similarity to mitochondrial aldehyde dehydrogenase ald1p;hypothetical 137.5 kd protein in mpl1-ppc1 intergenic region] [gcfc:1.1:2.2] [kegfc:14.2] [sgdfe:1.5:1.2:6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4305	33207500_c2_6	3157	17260	1293	431	YKR096W	402	1.5(10)-38	Saccharomyces cerevisiae	[ui:ykr096w] [pn:similarity to mitochondrial aldehyde dehydrogenase ald1p;hypothetical 137.5 kd protein in mpl1-ppc1 intergenic region] [gcfc:1.1:2.2] [kegfc:14.2] [sgdfe:1.5:1.2:6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG525	5084437_f3_1	3158	17261	843	281	YKR096W	132	1.5(10)-5	Saccharomyces cerevisiae	[ui:ykr096w] [pn:similarity to mitochondrial aldehyde dehydrogenase ald1p;hypothetical 137.5 kd protein in mpl1-ppc1 intergenic region] [gcfc:1.1:2.2] [kegfc:14.2] [sgdfe:1.5:1.2:6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5031	1968761_c3_7	3159	17262	591	197	YLR174W	694	1.7(10)-68	Saccharomyces cerevisiae	[ui:ykr174w] [pn:isocitrate dehydrogenase, cytosolic;isocitrate dehydrogenase:nadp cytoplasmic;oxalosuccinate decarboxylase:ldh:nadp+-specific icdh:ldp] [gn:ldp2:19470] [gcfc:1.1:1.2:2.5:6.16] [ec:1.1.1.42] [kegfc:1.2:2.4:6.9] [sgdf

CONTIG5812	4788275_c3_33	3160	17263	921	307	YLR286C	867	8.0(10)-87	Saccharomyces cerevisiae	[ui:ylr286c] [pn:endochitinase:endochitinase precursor] [gn:csl:18003] [gclfc:1.1.4.7.2] [ec:3.2.1.14] [keggfc:4.4] [sgdfe:1.5.1.3.9.0] [db:gic-saccharomyces cerevisiae]
CONTIG5786	20954511_f2_9	3161	17264	1296	432	YLR300W	1277	2.7(10)-130	Saccharomyces cerevisiae	[ui:ylr300w] [pn:exo-beta-1,3-glucanase:i/i, major isoform:glucan 1,3-beta-glucosidase i/ii precursor:exo-1,3-beta-glucanase i/ii] [gn:exgl:18003] [gclfc:1.1.12.15:12.8:12.9] [ec:3.2.1.58] [keggfc:14.1] [sgdfe:1.5.1.3.1.0.3.3.0.3.4.]
CONTIG4035	33699013_c3_11	3162	17265	1167	389	YLR304C	1478	1.3(10)-151	Saccharomyces cerevisiae	[ui:ylr304c] [pn:aconitate hydratase:aconitate hydratase, mitochondrial precursor:citrate hydro-lyase:aconitase] [gn:acol:glul:18003] [gclfc:1.1.1.2.1.9.2.5:2.8] [ec:4.2.1.3] [keggfc:1.2.1.9.2.4] [sgdfe:1.5.1.2.4.0.9.7.0] [db:gic-sacc
CONTIG5600	22453250_c2_22	3163	17266	1278	426	YLR304C	1732	1.7(10)-178	Saccharomyces cerevisiae	[ui:ylr304c] [pn:aconitate hydratase:aconitate hydratase, mitochondrial precursor:citrate hydro-lyase:aconitase] [gn:acol:glul:18003] [gclfc:1.1.1.2.1.9.2.5:2.8] [ec:4.2.1.3] [keggfc:1.2.1.9.2.4] [sgdfe:1.5.1.2.4.0.9.7.0] [db:gic-sacc

CONTIG5536	22286518_f3_5	3164	17267	1224	408	YLR308W	647	1.6(10)-63	Saccharomyces cerevisiae	[ui:y/r308w] [pn:sporulation-specific chitin deacetylase] [gn:cdaz] [gdcf:1.2.15.1.4.7.2] [keggfc:14.2] [sgdfe:1.5.1.3.4.0] [db:glc-saccharomyces cerevisiae]
CONTIG4773	24297055_c3_10	3165	17268	1689	563	YLR342W	2594	7.7(10)-270	Saccharomyces cerevisiae	[ui:y/r342w] [pn:1.3-beta-d-glucan synthase, catalytic subunit:1.3- beta-glucan synthase component gls1:1.3-beta-d-glucan-udp glucosyltransferase:cdl1 protein:cwn3 protein:rls1 protein:papulacandin b sensitivity protein 1] [gn:gls1:cn]
CONTIG5533	20395001_c1_7	3166	17269	1185	395	YML086C	1011	4.4(10)-102	Saccharomyces cerevisiae	[ui:y/ml086c] [pn:d-arabinono-1,4-lactone oxidase:alo1- galactonolactone oxidase:1-xylo-1,4-lactone oxidase] [gn:alo] [gdcf:1.1.4.3] [ec:1.1.3.24] [keggfc:4.3] [sgdfe:1.5.1] [db:glc-saccharomyces cerevisiae]
CONTIG1090	36132942_f2_1	3167	17270	351	117	YML054C	323	1.6(10)-28	Saccharomyces cerevisiae	[ui:y/ml054c] [pn:lactate dehydrogenase cytochrome b2:cytochrome b2 precursor:l-lactate dehydrogenase:cytochrome:l-lactate fericytochrome c oxidoreductase:l-lcr] [gn:cyb2:ym9958] [gdcf:1.1.1.8.2.8] [ec:1.1.2.3] [keggfc:1.8] [sgdfe:1.

b1x17434.y	20566405_f2_1	3168	17271	612	204	YML054C	462	6.5(10)-44	Saccharomyces cerevisiae	[ui:ym1054c] [pn:lactate dehydrogenase cytochrome b2:cytochrome b2 precursor:l-lactate dehydrogenase:cytochrome:l-lactate ferricytochrome c oxidoreductase:l-ler] [gn:cyb2:ym9958] [gdcf:1.1:1.8:2.8] [ec:1.1.2.3] [keggfc:1.8] [sgdfe:1.
CONTIG5466	36367167_c1_10	3169	17272	2241	747	YMR261C	1328	4.5(10)-165	Saccharomyces cerevisiae	[ui:ymr261c] [pn:alpha.alpha-trehalose-phosphate synthase, 115 kd subunit:alpha.alpha-trehalose-phosphate synthase:udp-forming 115 kd subunit:trehalose-6-phosphate synthase:udp- glucose-glucosephosphate glucosyltransferase] [gn:ipps3.y
CONTIG5308	34079140_f3_5	3170	17273	1641	547	YMR278W	946	8.6(10)-102	Saccharomyces cerevisiae	[ui:ymr278w] [pn:similarity to phosphomannomutases] [gdcf:1.1] [keggfc:14.2] [sgdfe:1.5.1] [db:gic-saccharomyces cerevisiae]
b1x15395.x	165937_c3_2	3171	17274	612	204	YMR306W	492	1.5(10)-45	Saccharomyces cerevisiae	[ui:ymr306w] [pn:similarity to 1,3-beta-glucan synthases] [gdcf:1.1] [keggfc:14.2] [sgdfe:1.5.1] [db:gic-saccharomyces cerevisiae]
CONTIG4903	3381880_c3_8	3172	17275	1089	363	YMR318C	704	1.5(10)-69	Saccharomyces cerevisiae	[ui:ymr318c] [pn:similarity to alcohol-dehydrogenase] [gdcf:1.1:2.2] [keggfc:14.2] [sgdfe:1.5.1:2.6.0] [db:gic-saccharomyces cerevisiae]

CONTIG1076	213538_fl_1	3173	17276	1149	383	YNL283C	122	7.0(10) ⁻⁷	Saccharomyces cerevisiae	[ui:ynl283c] [pn:glucoamylase iii:alpha-1,4-glucan- glucosidase:hyposhethical 52.3 kd protein in mrp110-erg24 intergenic region precursor] [gn:n0583] [gicfc:1.1] [keggfc:14.2] [sgdfe:1.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2028	12236555_fl_1	3174	17277	1839	613	YNL283C	105	0.00559	Saccharomyces cerevisiae	[ui:ynl283c] [pn:glucoamylase iii:alpha-1,4-glucan- glucosidase:hyposhethical 52.3 kd protein in mrp110-erg24 intergenic region precursor] [gn:n0583] [gicfc:1.1] [keggfc:14.2] [sgdfe:1.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG243	25627043_fl_1	3175	17278	477	159	YNL283C	91	0.0061	Saccharomyces cerevisiae	[ui:ynl283c] [pn:glucoamylase iii:alpha-1,4-glucan- glucosidase:hyposhethical 52.3 kd protein in mrp110-erg24 intergenic region precursor] [gn:n0583] [gicfc:1.1] [keggfc:14.2] [sgdfe:1.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4673	3907182_c2_9	3176	17279	435	145	YNL283C	203	1.2(10) ⁻¹⁵	Saccharomyces cerevisiae	[ui:ynl283c] [pn:glucoamylase iii:alpha-1,4-glucan- glucosidase:hyposhethical 52.3 kd protein in mrp110-erg24 intergenic region precursor] [gn:n0583] [gicfc:1.1] [keggfc:14.2] [sgdfe:1.5.1] [db:gtc-saccharomyces cerevisiae]

CONTIG4971	24609436_f3_4	3177	17280	1182	394	YNL283C	102	0.00889	Saccharomyces cerevisiae	[ui:ynl283c] [pn:glucoamylase iii:alpha-1,4-glucan-glucosidase:hypothetical 52.3 kd protein in mrp110-erg24 intergenic region precursor] [gn:n0583] [gicfc:1.1] [keggfc:14.2] [sgdfe:1.5.1] [db:gic-saccharomyces cerevisiae]
CONTIG5359	22366063_c1_11	3178	17281	1824	608	YNL283C	110	0.0032	Saccharomyces cerevisiae	[ui:ynl283c] [pn:glucoamylase iii:alpha-1,4-glucan-glucosidase:hypothetical 52.3 kd protein in mrp110-erg24 intergenic region precursor] [gn:n0583] [gicfc:1.1] [keggfc:14.2] [sgdfe:1.5.1] [db:gic-saccharomyces cerevisiae]
CONTIG5420	26834811_f1_3	3179	17282	2226	742	YNL283C	101	0.047	Saccharomyces cerevisiae	[ui:ynl283c] [pn:glucoamylase iii:alpha-1,4-glucan-glucosidase:hypothetical 52.3 kd protein in mrp110-erg24 intergenic region precursor] [gn:n0583] [gicfc:1.1] [keggfc:14.2] [sgdfe:1.5.1] [db:gic-saccharomyces cerevisiae]
CONTIG5597	26285926_c3_20	3180	17283	1125	375	YNL283C	112	0.00064	Saccharomyces cerevisiae	[ui:ynl283c] [pn:glucoamylase iii:alpha-1,4-glucan-glucosidase:hypothetical 52.3 kd protein in mrp110-erg24 intergenic region precursor] [gn:n0583] [gicfc:1.1] [keggfc:14.2] [sgdfe:1.5.1] [db:gic-saccharomyces cerevisiae]

CONTIG4516	4897181_c1_7	3181	17284	1059	353	YNL274C	849	6.4(10)-85	Saccharomyces cerevisiae	[ui:ynl274c] [pn:similarity to glycerate- and formate-dehydrogenases:hypothetical 38.8 kd protein in me2-sec2 intergenic region] [gn:n0631] [gtcf:1.1] [keggtc:14.2] [sgdgc:1.5.1] [db:glc-saccharomyces cerevisiae]
CONTIG4829	4328177_f2_3	3182	17285	501	167	YNL274C	308	1.3(10)-27	Saccharomyces cerevisiae	[ui:ynl274c] [pn:similarity to glycerate- and formate-dehydrogenases:hypothetical 38.8 kd protein in me2-sec2 intergenic region] [gn:n0631] [gtcf:1.1] [keggtc:14.2] [sgdgc:1.5.1] [db:glc-saccharomyces cerevisiae]
CONTIG4829	1069078_f2_4	3183	17286	492	164	YNL274C	457	2.2(10)-43	Saccharomyces cerevisiae	[ui:ynl274c] [pn:similarity to glycerate- and formate-dehydrogenases:hypothetical 38.8 kd protein in me2-sec2 intergenic region] [gn:n0631] [gtcf:1.1] [keggtc:14.2] [sgdgc:1.5.1] [db:glc-saccharomyces cerevisiae]
CONTIG5786	9938825_c2_27	3184	17287	1095	365	YNL274C	889	3.7(10)-89	Saccharomyces cerevisiae	[ui:ynl274c] [pn:similarity to glycerate- and formate-dehydrogenases:hypothetical 38.8 kd protein in me2-sec2 intergenic region] [gn:n0631] [gtcf:1.1] [keggtc:14.2] [sgdgc:1.5.1] [db:glc-saccharomyces cerevisiae]

CONTIG4392	50906_c3_10	3185	17288	744	248	YNL241C	617	2.5(10)-60	Saccharomyces cerevisiae	[ui:ynl241c] [pn:glucose-6-phosphate 1-dehydrogenase:glucose-6-phosphate 1-dehydrogenase:g6pd] [gn:zwf1:met19:n1110] [gtcf:1.1:3.6:16] [ec:1.1.1.49] [kegfc:1.3:6:9] [sgdfc:1.5:1:2.3:0:9:2:0] [db:gtc-saccharomyces cerevisiae]
b9x10k86.y	23725010_c1_2	3186	17289	243	81	YNL241C	226	4.0(10)-18	Saccharomyces cerevisiae	[ui:ynl241c] [pn:glucose-6-phosphate 1-dehydrogenase:glucose-6-phosphate 1-dehydrogenase:g6pd] [gn:zwf1:met19:n1110] [gtcf:1.1:3.6:16] [ec:1.1.1.49] [kegfc:1.3:6:9] [sgdfc:1.5:1:2.3:0:9:2:0] [db:gtc-saccharomyces cerevisiae]
b9x10k86.y	14116439_c1_1	3187	17290	210	70	YNL241C	226	4.0(10)-18	Saccharomyces cerevisiae	[ui:ynl241c] [pn:glucose-6-phosphate 1-dehydrogenase:glucose-6-phosphate 1-dehydrogenase:g6pd] [gn:zwf1:met19:n1110] [gtcf:1.1:3.6:16] [ec:1.1.1.49] [kegfc:1.3:6:9] [sgdfc:1.5:1:2.3:0:9:2:0] [db:gtc-saccharomyces cerevisiae]
CONTIG765	4345332_13_2	3188	17291	333	111	YNL219C	119	1.7(10)-6	Saccharomyces cerevisiae	[ui:ynl219c] [pn:mannosyltransferase:hydropoetic al 63.8 kd protein in adel2-rap1 intergenic region] [gn:alg9:n1295] [gtcf:1.1:3.4:8:1:8:2] [kegfc:14:2] [sgdfc:1.5:1:1:6:1] [db:gtc-saccharomyces cerevisiae]

CONTIG2407	11883593_f3_3	3189	17292	1002	334	YNL192W	771	3.0(10)-76	Saccharomyces cerevisiae	[ui:ynl192w] [pn:chitin synthase i:chitin synthase 1:chitin-udp acetyl-glucosaminyl transferase 1] [gn:chs1:n1404] [gctc:11.4:7.2] [ec:2.4.1.16] [keggfc:4.4] [sgdfc:1.5:1.3:3.0:3.4:0.3:9.0:9.1:0.9.9.0] [db:gic-saccharomyces cerevisia
CONTIG605	24417067_f3_1	3190	17293	342	114	YNL192W	150	2.1(10)-9	Saccharomyces cerevisiae	[ui:ynl192w] [pn:chitin synthase i:chitin synthase 1:chitin-udp acetyl-glucosaminyl transferase 1] [gn:chs1:n1404] [gctc:11.4:7.2] [ec:2.4.1.16] [keggfc:4.4] [sgdfc:1.5:1.3:3.0:3.4:0.3:9.0:9.1:0.9.9.0] [db:gic-saccharomyces cerevisia
CONTIG933	782035_c3_5	3191	17294	867	289	YNL192W	172	1.3(10)-10	Saccharomyces cerevisiae	[ui:ynl192w] [pn:chitin synthase i:chitin synthase 1:chitin-udp acetyl-glucosaminyl transferase 1] [gn:chs1:n1404] [gctc:11.4:7.2] [ec:2.4.1.16] [keggfc:4.4] [sgdfc:1.5:1.3:3.0:3.4:0.3:9.0:9.1:0.9.9.0] [db:gic-saccharomyces cerevisia
CONTIG5805	882825_c3_40	3192	17295	888	296	YNL117W	808	1.3(10)-80	Saccharomyces cerevisiae	[ui:ynl117w] [pn:malate synthase 1:malate synthase 1, glyoxysomal] [gn:misl:n1921] [gctc:1.1:1.8:1.9:12.6] [ec:4.1.3.2] [keggfc:1.8:1.9] [sgdfc:1.5:1.2:8.0:9.8.0] [db:gic-saccharomyces cerevisiae]

CONTIG3805	12203265_c2_31	3193	17296	804	268	YNL048W	708	5.5(10)-70	Saccharomyces cerevisiae	[ui:ynl117w] [pn:malate synthase 1:malate synthase 1, glyoxysomal] [gn:mls1:n1921] [gcf:1.1.1.8:1.9:12.6] [ec:4.1.3.2] [kegfc:1.8:1.9] [sgdfc:1.5:1.2.8.0:9.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1926	20345077_c1_1	3194	17297	843	281	YNL048W	335	5.2(10)-30	Saccharomyces cerevisiae	[ui:ynl048w] [pn:required for asparagine-linked glycosylation:hypothetical 63.1 kd protein in cox5a-yip3 intergenic region] [gn:alg1:n2510:ynl2510w] [gcf:1.1:10.7] [kegfc:14.2] [sgdfc:1.5:1.6:3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3977	165932_f2_5	3195	17298	780	260	YNL048W	284	2.2(10)-24	Saccharomyces cerevisiae	[ui:ynl048w] [pn:required for asparagine-linked glycosylation:hypothetical 63.1 kd protein in cox5a-yip3 intergenic region] [gn:alg1:n2510:ynl2510w] [gcf:1.1:10.7] [kegfc:14.2] [sgdfc:1.5:1.6:3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3864	25424128_c2_3	3196	17299	378	126	YNL037C	192	1.0(10)-18	Saccharomyces cerevisiae	[ui:ynl037c] [pn:nad+ subunit 1, mitochondrial:isocitrate dehydrogenase:nad, mitochondrial subunit 1 precursor:isocitric dehydrogenase:nad+-specific icdh] [gn:icdh1:n2690] [gcf:1.1:1.2.2.8:10.2] [ec:1.1.1.41] [kegfc:1.2] [sgdfc:1.5]

CONTIG4323	25424128_cl_5	3197	17300	189	63	YNL037C	167	4.7(10)-12	Saccharomyces cerevisiae	[ui:ynl037c] [pn:nad+ subunit 1, mitochondrial:isocitrate dehydrogenase:nad, mitochondrial subunit 1 precursor:isocitric dehydrogenase:nad+-specific icdh] [gn:icdh1:n2690] [gcfc:1.1:2.2:8:10.2] [ec:1.1.1.41] [keggfc:1.2] [sgdfc:1.5]
CONTIG5615	31285037_f2_6	3198	17301	582	194	YNL037C	549	4.0(10)-53	Saccharomyces cerevisiae	[ui:ynl037c] [pn:nad+ subunit 1, mitochondrial:isocitrate dehydrogenase:nad, mitochondrial subunit 1 precursor:isocitric dehydrogenase:nad+-specific icdh] [gn:icdh1:n2690] [gcfc:1.1:2.2:8:10.2] [ec:1.1.1.41] [keggfc:1.2] [sgdfc:1.5]
CONTIG5615	33785937_f3_14	3199	17302	528	176	YNL037C	607	2.7(10)-59	Saccharomyces cerevisiae	[ui:ynl037c] [pn:nad+ subunit 1, mitochondrial:isocitrate dehydrogenase:nad, mitochondrial subunit 1 precursor:isocitric dehydrogenase:nad+-specific icdh] [gn:icdh1:n2690] [gcfc:1.1:2.2:8:10.2] [ec:1.1.1.41] [keggfc:1.2] [sgdfc:1.5]

CONTIG4480	203183_c1_7	3200	17303	309	103	YNL037C	94	1.0(10)-10	Saccharomyces cerevisiae	[ui:yn037c] [pn:nad+ subunit 1, mitochondrial:isocitrate dehydrogenase:nad, mitochondrial subunit 1 precursor:isocitric dehydrogenase:nad+-specific icdh] [gn:ich1:n2690] [gctc:1.1:1.2:2.8:10.2] [ec:1.1.1.41] [keggfc:1.2] [sgdfe:1.5]
CONTIG3933	34408518_c2_8	3201	17304	1200	400	YNR001C	1631	8.6(10)-168	Saccharomyces cerevisiae	[ui:ynr001c] [pn:citrate:si-synthase, mitochondrial:citrate synthase, mitochondrial precursor] [gn:cit1:lys6:glu3:n2019] [gctc:1.1:1.2:1.9:2.8] [ec:4.1.3.7] [keggfc:1.2:1.9] [sgdfe:1.5:1.2:4.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5102	20392202_c3_6	3202	17305	1170	390	YNR059W	137	3.7(10)-6	Saccharomyces cerevisiae	[ui:ynr059w] [pn:similarity to to alpha-1,3-mannosyltransferase:hypothetical 68.1 kd protein in bio3-hxt17 intergenic region] [gn:n3514] [gctc:1.1:1.5:7.1:8.5:10.7:11.3:11.4] [ec:2.4.1.-] [keggfc:1.5:7.2:7.3:8.5] [sgdfe:1.5:1:6.3.0]
CONTIG4580	33244763_f3_4	3203	17306	1167	389	YOL155C	114	0.0023	Saccharomyces cerevisiae	[ui:yol155c] [pn:similarity to glucan 1,4-alpha-glucosidase mal5p] [gctc:1.1] [keggfc:14.2] [sgdfe:1.5.1] [db:gtc-saccharomyces cerevisiae]

CONTIG5313	4329050_c2_10	3204	17307	2481	827	YOL155C	144	7.4(10)-7	Saccharomyces cerevisiae	[ui:yol155c] [pn:similarity to glucan 1,4-alpha-glucosidase mal5p] [gicfc:1.1] [keggfc:1.4.2] [sgdfe:1.5.1] [db:gic-saccharomyces cerevisiae]
CONTIG1522	23990637_c1_2	3205	17308	1407	469	YOR002W	712	6.9(10)-75	Saccharomyces cerevisiae	[ui:yor002w] [pn:glucosyltransferase] [gn:alg6] [gicfc:1.1:10.7] [keggfc:1.4.2] [sgdfe:1.5.1:6.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG3696	24501625_c3_7	3206	17309	798	266	YOR067C	630	1.0(10)-61	Saccharomyces cerevisiae	[ui:yor067c] [pn:glucosyltransferase] [gn:alg8] [gicfc:1.1:1.5:7.1:8.5:10.7:11.3:11.4:12.16] [ec:2.4.1.-] [keggfc:1.5:7.2:7.3:8.5] [sgdfe:1.5.1:6.3.0:9.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG5602	31689583_f2_5	3207	17310	312	104	YOR085W	167	4.4(10)-12	Saccharomyces cerevisiae	[ui:yor085w] [pn:oligosaccharyltransferase gamma subunit:dolichyl-diphosphooligosaccharide--protein glycosyltransferase gamma subunit precursor:oligosaccharyl transferase gamma subunit:oligosaccharyl transferase 34 kd subunit] [gn:osi3]

CONTIG5602	24801576_13_8	3208	17311	729	243	YOR085W	267	3.0(10)-23	Saccharomyces cerevisiae	[ui:yor085w] [pn:oligosaccharyltransferase gamma subunit:dolichyl-diphosphooligosaccharide--protein glycosyltransferase gamma subunit precursor:oligosaccharyl transferase gamma subunit:oligosaccharyl transferase 34 kd subunit] [gn:os3
CONTIG5667	804501_c2_22	3209	17312	723	241	YOR085W	128	3.2(10)-6	Saccharomyces cerevisiae	[ui:yor085w] [pn:oligosaccharyltransferase gamma subunit:dolichyl-diphosphooligosaccharide--protein glycosyltransferase gamma subunit precursor:oligosaccharyl transferase gamma subunit:oligosaccharyl transferase 34 kd subunit] [gn:os3
CONTIG337	15830465_c2_3	3210	17313	255	85	YOR099W	322	4.5(10)-29	Saccharomyces cerevisiae	[ui:yor099w] [pn:strong similarity to mannosyltransferases:probable mannosyltransferase ktr1] [gn:ktr1:yor3189w] [gclfc:1.7.1:10.7.11.3:12.16] [ec:2.4.1.131] [kegglc:7.2] [sgdgc:1.5.1:6.3.0.9.4.0] [db-gtc-saccharomyces cerevisiae]

CONTIG3056	4100277_c3_5	3211	17314	537	179	YOR103C	117	1.1(10)-15	Saccharomyces cerevisiae	[ui:yor103c] [pn:oligosacharyltransferase epsilon subunit:dolichyl-diphosphooligosaccharide--protein glycosyltransferase epsilon subunit:oligosacharyl transferase epsilon subunit:oligosacharyl transferase 16 kd subunit] [gn:ost2.yor]
CONTIG274	10397135_f1_1	3212	17315	831	277	YOR120W	588	2.8(10)-57	Saccharomyces cerevisiae	[ui:yor120w] [pn:galactose-induced protein of aldo/keto reductase family:gey protein] [gn:gey1:gey:031567.yor3269w] [gclfc:1.1:1.1:1.5:1.6:1.7:3.5:4:3:5.13:5:3:5:9:9:3] [ec:1.1.1.-] [keggfc:1.5:1.6:1.7:1.1:1.3:5:4:3:5:3:5:9:5:13:9:3]
CONTIG3907	16103382_c3_4	3213	17316	873	291	YOR120W	608	2.2(10)-59	Saccharomyces cerevisiae	[ui:yor120w] [pn:galactose-induced protein of aldo/keto reductase family:gey protein] [gn:gey1:gey:031567.yor3269w] [gclfc:1.1:1.1:1.5:1.6:1.7:3.5:4:3:5.13:5:3:5:9:9:3] [ec:1.1.1.-] [keggfc:1.5:1.6:1.7:1.1:1.3:5:4:3:5:3:5:9:5:13:9:3]
CONTIG5471	30603437_c3_28	3214	17317	810	270	YOR126C	286	7.5(10)-38	Saccharomyces cerevisiae	[ui:yor126c] [pn:isoamyl acetate hydrolytic enzyme:hyphothetical 27.3 kd protein in cat5-rgal intergenic region] [gn:est2:03287] [gclfc:1.1:2:2] [keggfc:14:2] [sgdfe:1.5:1:2:6:0] [db:glc-saccharomyces cerevisiae]

CONTIG2708	6735432_fl_1	3215	17318	1089	363	YOR136W	1190	4.7(10)-121	Saccharomyces cerevisiae	[ui:yor136w] [pn:nad+ subunit 2, mitochondrial:isocitrate dehydrogenase:nad, mitochondrial subunit 2 precursor:isocitric dehydrogenase:nad+- specific icdh] [gn:dh2:o3326.yor3326w] [gtcf:1.1:2.2:8:10.2] [ec:1.1.4.1] [kegfc:1.2] [
CONTIG2324	2157751_fl_1	3216	17319	1107	369	YOR190W	491	5.5(10)-47	Saccharomyces cerevisiae	[ui:yor190w] [pn:exo-1,3-beta-glucanase precursor:sporulation-specific glucan 1,3-beta-glucosidase precursor:exo-1,3-beta-glucanase] [gn:sprl:ssg1] [gtcf:1.1:1.1:12.15] [ec:3.2.1.58] [kegfc:14.1] [sgdfe:1.5:1.3:4.0:9.1.0] [db:gtc-s
CONTIG1230	34251586_c2_2	3217	17320	834	278	YOR299W	301	9.3(10)-36	Saccharomyces cerevisiae	[ui:yor299w] [pn:weak similarity to csd3p] [gtcf:1.1] [kegfc:14.2] [sgdfe:1.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3825	22454200_fl_3	3218	17321	423	141	YOR299W	441	4.9(10)-41	Saccharomyces cerevisiae	[ui:yor299w] [pn:weak similarity to csd3p] [gtcf:1.1] [kegfc:14.2] [sgdfe:1.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3825	36111388_fl_4	3219	17322	933	311	YOR299W	346	1.1(10)-30	Saccharomyces cerevisiae	[ui:yor299w] [pn:weak similarity to csd3p] [gtcf:1.1] [kegfc:14.2] [sgdfe:1.5.1] [db:gtc-saccharomyces cerevisiae]

CONTIG4154	2116531_f2_2	3220	17323	1134	378	YOR321W	634	3.8(10)-62	Saccharomyces cerevisiae	[ui:yor321w] [pn:mannosyltransferase:dolichyl-phosphate-mannose--protein mannosyltransferase 3] [gn:pmt3:o6148] [gicfc:1.1:7.1:10.7:11.3:12.16] [ec:2.4.1.109] [keggfc:7.2] [sgdffc:1.5.1:6.3:0:9:4.0] [db:gic-saccharomyces cerevisiae]
CONTIG4154	36573817_f1_1	3221	17324	1134	378	YOR321W	719	3.7(10)-71	Saccharomyces cerevisiae	[ui:yor321w] [pn:mannosyltransferase:dolichyl-phosphate-mannose--protein mannosyltransferase 3] [gn:pmt3:o6148] [gicfc:1.1:7.1:10.7:11.3:12.16] [ec:2.4.1.109] [keggfc:7.2] [sgdffc:1.5.1:6.3:0:9:4.0] [db:gic-saccharomyces cerevisiae]
CONTIG5263	24336527_c2_12	3222	17325	1935	645	YOR336W	261	9.5(10)-19	Saccharomyces cerevisiae	[ui:yor336w] [pn:killer toxin-resistance protein:killer toxin-resistance protein 5 precursor] [gn:kres5] [gicfc:1.1:12.16:12.8] [keggfc:14.2] [sgdffc:1.5.1:3.1:0:9:4.0] [db:gic-saccharomyces cerevisiae]
CONTIG5263	3907950_c3_13	3223	17326	1086	362	YOR336W	152	2.5(10)-7	Saccharomyces cerevisiae	[ui:yor336w] [pn:killer toxin-resistance protein:killer toxin-resistance protein 5 precursor] [gn:kres5] [gicfc:1.1:12.16:12.8] [keggfc:14.2] [sgdffc:1.5.1:3.1:0:9:4.0] [db:gic-saccharomyces cerevisiae]

CONTIG5649	15907187_c2_18	3224	17327	1509	503	YOR377W	133	1.5(10)-5	Saccharomyces cerevisiae	[ui:yor377w] [pn:alcohol acetyltransferase:alcohol o-acetyltransferase:aatase] [gn:atf1] [gicfc:1.1] [ec:2.3.1.84] [kegfc:14.1] [sgdfe:1.5.1] [db:gic-saccharomyces cerevisiae]
CONTIG5202	30521890_c2_8	3225	17328	321	107	YPL227C	304	3.6(10)-27	Saccharomyces cerevisiae	[ui:yp1227c] [pn:dolichol-p-glucose synthetase:dolichyl-phosphate beta-glucosyltransferase] [gn:alg5p1437] [gicfc:1.17.1:10.7:11.3:12.16] [ec:2.4.1.117] [kegfc:7.2] [sgdfe:1.5.1:6.3:0.9:4.0] [db:gic-saccharomyces cerevisiae]
CONTIG5202	11756513_c1_6	3226	17329	687	229	YPL227C	443	6.7(10)-42	Saccharomyces cerevisiae	[ui:yp1227c] [pn:dolichol-p-glucose synthetase:dolichyl-phosphate beta-glucosyltransferase] [gn:alg5p1437] [gicfc:1.17.1:10.7:11.3:12.16] [ec:2.4.1.117] [kegfc:7.2] [sgdfe:1.5.1:6.3:0.9:4.0] [db:gic-saccharomyces cerevisiae]
CONTIG3289	25878901_c3_4	3227	17330	396	132	YPL175W	219	1.8(10)-17	Saccharomyces cerevisiae	[ui:yp1175w] [pn:n-acetylglucosaminyl-phosphatidylinositol biosynthetic protein:glucac-pi synthesis protein] [gn:spt14:gp13] [gicfc:1.13.4:8.1:8.2:10.2] [kegfc:14.2] [sgdfe:1.5.1:1.6.1:9.5:0] [db:gic-

CONTIG3690	20603387_c2_6	3228	17331	213	71	YPL175W	233	5.2(10)-19	Saccharomyces cerevisiae	[ui:yp1175w] [pn:n-acetylglucosaminyltransferase:n-acetylglucosaminyl-phosphatidylinositol biosynthetic protein:glcnac-pi synthesis protein] [gn:spt14:gp13] [gicfc:1.1:3.4:8.1:8.2:10.2] [keggfc:14.2] [sgdfe:1.5.1:1.6.1:9.5.0] [db:gtc-
b9x13v36.y	2635466_f1_1	3229	17332	354	118	YPL175W	311	7.7(10)-28	Saccharomyces cerevisiae	[ui:yp1175w] [pn:n-acetylglucosaminyltransferase:n-acetylglucosaminyl-phosphatidylinositol biosynthetic protein:glcnac-pi synthesis protein] [gn:spt14:gp13] [gicfc:1.1:3.4:8.1:8.2:10.2] [keggfc:14.2] [sgdfe:1.5.1:1.6.1:9.5.0] [db:gtc-
b9x13v36.y	12319055_f1_2	3230	17333	459	153	YPL175W	347	1.0(10)-31	Saccharomyces cerevisiae	[ui:yp1175w] [pn:n-acetylglucosaminyltransferase:n-acetylglucosaminyl-phosphatidylinositol biosynthetic protein:glcnac-pi synthesis protein] [gn:spt14:gp13] [gicfc:1.1:3.4:8.1:8.2:10.2] [keggfc:14.2] [sgdfe:1.5.1:1.6.1:9.5.0] [db:gtc-
CONTIG5435	23706287_f1_2	3231	17334	894	298	YPL113C	167	3.5(10)-10	Saccharomyces cerevisiae	[ui:yp1113c] [pn:similarity to glycerate dehydrogenases] [gicfc:1.1] [keggfc:14.2] [sgdfe:1.5.1] [db:gtc-saccharomyces cerevisiae]

CONTIG5451	24394162_r3_7	3232	17335	1170	390	YPL113C	314	3.2(10)-28	Saccharomyces cerevisiae	[ui:ypi113c] [pn:similarity to glycinate dehydrogenases] [gctc:1.1] [keggc:14.2] [sgdfe:1.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG1756	23833126_c2_7	3233	17336	1143	381	YPL088W	833	3.2(10)-83	Saccharomyces cerevisiae	[ui:ypi088w] [pn:similarity to aryl-alcohol dehydrogenases] [gctc:1.1:2.2] [keggc:14.2] [sgdfe:1.5.1:2.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2214	30672192_c3_6	3234	17337	210	70	YPL088W	96	0.00025	Saccharomyces cerevisiae	[ui:ypi088w] [pn:similarity to aryl-alcohol dehydrogenases] [gctc:1.1:2.2] [keggc:14.2] [sgdfe:1.5.1:2.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2434	12540625_c1_3	3235	17338	867	289	YPL088W	714	1.3(10)-70	Saccharomyces cerevisiae	[ui:ypi088w] [pn:similarity to aryl-alcohol dehydrogenases] [gctc:1.1:2.2] [keggc:14.2] [sgdfe:1.5.1:2.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3939	26641500_f2_1	3236	17339	1074	358	YPL088W	821	6.0(10)-82	Saccharomyces cerevisiae	[ui:ypi088w] [pn:similarity to aryl-alcohol dehydrogenases] [gctc:1.1:2.2] [keggc:14.2] [sgdfe:1.5.1:2.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4675	14490927_c1_5	3237	17340	666	222	YPL088W	483	3.8(10)-46	Saccharomyces cerevisiae	[ui:ypi088w] [pn:similarity to aryl-alcohol dehydrogenases] [gctc:1.1:2.2] [keggc:14.2] [sgdfe:1.5.1:2.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4675	9804525_c2_6	3238	17341	1101	367	YPL088W	812	5.4(10)-81	Saccharomyces cerevisiae	[ui:ypi088w] [pn:similarity to aryl-alcohol dehydrogenases] [gctc:1.1:2.2] [keggc:14.2] [sgdfe:1.5.1:2.6.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4704	23907186_f2_2	3239	17342	1062	354	YPL088W	825	2.2(10)-82	Saccharomyces cerevisiae	[ui:yp1088w] [pn:similarity to aryl-alcohol dehydrogenases] [gicfc:1.1:2.2] [keggfc:14.2] [sgdfe:1.5:1.2:6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5081	100927_f3_5	3240	17343	1101	367	YPL088W	927	3.5(10)-93	Saccharomyces cerevisiae	[ui:yp1088w] [pn:similarity to aryl-alcohol dehydrogenases] [gicfc:1.1:2.2] [keggfc:14.2] [sgdfe:1.5:1.2:6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5285	35199055_c3_14	3241	17344	297	99	YPL088W	189	1.3(10)-14	Saccharomyces cerevisiae	[ui:yp1088w] [pn:similarity to aryl-alcohol dehydrogenases] [gicfc:1.1:2.2] [keggfc:14.2] [sgdfe:1.5:1.2:6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5285	4806253_c1_8	3242	17345	738	246	YPL088W	572	1.5(10)-55	Saccharomyces cerevisiae	[ui:yp1088w] [pn:similarity to aryl-alcohol dehydrogenases] [gicfc:1.1:2.2] [keggfc:14.2] [sgdfe:1.5:1.2:6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG214	20348424_c1_3	3243	17346	801	267	YPL088W	650	7.9(10)-64	Saccharomyces cerevisiae	[ui:yp1088w] [pn:similarity to aryl-alcohol dehydrogenases] [gicfc:1.1:2.2] [keggfc:14.2] [sgdfe:1.5:1.2:6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5702	14142011_f2_6	3244	17347	3306	1102	YPR026W	1514	8.1(10)-168	Saccharomyces cerevisiae	[ui:yp1088w] [pn:acid trehalase, vacuolar:ath1 protein] [gn:ath1:yp9367] [gicfc:1.1:7.1:7.2:13.2] [keggfc:14.2] [sgdfe:1.5:1.2:7.0:1.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4820	23912551_f2_2	3245	17348	2046	682	YPR074C	2244	9.5(10)-233	Saccharomyces cerevisiae	[ui:yp1074c] [pn:transketolase 1:ik 1] [gn:tkl1:yp9499] [gdcf:1.1:1.3:2.4:6:6] [cc:2.2.1.1] [keggcf:1.3:2.3] [sgdgc:1.1:1.5.1.2:3.0:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG1006	26572091_f2_1	3246	17349	954	318	YPR159W	758	2.7(10)-75	Saccharomyces cerevisiae	[ui:yp159w] [pn:glucan synthase subunit:beta-glucan synthase-associated protein:killer toxin-resistance protein 6] [gn:kre6] [gdcf:1.1:1.2.16:12.8] [keggcf:14.2] [sgdgc:1.5:1.3.1.0:9.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG330	29492067_f1_1	3247	17350	360	120	YPR159W	384	7.2(10)-35	Saccharomyces cerevisiae	[ui:yp159w] [pn:glucan synthase subunit:beta-glucan synthase-associated protein:killer toxin-resistance protein 6] [gn:kre6] [gdcf:1.1:1.2.16:12.8] [keggcf:14.2] [sgdgc:1.5:1.3.1.0:9.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG444	34611628_c2_2	3248	17351	291	97	YPR159W	377	4.2(10)-34	Saccharomyces cerevisiae	[ui:yp159w] [pn:glucan synthase subunit:beta-glucan synthase-associated protein:killer toxin-resistance protein 6] [gn:kre6] [gdcf:1.1:1.2.16:12.8] [keggcf:14.2] [sgdgc:1.5:1.3.1.0:9.4.0] [db:gic-saccharomyces cerevisiae]

CONTIG5086	3940890_c2_5	3249	17352	1878	626	YPR159W	1080	2.1(10)-109	Saccharomyces cerevisiae	[ui:ypri59w] [pn:glucan synthase subunit:beta-glucan synthesis-associated protein:killer toxin-resistance protein 6] [gn:kref6] [gtcf:1.1:12.16:12.8] [keggfc:14.2] [sgdfc:1.5.1:3.1:0.9:4.0] [db-gtc-saccharomyces cerevisiae]
CONTIG5456	4878288_c1_6	3250	17353	2232	744	YPR159W	1905	8.0(10)-197	Saccharomyces cerevisiae	[ui:ypri59w] [pn:glucan synthase subunit:beta-glucan synthesis-associated protein:killer toxin-resistance protein 6] [gn:kref6] [gtcf:1.1:12.16:12.8] [keggfc:14.2] [sgdfc:1.5.1:3.1:0.9:4.0] [db-gtc-saccharomyces cerevisiae]
CONTIG2523	11723543_f3_2	3251	17354	1107	369	YPR160W	1151	6.4(10)-117	Saccharomyces cerevisiae	[ui:ypri60w] [pn:glycogen phosphorylase] [gn:gph1:p9584] [gtcf:1.1:7.1:7.2] [ec:2.4.1.1] [keggfc:7.1] [sgdfc:1.5.1:2.7:0.9:2.0] [db-gtc-saccharomyces cerevisiae]
CONTIG3133	85313_f2_1	3252	17355	1428	476	YPR160W	1727	5.9(10)-178	Saccharomyces cerevisiae	[ui:ypri60w] [pn:glycogen phosphorylase] [gn:gph1:p9584] [gtcf:1.1:7.1:7.2] [ec:2.4.1.1] [keggfc:7.1] [sgdfc:1.5.1:2.7:0.9:2.0] [db-gtc-saccharomyces cerevisiae]
CONTIG2300	9798291_f1_1	3253	17356	201	67	YPR184W	98	0.001	Saccharomyces cerevisiae	[ui:ypri84w] [pn:similarity to glycogen debranching enzymes] [gtcf:1.1:7.1:7.2] [keggfc:14.2] [sgdfc:1.5.1:2.7:0] [db-gtc-saccharomyces cerevisiae]

CONTIG2300	22462507_f1_2	3254	17357	1263	421	YPR184W	1492	4..7(10)-153	Saccharomyces cerevisiae	[ui:ypri84w] [pn:similarity to glycogen debranching enzymes] [gtcf:1.1:7.1:7.2] [keggfc:14.2] [sgdfc:1.5.1:2.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2669	158443_c1_4	3255	17358	957	319	YPR184W	955	2..7(10)-95	Saccharomyces cerevisiae	[ui:ypri84w] [pn:similarity to glycogen debranching enzymes] [gtcf:1.1:7.1:7.2] [keggfc:14.2] [sgdfc:1.5.1:2.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2669	2478427_c2_5	3256	17359	771	257	YPR184W	482	1..3(10)-44	Saccharomyces cerevisiae	[ui:ypri84w] [pn:similarity to glycogen debranching enzymes] [gtcf:1.1:7.1:7.2] [keggfc:14.2] [sgdfc:1.5.1:2.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2907	22366535_c3_11	3257	17360	897	299	YPR184W	441	3..1(10)-40	Saccharomyces cerevisiae	[ui:ypri84w] [pn:similarity to glycogen debranching enzymes] [gtcf:1.1:7.1:7.2] [keggfc:14.2] [sgdfc:1.5.1:2.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG812	29333590_c3_2	3258	17361	534	178	YPR184W	329	2..7(10)-28	Saccharomyces cerevisiae	[ui:ypri84w] [pn:similarity to glycogen debranching enzymes] [gtcf:1.1:7.1:7.2] [keggfc:14.2] [sgdfc:1.5.1:2.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5611	21675410_f3_5	3259	17362	2181	727	YBR204C	101	0.04	Saccharomyces cerevisiae	[ui:ybr204c] [pn:weak similarity to peroxisomal serine-active lipase:putative peroxisomal lipase in cdc47-ktr3 intergenic region] [gn:ybr1444] [gtcf:1.1:3.2:12.6] [ec:3.1.1.-] [keggfc:1.11] [sgdfc:1.6.2:9.8.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1651	36207628_c3_4	3260	17363	261	87	YJR107W	106	1.8(10)-5	Saccharomyces cerevisiae	[ui:yjr107w] [pn:weak similarity to acylglycerol lipase:hyphothetical lipase in sod1-cpa2 intergenic region] [gn:j1983] [gctc:1.113.2] [ec:3.1.1.-] [keggfc:1.11] [sgdfe:1.6.2] [db:gtc-saccharomyces cerevisiae]
CONTIG5765	24882762_f2_8	3261	17364	1092	364	YJR107W	476	2.2(10)-45	Saccharomyces cerevisiae	[ui:yjr107w] [pn:weak similarity to acylglycerol lipase:hyphothetical lipase in sod1-cpa2 intergenic region] [gn:j1983] [gctc:1.113.2] [ec:3.1.1.-] [keggfc:1.11] [sgdfe:1.6.2] [db:gtc-saccharomyces cerevisiae]
CONTIG2727	14569682_f2_1	3262	17365	1299	433	YKL140W	317	2.6(10)-58	Saccharomyces cerevisiae	[ui:ykl140w] [pn:triacylglycerol lipase:triacylglycerol lipase-cholesterol esterase] [gn:igl1:ykl5] [gctc:1.113.2] [ec:3.1.1.-] [keggfc:1.11] [sgdfe:1.6.2] [db:gtc-saccharomyces cerevisiae]
CONTIG5686	22444052_c2_21	3263	17366	1656	552	YKL140W	1029	2.7(10)-109	Saccharomyces cerevisiae	[ui:ykl140w] [pn:triacylglycerol lipase:triacylglycerol lipase-cholesterol esterase] [gn:igl1:ykl5] [gctc:1.113.2] [ec:3.1.1.-] [keggfc:1.11] [sgdfe:1.6.2] [db:gtc-saccharomyces cerevisiae]
CONTIG2760	23941075_c2_2	3264	17367	183	61	YML126C	125	3.2(10)-7	Saccharomyces cerevisiae	[ui:yml126c] [pn:hydroxymethylglutaryl-coa synthase:hmg-coa synthase:3-hydroxy-3-methylglutaryl coenzyme a synthase] [gn:hmgc:hmgc:ym4987] [gctc:1.113.3.3.4.5.6.8.1.8.2] [ec:4.1.3.5] [keggfc:1.113.3.3.5.6] [sgdfe:1.6.1] [db:gtc-sac]

CONTIG2760	2422938_c2_1	3265	17368	828	276	YML126C	1032	2.6(10)-104	Saccharomyces cerevisiae	[ui:ym1 26c] [pn:hydroxymethylglutaryl-coa synthase:hmg-coa synthase:3-hydroxy-3-methylglutaryl coenzyme a synthase] [gn:hmgc:hmg:ym4987] [gcfc:1.11.3.3.4.5.6.8.1.8.2] [ec:4.1.3.5] [keggfc:1.11.3.3.5.6] [sgdfe:1.6.1] [db:gtc-sacc
CONTIG3692	35204410_f3_3	3266	17369	324	108	YML126C	319	1.6(10)-28	Saccharomyces cerevisiae	[ui:ym1 26c] [pn:hydroxymethylglutaryl-coa synthase:hmg-coa synthase:3-hydroxy-3-methylglutaryl coenzyme a synthase] [gn:hmgc:hmg:ym4987] [gcfc:1.11.3.3.4.5.6.8.1.8.2] [ec:4.1.3.5] [keggfc:1.11.3.3.5.6] [sgdfe:1.6.1] [db:gtc-sacc
CONTIG1947	24646887_f1_1	3267	17370	1242	414	YMR108W	1544	1.3(10)-158	Saccharomyces cerevisiae	[ui:ymr108w] [pn:acetylacate synthase:acetylacate synthase precursor:acetylhydroxy-acid synthase:als:ahas] [gn:ilv2:smr1:ym9718] [gcfc:1.11.1.12.2.8.5.7.6.9.5] [ec:4.1.3.18] [keggfc:1.11.1.12.5.7.9.5] [sgdfe:1.1.1.9.7.0] [db:gtc-s

CONTIG625	24297127_f1_1	3268	17371	801	267	YMR108W	725	8.9(10)-72	Saccharomyces cerevisiae	[ui:ymr108w] [pn:acetylacate synthase:acetylacate synthase precursor:acetylacate synthase synthase:als:ahas] [gn:ilv2:smr:ym9718] [gicf:1.11.1.12.2.8.5.7.6.9.5] [ec:4.1.3.18] [keggf:1.11.1.12.5.7.9.5] [sgdf:1.1.1.9.7.0] [db:gic-s
CONTIG5413	16413900_f3_12	3269	17372	390	130	YPR051W	114	5.0(10)-7	Saccharomyces cerevisiae	[ui:yp051w] [pn:n-acetyltransferase:-1a virus gag protein n-acetyltransferase] [gn:mak3:yp9499] [gicf:1.11.5.12.5.13.5.6.5.8.6.14.6.8.7.1:10.7] [ec:2.3.1.-] [keggf:1.11.4.4.5.6.5.8.5.12.5.13.6.7] [sgdf:6.3.0.9.2.0] [db:gic-sacchar
blx11654.x	2402080_f3_1	3270	17373	696	232	YPR051W	453	5.9(10)-43	Saccharomyces cerevisiae	[ui:yp051w] [pn:n-acetyltransferase:-1a virus gag protein n-acetyltransferase] [gn:mak3:yp9499] [gicf:1.11.5.12.5.13.5.6.5.8.6.14.6.8.7.1:10.7] [ec:2.3.1.-] [keggf:1.11.4.4.5.6.5.8.5.12.5.13.6.7] [sgdf:6.3.0.9.2.0] [db:gic-sacchar
CONTIG3642	22658550_c2_7	3271	17374	1590	530	YJL200C	1704	1.6(10)-175	Saccharomyces cerevisiae	[ui:yj200c] [pn:strong similarity to aconitase in prp21-ubp12 intergenic region] [gn:j0327] [gicf:1.2.1.9.2.5] [ec:4.2.1.3] [keggf:1.2.1.9.2.4] [sgdf:2.4.0] [db:gic-saccharomyces cerevisiae]

CONTIG1617	26757637_c3_7	3272	17375	336	112	YPL262W	195	8.5(10)-15	Saccharomyces cerevisiae	[ui:ypi262w] [pn:fumarate hydratase, mitochondrial precursor:fumarase] [gn:fum1] [gtcf:1.2:2.5:2.8] [ec:4.2.1.2] [keggf:1.2:2.4] [sgdfc:2.4:0.9:2.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4281	36039137_c3_6	3273	17376	456	152	YPL262W	469	1.2(10)-44	Saccharomyces cerevisiae	[ui:ypi262w] [pn:fumarate hydratase, mitochondrial precursor:fumarase] [gn:fum1] [gtcf:1.2:2.5:2.8] [ec:4.2.1.2] [keggf:1.2:2.4] [sgdfc:2.4:0.9:2.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5810	32119037_c1_26	3274	17377	873	291	YPL262W	1044	1.3(10)-105	Saccharomyces cerevisiae	[ui:ypi262w] [pn:fumarate hydratase, mitochondrial precursor:fumarase] [gn:fum1] [gtcf:1.2:2.5:2.8] [ec:4.2.1.2] [keggf:1.2:2.4] [sgdfc:2.4:0.9:2.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
b2x18261.y	35236700_f2_2	3275	17378	597	199	YPL262W	775	4.5(10)-77	Saccharomyces cerevisiae	[ui:ypi262w] [pn:fumarate hydratase, mitochondrial precursor:fumarase] [gn:fum1] [gtcf:1.2:2.5:2.8] [ec:4.2.1.2] [keggf:1.2:2.4] [sgdfc:2.4:0.9:2.0:9.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4206	34256511_f2_2	3276	17379	906	302	YLL041C	1110	1.3(10)-112	Saccharomyces cerevisiae	[ui:yhl041c] [pn:succinate dehydrogenase iron-sulfur protein subunit:succinate dehydrogenase:ubiquinone iron-sulfur protein precursor:ip] [gn:sdh2:sdh:sdh] [gicf:1.2.2.1:2.8.9.12] [ec:1.3.5.1] [keggf:2.1] [sgdf:2.4.0:9.7.0] [db:gt]
CONTIG1106	9938400_f1_1	3277	17380	465	155	YMR118C	196	1.0(10)-15	Saccharomyces cerevisiae	[ui:ymr118c] [pn:strong similarity to succinate dehydrogenase] [gicf:1.2] [keggf:14.2] [sgdf:2.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG2847	595252_c3_2	3278	17381	768	256	YHL011C	965	3.2(10)-97	Saccharomyces cerevisiae	[ui:yhl011c] [pn:ribose-phosphate pyrophosphokinase:ribose-phosphate pyrophosphokinase 3:phosphoribosyl pyrophosphate synthetase 3] [gn:prps3:prps3] [gicf:1.3:4.1:4.2] [ec:2.7.6.1] [keggf:1.3:4.1] [sgdf:1.3.1:1.3.2] [db:gic-saccharo]
CONTIG5817	24005252_c3_60	3279	17382	999	333	YHL011C	1412	1.3(10)-144	Saccharomyces cerevisiae	[ui:yhl011c] [pn:ribose-phosphate pyrophosphokinase:ribose-phosphate pyrophosphokinase 3:phosphoribosyl pyrophosphate synthetase 3] [gn:prps3:prps3] [gicf:1.3:4.1:4.2] [ec:2.7.6.1] [keggf:1.3:4.1] [sgdf:1.3.1:1.3.2] [db:gic-saccharo]

CONTIG4001	10156580_c1_11	3280	17383	1146	382	YKL181W	954	1.8(10)-127	Saccharomyces cerevisiae	[ui:ykl181w] [pn:ribose-phosphate pyrophosphokinase:ribose-phosphate pyrophosphokinase l:phosphoribosyl pyrophosphate synthetase 1] [gn:prps1:prps1:prps:prp1:prps1] [glcfc:1.3:4.1:4.2:12.8] [keggfc:1.3:4.1] [sgdfc:1.3:1.3:2.3:2.0] [db
CONTIG1091	1361015_c1_4	3281	17384	903	301	YBL015W	1146	2.2(10)-116	Saccharomyces cerevisiae	[ui:ybl015w] [pn:acetyl-coa hydroxylase:acetyl-coa deacetylase:acetyl-coa acylase] [gn:ach1:ybl0304:ybl03] [glcfc:1.8:10.2:12.15] [ec:3.1.2.1] [keggfc:1.8] [sgdfc:1.6:4.3:4.0:9.2.0] [db:glc-saccharomyces cerevisiae]
CONTIG2621	16494027_f1_1	3282	17385	504	168	YBL015W	652	4.7(10)-64	Saccharomyces cerevisiae	[ui:ybl015w] [pn:acetyl-coa hydroxylase:acetyl-coa deacetylase:acetyl-coa acylase] [gn:ach1:ybl0304:ybl03] [glcfc:1.8:10.2:12.15] [ec:3.1.2.1] [keggfc:1.8] [sgdfc:1.6:4.3:4.0:9.2.0] [db:glc-saccharomyces cerevisiae]
CONTIG2362	23600010_f3_2	3283	17386	996	332	YML004C	737	4.7(10)-73	Saccharomyces cerevisiae	[ui:yml004c] [pn:lactoylglutathione lyase:methylglyoxalase:aldoketomutase:glyoxalase ii] [gn:glol:ym9571] [glcfc:1.8:5.3] [ec:4.4.1.5] [keggfc:1.8] [sgdfc:1.1:4] [db:glc-saccharomyces cerevisiae]

CONTIG4996	12925905_f1_1	3284	17387	1323	441	YNL104C	1622	7.9(10)-167	Saccharomyces cerevisiae	[ui:ynl104c] [pn:2-isopropylmalate synthase:2-isopropylmalate synthase:alpha-isopropylmalate synthase:alpha-ipm synthetase] [gn:leu4:n2173] [gctc:1.8:2.8:5.7:6.6] [ec:4.1.3.12] [keggfc:1.8:5.7] [sgdfc:1.1:1.9:2.0:9.7.0] [db:gtc-sac
CONTIG4996	26369676_f2_6	3285	17388	426	142	YNL104C	199	5.0(10)-15	Saccharomyces cerevisiae	[ui:ynl104c] [pn:2-isopropylmalate synthase:2-isopropylmalate synthase:alpha-isopropylmalate synthase:alpha-ipm synthetase] [gn:leu4:n2173] [gctc:1.8:2.8:5.7:6.6] [ec:4.1.3.12] [keggfc:1.8:5.7] [sgdfc:1.1:1.9:2.0:9.7.0] [db:gtc-sac
CONTIG5795	9878125_f2_11	3286	17389	1779	593	YNL104C	2107	3.2(10)-218	Saccharomyces cerevisiae	[ui:ynl104c] [pn:2-isopropylmalate synthase:2-isopropylmalate synthase:alpha-isopropylmalate synthase:alpha-ipm synthetase] [gn:leu4:n2173] [gctc:1.8:2.8:5.7:6.6] [ec:4.1.3.12] [keggfc:1.8:5.7] [sgdfc:1.1:1.9:2.0:9.7.0] [db:gtc-sac

CONTIG4925	4789010_f3_4	3287	17390	2079	693	YNR033W	560	2.7(10)-54	Saccharomyces cerevisiae	[ui:ym033w] [pn:para-aminobenzoate synthase:p-aminobenzoic acid synthase:paba synthase] [gn:abz1:n3286] [gicfc:1.8.5.15.5.9.9.10.9.11.9.12] [ec:4.1.3.-] [keggfc:1.8.5.9.5.15.9.13] [sgdfe:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG674	12593901_f3_1	3288	17391	648	216	YNR033W	156	5.0(10)-15	Saccharomyces cerevisiae	[ui:ym033w] [pn:para-aminobenzoate synthase:p-aminobenzoic acid synthase:paba synthase] [gn:abz1:n3286] [gicfc:1.8.5.15.5.9.9.10.9.11.9.12] [ec:4.1.3.-] [keggfc:1.8.5.9.5.15.9.13] [sgdfe:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4320	9820379_c2_8	3289	17392	441	147	YNR033W	361	3.0(10)-32	Saccharomyces cerevisiae	[ui:ym033w] [pn:para-aminobenzoate synthase:p-aminobenzoic acid synthase:paba synthase] [gn:abz1:n3286] [gicfc:1.8.5.15.5.9.9.10.9.11.9.12] [ec:4.1.3.-] [keggfc:1.8.5.9.5.15.9.13] [sgdfe:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5377	4894063_c2_10	3290	17393	1155	385	YGL205W	885	9.9(10)-89	Saccharomyces cerevisiae	[ui:ygl205w] [pn:acyl-coa oxidase:acyl-coenzyme a oxidase] [gn:fox1:pox1] [gicfc:1.8.3.2.12.6] [ec:1.3.3.6] [keggfc:14.1] [sgdfe:1.6.2.8.0.9.8.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1030	7150251_F3_1	3291	17394	582	194	YHR179W	202	8.9(10)-16	Saccharomyces cerevisiae	[ui:Yhr179w] [pn:nadph dehydrogenase:old yellow enzyme, isoform 1:nadph dehydrogenase 2:old yellow enzyme 2] [gn:oye2] [gicf:1.8] [ec:1.6.99.1] [keggfc:1.4.1] [sgdfc:2.8.0] [db:gic-saccharomyces cerevisiae]
CONTIG1952	6_f1_1	3292	17395	699	233	YHR179W	459	1.3(10)-43	Saccharomyces cerevisiae	[ui:Yhr179w] [pn:nadph dehydrogenase:old yellow enzyme, isoform 1:nadph dehydrogenase 2:old yellow enzyme 2] [gn:oye2] [gicf:1.8] [ec:1.6.99.1] [keggfc:1.4.1] [sgdfc:2.8.0] [db:gic-saccharomyces cerevisiae]
CONTIG5235	22375926_F3_9	3293	17396	1260	420	YIL160C	945	4.2(10)-95	Saccharomyces cerevisiae	[ui:Yil160c] [pn:acetyl-coa c-acyltransferase, peroxisomal:3-ketoacyl-coa thiolase peroxisomal precursor:beta-ketothiolase:acetyl-coa acyltransferase:peroxisomal 3-oxoacyl-coa thiolase] [gn:fox3:pox3:pot1] [gicf:1.8.3.1:3.2.3.5.5.13:]
CONTIG592	24489218_f1_1	3294	17397	810	270	YIL160C	397	5.0(10)-37	Saccharomyces cerevisiae	[ui:Yil160c] [pn:acetyl-coa c-acyltransferase, peroxisomal:3-ketoacyl-coa thiolase peroxisomal precursor:beta-ketothiolase:acetyl-coa acyltransferase:peroxisomal 3-oxoacyl-coa thiolase] [gn:fox3:pox3:pot1] [gicf:1.8.3.1:3.2.3.5.5.13:]

CONTIG5551	23492192_f2_5	3295	17398	927	309	YML035C	145	1.6(10)-7	Saccharomyces cerevisiae	[ui:ym1035c] [pn:amp deaminase:myoadenylate deaminase] [gn:amd1:amd] [gctc:1.8:4.1] [ec:3.5.4.6] [keggfc:4.1] [sgdfe:1.3.1:2.8.0] [db:gic-saccharomyces cerevisiae]
CONTIG5551	19782502_f3_9	3296	17399	1833	611	YML035C	1997	1.3(10)-206	Saccharomyces cerevisiae	[ui:ym1035c] [pn:amp deaminase:myoadenylate deaminase] [gn:amd1:amd] [gctc:1.8:4.1] [ec:3.5.4.6] [keggfc:4.1] [sgdfe:1.3.1:2.8.0] [db:gic-saccharomyces cerevisiae]
b9x10f21.y	43438319_f3_1	3297	17400	189	63	YMR170C	184	1.5(10)-13	Saccharomyces cerevisiae	[ui:ymr170c] [pn:aldehyde dehydrogenase 2:nad+, mitochondrial:aldehyde dehydrogenase:nadp+ 2] [gn:ald5:ald2:ym8520] [gctc:1.8:2.8.5.11:5.12:5.13] [ec:1.2.1.5] [keggfc:5.11:5.12:5.13] [sgdfe:2.8.0:9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG1505	23862577_c3_5	3298	17401	879	293	YMR267W	719	3.7(10)-71	Saccharomyces cerevisiae	[ui:ymr267w] [pn:inorganic pyrophosphatase, mitochondrial:inorganic pyrophosphatase, mitochondrial precursor:pyrophosphate phosphohydrolase:ppase] [gn:ipp2:ppa2:ym8156] [gctc:1.8:2.1:2.8:13.10] [ec:3.6.1.1] [keggfc:2.1] [sgdfe:1.4.1]

CONTIG2769	21687625_f1_1	3299	17402	420	140	YPL171C	227	1.3(10)-18	Saccharomyces cerevisiae	[ui:ypi1171c] [pn:naph dehydrogenase:old yellow enzyme, isoform 3:nadph dehydrogenase 3:old yellow enzyme 3] [gn:oye3:p2291] [gltc:1.8] [ec:1.6.99.1] [keggfc:14.1] [sgdfe:2.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4510	14882132_c2_6	3300	17403	276	92	YPL171C	130	6.7(10)-8	Saccharomyces cerevisiae	[ui:ypi1171c] [pn:naph dehydrogenase:old yellow enzyme, isoform 3:nadph dehydrogenase 3:old yellow enzyme 3] [gn:oye3:p2291] [gltc:1.8] [ec:1.6.99.1] [keggfc:14.1] [sgdfe:2.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4694	25438582_f3_3	3301	17404	519	173	YPL171C	167	1.6(10)-22	Saccharomyces cerevisiae	[ui:ypi1171c] [pn:naph dehydrogenase:old yellow enzyme, isoform 3:nadph dehydrogenase 3:old yellow enzyme 3] [gn:oye3:p2291] [gltc:1.8] [ec:1.6.99.1] [keggfc:14.1] [sgdfe:2.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4702	22456326_f3_4	3302	17405	1197	399	YPL171C	706	9.1(10)-70	Saccharomyces cerevisiae	[ui:ypi1171c] [pn:naph dehydrogenase:old yellow enzyme, isoform 3:nadph dehydrogenase 3:old yellow enzyme 3] [gn:oye3:p2291] [gltc:1.8] [ec:1.6.99.1] [keggfc:14.1] [sgdfe:2.8.0] [db:gtc-saccharomyces cerevisiae]

CONTIG567	25508462_c3_4	3303	17406	591	197	YPL171C	383	1.5(10)-35	Saccharomyces cerevisiae	[ui:yp1171c] [pn:naphd dehydrogenase:old yellow enzyme, isoform 3:nadph dehydrogenase 3:old yellow enzyme 3] [gn:oye3:p2291] [gltc:1.8] [ec:1.6.99.1] [keggfc:14.1] [sgdfe:2.8.0] [db:glc-saccharomyces cerevisiae]
CONTIG4807	24318752_f1_1	3304	17407	285	95	YGR204W	404	1.1(10)-36	Saccharomyces cerevisiae	[ui:ygr204w] [pn:c1-tetrahydrofolate synthase:trifunctional enzyme,cytoplasmic:c-1-tetrahydrofolate synthase, cytoplasmic:methylenetetrahydrofolate dehydrogenase / methylenetetrahydrofolate cyclohydrolase / formyltetrahydrofolate synthase]
CONTIG5544	4775775_c1_14	3305	17408	984	328	YKR080W	957	2.2(10)-96	Saccharomyces cerevisiae	[ui:ykr080w] [pn:methylenetetrahydrofolate dehydrogenase:nad+] [gn:mdl.ykr400] [gltc:10.7.1.9:4.1.9.6] [keggfc:1.9.9.8] [sgdfe:1.3.1.9.2.0] [db:glc-saccharomyces cerevisiae]
CONTIG1765	30738136_f2_1	3306	17409	249	83	YBL099W	197	6.5(10)-15	Saccharomyces cerevisiae	[ui:ybl099w] [pn:f1f0-arpase complex, f1 alpha subunit:atp synthase alpha chain, mitochondrial precursor] [gn:ap1.ybl0827] [gltc:2.1.2.8:12.6] [ec:3.6.1.34] [keggfc:2.1] [sgdfe:1.8.2.2.5.0:7.8.0:8.2.0:9.7.0] [db:glc-saccharomyces ce]

CONTIG2935	14548883_F3_5	3307	17410	225	75	YBL099W	165	1.8(10)-11	Saccharomyces cerevisiae	[ui:ybl099w] [pn:flb-atpase complex, fl alpha subunit:atp synthase alpha chain, mitochondrial precursor] [gn:ap1:ybl0827] [gncf:2.1:2.8:12.6] [ec:3.6.1.34] [keggfc:2.1] [sgdfc:1.8:2.2:5.0:7.8:0.8:2.0:9.7.0] [db:gic-saccharomyces ce
CONTIG2935	4069812_f1_2	3308	17411	201	67	YBL099W	163	3.1(10)-11	Saccharomyces cerevisiae	[ui:ybl099w] [pn:flb-atpase complex, fl alpha subunit:atp synthase alpha chain, mitochondrial precursor] [gn:ap1:ybl0827] [gncf:2.1:2.8:12.6] [ec:3.6.1.34] [keggfc:2.1] [sgdfc:1.8:2.2:5.0:7.8:0.8:2.0:9.7.0] [db:gic-saccharomyces ce
CONTIG3694	16411067_c2_6	3309	17412	654	218	YBL099W	862	2.7(10)-86	Saccharomyces cerevisiae	[ui:ybl099w] [pn:flb-atpase complex, fl alpha subunit:atp synthase alpha chain, mitochondrial precursor] [gn:ap1:ybl0827] [gncf:2.1:2.8:12.6] [ec:3.6.1.34] [keggfc:2.1] [sgdfc:1.8:2.2:5.0:7.8:0.8:2.0:9.7.0] [db:gic-saccharomyces ce
CONTIG5727	32432775_c2_22	3310	17413	1464	488	YBL045C	754	7.5(10)-75	Saccharomyces cerevisiae	[ui:ybl045c] [pn:ubiquinol-cytochrome-c reductase 44k core protein:ubiquinol-cytochrome-c reductase complex core protein i precursor] [gn:qcr1:cor1:ybl0403] [gncf:2.1:2.8] [ec:1.10.2.2] [keggfc:2.1] [sgdfc:2.5:0.9:7.0] [db:gic-saccha

CONTIG3623	20319502_f1_1	3311	17414	240	80	YBR011C	284	4.7(10)-25	Saccharomyces cerevisiae	[ui:yr011c] [pn:inorganic pyrophosphatase, cytoplasmic:inorganic pyrophosphatase:pyrophosphate phospho-hydrolase:ppase] [gn:ippl:ppal:ppa:yr0202] [gctc:2.1:13.10] [ec:3.6.1.1] [keggfc:2.1] [sgdfe:1.4.1:9.2.0] [db:gtc-saccharomyces]
CONTIG3623	15742305_f2_3	3312	17415	624	208	YBR011C	638	1.5(10)-62	Saccharomyces cerevisiae	[ui:yr011c] [pn:inorganic pyrophosphatase, cytoplasmic:inorganic pyrophosphatase:pyrophosphate phospho-hydrolase:ppase] [gn:ippl:ppal:ppa:yr0202] [gctc:2.1:13.10] [ec:3.6.1.1] [keggfc:2.1] [sgdfe:1.4.1:9.2.0] [db:gtc-saccharomyces]
CONTIG2846	33719567_c1_4	3313	17416	552	184	YBR039W	533	2.0(10)-51	Saccharomyces cerevisiae	[ui:yr039w] [pn:flb-ai-pase complex, fl gamma subunit:ai-p synthase gamma chain, mitochondrial precursor] [gn:atp3:yr0408] [gctc:2.1:2.8:12.6] [ec:3.6.1.34] [keggfc:2.1] [sgdfe:1.8.2:2.5:0:7.8:0.8:2.0:9.7.0] [db:gtc-saccharomyces ce]
CONTIG4062	89787_c2_7	3314	17417	846	282	YBR127C	1250	2.1(10)-127	Saccharomyces cerevisiae	[ui:yr127c] [pn:h+-ai-pase v1 domain 60 kd subunit, vacuolar:vacuolar ai-p synthase subunit b-v-ai-pase 57 kd subunit] [gn:vma2:vat2:yr1002] [gctc:2.1:12.13:12.16:12.5:12.6] [ec:3.6.1.34] [keggfc:2.1] [sgdfe:1.8.2:7.2:7.8:0.8:5.0:9.]

CONTIG4062	4726061_c1_6	3315	17418	747	249	YBR127C	1092	1.1(10)-110	Saccharomyces cerevisiae	[ui:y:br127c] [pn:h+-atpase v1 domain 60 kd subunit, vacuolar: vacuolar atp synthase subunit b:v-atpase 57 kd subunit] [gn: vma2:va2:y:br1002] [gicfc:2.1:12.13:12.16:12.5:12.6] [ec:3.6.1.34] [keggfc:2.1] [sgdfc:1.8.2:7.2.7.8.0:8.5:0:9.
CONTIG269	24096875_f1_1	3316	17419	477	159	YDL185W	551	2.3(10)-52	Saccharomyces cerevisiae	[ui:y:dl185w] [pn:h+-atpase v1 domain 69 kd catalytic subunit, vacuolar: vacuolar atp synthase catalytic subunit a: contains: vma1-derived endonuclease: vde: pi-sce i endonuclease] [gn: vma1: ttp1: c: s8: d1286: vde] [gicfc:2.1:12.13:12.16:12.5:12
CONTIG5373	10643761_c3_11	3317	17420	504	168	YDL185W	750	3.2(10)-74	Saccharomyces cerevisiae	[ui:y:dl185w] [pn:h+-atpase v1 domain 69 kd catalytic subunit, vacuolar: vacuolar atp synthase catalytic subunit a: contains: vma1-derived endonuclease: vde: pi-sce i endonuclease] [gn: vma1: ttp1: c: s8: d1286: vde] [gicfc:2.1:12.13:12.16:12.5:12
CONTIG5373	4461_c3_10	3318	17421	1368	456	YDL185W	1270	3.5(10)-215	Saccharomyces cerevisiae	[ui:y:dl185w] [pn:h+-atpase v1 domain 69 kd catalytic subunit, vacuolar: vacuolar atp synthase catalytic subunit a: contains: vma1-derived endonuclease: vde: pi-sce i endonuclease] [gn: vma1: ttp1: c: s8: d1286: vde] [gicfc:2.1:12.13:12.16:12.5:12

CONTIG5447	10003338_f2_5	3319	17422	627	209	YDL004W	372	2.2(10)-34	Saccharomyces cerevisiae	[ui:ydl004w] [pn:fl0-atpase complex, fl delta subunit:atp synthase delta chain, mitochondrial precursor] [gn:atp16:atp4:atp14:ydb119] [gdcf:2.1:2.8:12.6] [ec:3.6.1.34] [keggfc:2.1] [sgdc:1.8.2:2.5:0.7:8.0:8.2:0.9:7.0] [db:gic-sacch]
CONTIG5720	15039087_f3_15	3320	17423	687	229	YDR298C	492	4.4(10)-47	Saccharomyces cerevisiae	[ui:ydr298c] [pn:fl0-atpase complex, osep subunit:atp synthase oligomycin sensitivity conferral protein precursor, mitochondrial:osep:atp synthase chain 5] [gn:atp5:osep:d9740] [gdcf:2.1:2.8:12.6] [ec:3.6.1.34] [keggfc:2.1] [sgdc:1]
CONTIG1452	408442_f1_2	3321	17424	387	129	YDR529C	271	1.1(10)-23	Saccharomyces cerevisiae	[ui:ydr529c] [pn:ubiquinol cytochrome-c reductase subunit 7:ubiquinol-cytochrome c reductase complex 14 kd protein:complex iii subunit vii] [gn:qr7:cro1:uer7:d9719] [gdcf:2.1:2.8] [ec:1.10.2.21] [keggfc:2.1] [sgdc:2.5:0.9:7.0] [db:g]
CONTIG1518	10969056_f1_2	3322	17425	576	192	YEL051W	683	2.5(10)-67	Saccharomyces cerevisiae	[ui:yel051w] [pn:h+-atpsynthase v1 domain 32 kd subunit, vacuolar:vacuolar atp synthase subunit d:v-atpase d subunit] [gn:yma8:sgp-orf11] [gdcf:2.1:12.13:12.16:12.5:12.6] [ec:3.6.1.34] [keggfc:2.1] [sgdc:1.8.2:7.2:2.7:8.0:8.5:0.9:1]

CONTIG347	969003_c2_3	3323	17426	315	105	YEL051W	182	3.1(10)-14	Saccharomyces cerevisiae	[ui:ye1051w] [pn:h+-atp synthase v1 domain 32 kd subunit, vacuolar: vacuolar atp synthase subunit d: v-atpase d subunit] [gn: vma8: sygp-orf11] [gtrfc: 2.1:12.13:12.16:12.5:12.6] [ec: 3.6.1.34] [keggfc: 2.1] [sgdfe: 1.8.2:7.2.2:7.8.0:8.5.0:9.1
CONTIG5740	10053126_f3_9	3324	17427	600	200	YEL024W	742	1.3(10)-73	Saccharomyces cerevisiae	[ui:ye1024w] [pn: ubiquinol--cytochrome-c reductase iron-sulfur protein precursor: ubiquinol-cytochrome c reductase iron-sulfur subunit precursor: rieske iron-sulfur protein: risp] [gn: rip1] [gtrfc: 2.1:2.8] [ec: 1.10.2.2] [keggfc: 2.1] [sgd
CONTIG4983	26375431_c1_10	3325	17428	351	117	YFR033C	193	2.1(10)-15	Saccharomyces cerevisiae	[ui:yfr033c] [pn: ubiquinol--cytochrome-c reductase 17k protein: ubiquinol-cytochrome c reductase complex 17 kd protein: mitochondrial hinge protein: complex iii polypeptide vi] [gn: qcr6: ucr6] [gtrfc: 2.1:2.8] [ec: 1.10.2.2] [keggfc: 2.1] [s
CONTIG3417	34259840_c2_4	3326	17429	504	168	YGL191W	289	1.3(10)-25	Saccharomyces cerevisiae	[ui:ygl191w] [pn: cytochrome-c oxidase chain via: cytochrome c oxidase polypeptide via precursor] [gn: cox13: g1341] [gtrfc: 2.1:2.8] [ec: 1.9.3.1] [keggfc: 2.1] [sgdfe: 2.5.0:9.7.0] [db: gic-saccharomyces cerevisiae]

CONTIG3435	1048127_f1_1	3327	17430	492	164	YGL187C	371	2.8(10)-34	Saccharomyces cerevisiae	[ui:yg1187c] [pn:cytochrome-c oxidase chain iv:cytochrome c oxidase polypeptide iv precursor] [gn:cox4:g1362] [gctc:2.1:2.8] [ec:1.9.3.1] [keggc:2.1] [sgdgc:2.5.0.9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2979	26267512_c3_12	3328	17431	495	165	YGR020C	417	3.8(10)-39	Saccharomyces cerevisiae	[ui:yg020c] [pn:h+-atpase v1 domain 14 kda subunit, vacuolar:vacuolar atp synthase 14 kd subunit:v-atpase f subunit] [gn:vma7] [gctc:2.1:12.13:12.16:12.5:12.6] [ec:3.6.1.34] [keggc:2.1] [sgdgc:1.8.2:7.2.2:7.8.0:8.5.0.9.10.0] [db:gt]
CONTIG3241	11223961_c3_7	3329	17432	222	74	YGR020C	251	1.5(10)-21	Saccharomyces cerevisiae	[ui:yg020c] [pn:h+-atpase v1 domain 14 kda subunit, vacuolar:vacuolar atp synthase 14 kd subunit:v-atpase f subunit] [gn:vma7] [gctc:2.1:12.13:12.16:12.5:12.6] [ec:3.6.1.34] [keggc:2.1] [sgdgc:1.8.2:7.2.2:7.8.0:8.5.0.9.10.0] [db:gt]
CONTIG3488	9807927_f3_3	3330	17433	240	80	YGR183C	111	1.0(10)-6	Saccharomyces cerevisiae	[ui:yg183c] [pn:ubiquinol cytochrome-c reductase subunit 9:ubiquinol-cytochrome c reductase complex 7.3 kd protein:complex iii polypeptide ix] [gn:qcr9:ucr9] [gctc:2.1:2.8] [ec:1.10.2.2] [keggc:2.1] [sgdgc:2.5.0.9.7.0] [db:gtc-sac]

CONTIG754	14570318_c2_2	3331	17434	321	107	YHR051W	328	1.0(10)-29	Saccharomyces cerevisiae	[ui:yhr051w] [pn:cytochrome c oxidase subunit vi:cytochrome c oxidase polypeptide vi precursor] [gn:cox6] [gcf:2.1:2.8] [ec:1.9.3.1] [keggfc:2.1] [sgdf:2.5:0.9:7.0] [db:glc-saccharomyces cerevisiae]
CONTIG5151	2128802_f2_3	3332	17435	345	115	YJL166W	331	5.0(10)-30	Saccharomyces cerevisiae	[ui:yjl166w] [pn:ubiquinol-cytochrome-c reductase chain viii:ubiquinol-cytochrome c reductase complex ubiquinone-binding protein qp-c:ubiquinol-cytochrome c reductase complex 11 kd protein:complex iii subunit viii] [gn:qcr8:j0526] [gt]
CONTIG5804	4725785_f2_22	3333	17436	1596	532	YJR121W	2122	8.1(10)-220	Saccharomyces cerevisiae	[ui:yjr121w] [pn:ft0-atpase complex, f1 beta subunit:atp synthase beta chain, mitochondrial precursor] [gn:atp2:j2041] [gcf:2.1:2.8:12.6] [ec:3.6.1.34] [keggfc:2.1] [sgdf:1.8:2.2:5.0:7.8:0.8:2.0:9.7.0] [db:glc-saccharomyces cerevi]
CONTIG3015	10680437_f2_2	3334	17437	369	123	YKL192C	131	5.9(10)-11	Saccharomyces cerevisiae	[ui:ykl192c] [pn:strong similarity to n.crassa s.pombe and a.thaliana acyl-carrier proteins:acyl carrier protein, mitochondrial precursor:acp:nadh-ubiquinone oxidoreductase 9,6 kd subunit] [gcf:2.1:2.8:3.4:8.1:8.2:9.12] [keggfc:2.1]

CONTIG5506	23447192_c1_9	3335	17438	336	112	YKL192C	172	3.5(10)-13	Saccharomyces cerevisiae	[ui:ykl192c] [pn:strong similarity to n. crassa s.pombe and a.thaliana acyl-carrier proteins:acyl carrier protein, mitochondrial precursor:acp:nadh- ubiquinone oxidoreductase 9.6 kd subunit] [gtcf:2.1:2.8:3.4:8.1:8.2:9.12] [kegfc:2.1]
CONTIG3620	33437811_f3_1	3336	17439	948	316	YKL080W	733	1.3(10)-72	Saccharomyces cerevisiae	[ui:ykl080w] [pn:ht-atpase v1 domain 42 kd subunit, vacuolar: vacuolar atp synthase subunit c:v- atpase c subunit:v- atpase 42 kd subunit] [gn:vma5:vat3:vatc:ykl1410] [gtcf:2.1:12.13:12.16:12.5:12.6] [ec:3.6.1.34] [kegfc:2.1] [sgdfc:1.1]
CONTIG4408	26182837_f3_3	3337	17440	645	215	YKL016C	441	1.1(10)-41	Saccharomyces cerevisiae	[ui:ykl016c] [pn:fl0-atpase complex, fo d subunit:atp synthase d chain, mitochondrial] [gn:atp7] [gtcf:2.1:2.8:12.6] [ec:3.6.1.34] [kegfc:2.1] [sgdfc:1.8:2.2:5.0:7.8:0.8:2.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3201	20391932_c2_8	3338	17441	267	89	YLR038C	294	4.2(10)-26	Saccharomyces cerevisiae	[ui:ylr038c] [pn:cytochrome-c oxidase, subunit vib:cytochrome c oxidase polypeptide vib:acd] [gn:cox12] [gtcf:2.1:2.8:12.16] [ec:1.9.3.1] [kegfc:2.1] [sgdfc:2.5:0.6:4.0:9.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5669	1032635_c2_26	3339	17442	315	105	YLR395C	112	8.0(10)-7	Saccharomyces cerevisiae	[ui:yhr395c] [pn:cytochrome-c oxidase chain viii:cytochrome c oxidase polypeptide viii precursor] [gn:cox8:l8084] [gdcf:2.1:2.8] [ec:1.9.3.11] [keggcf:2.1] [sgdfe:2.5:0.9:7.0] [db:gic-saccharomyces cerevisiae]
CONTIG5606	26047716_f1_1	3340	17443	1170	390	YLR447C	1082	1.3(10)-109	Saccharomyces cerevisiae	[ui:yhr447c] [pn:h+-atpase v0 domain 36 kd subunit, vacuolar:vacuolar atp synthase subunit ac39:v-atpase ac39 subunit:v-atpase subunit m39] [gn:yma6:l9324] [gdcf:2.1:12.13:12.16:12.5:12.6] [ec:3.6.1.34] [keggcf:2.1] [sgdfe:1.8:2:6.4]
CONTIG5103	4859512_f1_1	3341	17444	1956	652	YML120C	997	1.3(10)-100	Saccharomyces cerevisiae	[ui:yml120c] [pn:nadh-ubiquinone-6 oxidoreductase:rotenone-insensitive nadh-ubiquinone oxidoreductase precursor:internal nadh dehydrogenase] [gn:ndi1:ym7056] [gdcf:2.1:2.8:9.12] [ec:1.6.5.3] [keggcf:2.1:9.13] [sgdfe:1.7:2:9.7.0] [db:]
CONTIG5422	14897143_f3_9	3342	17445	591	197	YMR054W	500	3.8(10)-47	Saccharomyces cerevisiae	[ui:ymr054w] [pn:h+-atpase v0 domain 102 kd subunit, vacuolar:vacuolar atp synthase 101 kd subunit:v-atpase subunit ac115] [gn:stvl:ym9796] [gdcf:2.1:12.13:12.5:12.6] [ec:3.6.1.34] [keggcf:2.1] [sgdfe:1.8:2:7.2:7.8:0.8:5.0] [db:gic]

CONTIG218	24485885_f2_1	3343	17446	333	111	YMR256C	120	1.1(10)-7	Saccharomyces cerevisiae	[lui:ymr256c] [pn:cytochrome-c oxidase, subunit vii:cytochrome c oxidase polypeptide vii] [gn:cox7:ymr256w:ym9920] [gctc:2.1:2.8:12.16] [ec:1.9.3.1] [keggfc:2.1] [sgdfe:2.5:0:6:4:0:9:7:0] [db:gtc-saccharomyces cerevisiae]
CONTIG32	34586578_c2_5	3344	17447	315	105	YMR256C	151	5.9(10)-11	Saccharomyces cerevisiae	[lui:ymr256c] [pn:cytochrome-c oxidase, subunit vii:cytochrome c oxidase polypeptide vii] [gn:cox7:ymr256w:ym9920] [gctc:2.1:2.8:12.16] [ec:1.9.3.1] [keggfc:2.1] [sgdfe:2.5:0:6:4:0:9:7:0] [db:gtc-saccharomyces cerevisiae]
CONTIG3740	2441405_f1_2	3345	17448	528	176	YNL052W	332	3.8(10)-30	Saccharomyces cerevisiae	[lui:ynl052w] [pn:cytochrome-c oxidase chain v.a precursor:cytochrome c oxidase polypeptide va precursor] [gn:cox5a:n2474:ynl2474w] [gctc:2.1:2.8] [ec:1.9.3.1] [keggfc:2.1] [sgdfe:2.5:0:9:7:0] [db:gtc-saccharomyces cerevisiae]
CONTIG3408	10813307_c3_11	3346	17449	1080	360	YOR270C	331	3.3(10)-41	Saccharomyces cerevisiae	[lui:yor270c] [pn:h+-atpase v0 domain 95k subunit, vacuolar: vacuolar alp synthase 95.5 kd subunit] [gn:vpb1] [gctc:2.1:10.7:11.1:12.13:12.16:12.5:12.6] [ec:3.6.1.34] [keggfc:2.1] [sgdfe:1.8:2:6:2:0:6:4:0:7:2:2:7:8:0:8:5:0:9:10:0] [db:

CONTIG3408	9783405_c1_9	3347	17450	537	179	YOR270C	220	4.7(10)-17	Saccharomyces cerevisiae	[ui:yor270c] [pn:h+-atpase v0 domain 95k subunit, vacuolar: vacuolar atp synthase 95.5 kd subunit] [gn:vpb1] [gicf:2.1:10.7:11.1:12.13:12.16:12.5:12.6] [ec:3.6.1.34] [kegglc:2.1] [sgdfe:1.8:2:6.2:0:6.4:0:7.2:2:7.8:0:8.5:0:9.10:0] [db:
CONTIG2778	24644577_f3_3	3348	17451	1161	387	YOR270C	1323	3.7(10)-135	Saccharomyces cerevisiae	[ui:yor270c] [pn:h+-atpase v0 domain 95k subunit, vacuolar: vacuolar atp synthase 95.5 kd subunit] [gn:vpb1] [gicf:2.1:10.7:11.1:12.13:12.16:12.5:12.6] [ec:3.6.1.34] [kegglc:2.1] [sgdfe:1.8:2:6.2:0:6.4:0:7.2:2:7.8:0:8.5:0:9.10:0] [db:
CONTIG4314	10163206_c2_6	3349	17452	1275	425	YOR270C	916	5.0(10)-92	Saccharomyces cerevisiae	[ui:yor270c] [pn:h+-atpase v0 domain 95k subunit, vacuolar: vacuolar atp synthase 95.5 kd subunit] [gn:vpb1] [gicf:2.1:10.7:11.1:12.13:12.16:12.5:12.6] [ec:3.6.1.34] [kegglc:2.1] [sgdfe:1.8:2:6.2:0:6.4:0:7.2:2:7.8:0:8.5:0:9.10:0] [db:

CONTIG5422	13837780_f1_1	3350	17453	561	187	YOR270C	554	3.1(10)-53	Saccharomyces cerevisiae	[ui:yor270c] [pn:h+-atpase v0 domain 95k subunit, vacuolar: vacuolar atp synthase 95.5 kd subunit] [gn: yph1] [gicf: 2.1:10.7:11.1:12.13:12.16:12.5:12.6] [ec: 3.6.1.34] [keggfc: 2.1] [sgdfc: 1.8.2:6.2:0:6.4:0:7.2:2:7.8:0:8.5:0:9.10:0] [db:
CONTIG4036	24695253_c2_6	3351	17454	660	220	YOR332W	489	9.0(10)-47	Saccharomyces cerevisiae	[ui:yor332w] [pn:h+-atpase v1 domain 27 kd subunit, vacuolar: vacuolar atp synthase subunit e.v.-atpase e subunit: v.-atpase 27 kd subunit] [gn: yma4: yal5] [gicf: 2.1:12.13:12.16:12.5:12.6] [ec: 3.6.1.34] [keggfc: 2.1] [sgdfc: 1.8.2:6.4:0:7.2
CONTIG5236	34664087_f3_7	3352	17455	780	260	YPL078C	621	9.3(10)-61	Saccharomyces cerevisiae	[ui:ypl078c] [pn:f10-atpase complex, f1 delta subunit] [gn: atp4] [gicf: 2.1:2.8:12.6] [ec: 3.6.1.34] [keggfc: 2.1] [sgdfc: 1.8.2:2.5:0:7.8:0:8.2:0:9.7:0] [db: gic-saccharomyces cerevisiae]
CONTIG4312	22297800_c3_7	3353	17456	1407	469	YPR036W	350	4.9(10)-32	Saccharomyces cerevisiae	[ui:ypr036w] [pn:h+-atpase v1 domain 54 kd subunit, vacuolar: vacuolar atp synthase 54 kd subunit: v.-atpase 54 kd subunit] [gn: yma13: csl1: yps3085] [gicf: 2.1:12.13:12.16:12.5:12.6] [ec: 3.6.1.34] [keggfc: 2.1] [sgdfc: 1.8.2:7.2:2.7:8.0:8.

CONTIG3838	10659407_c2_2	3354	17457	1149	383	YPR191W	578	3.3(10)-56	Saccharomyces cerevisiae	[ui:ypri91w] [pn:ubiquinol-cytochrome-c reductase 40kd chain ii:ubiquinol-cytochrome c reductase complex core protein 2 precursor] [gn:qr2:cor2:ucr2:p9677] [glcf:2.12.8.12.16] [ec:1.10.2.2] [keggglc:2.1] [sgdgc:2.5.0.6.4.0.9.7.0] [d
CONTIG4568	212950_c2_7	3355	17458	369	123	YBR263W	346	3.7(10)-31	Saccharomyces cerevisiae	[ui:ybr263w] [pn:serine hydroxymethyltransferase precursor, mitochondrial:serine hydroxymethyltransferase, mitochondrial precursor:serine methylase:glycine hydroxymethyltransferase:shml] [gn:shml:shml:ybr1732] [glcf:2.2.2.8.3.4.4.1.5
CONTIG5207	3395261_f1_2	3356	17459	840	280	YBR263W	809	1.1(10)-80	Saccharomyces cerevisiae	[ui:ybr263w] [pn:serine hydroxymethyltransferase precursor, mitochondrial:serine hydroxymethyltransferase, mitochondrial precursor:serine methylase:glycine hydroxymethyltransferase:shml] [gn:shml:shml:ybr1732] [glcf:2.2.2.8.3.4.4.1.5

CONTIG1516	10972807_r2_2	3357	17460	621	207	YDL198C	828	1.1(10)-82	Saccharomyces cerevisiae	[ui:ydl198c] [pn:member of the mitochondrial carrier family:mcf:putative mitochondrial carrier protein yhm1/shm1] [gn:yhm1:shm1:d1214] [gctc:2.2:8.5:3.5:9.6:5.9:3.9:6:12.2] [ec:2.1.2.1] [keggc:2.2:5.3:5.9:6:5.9:3.9:8] [sgdfe:7.3.0]
CONTIG2782	22069376_f3_2	3358	17461	291	97	YDL198C	283	6.0(10)-25	Saccharomyces cerevisiae	[ui:ydl198c] [pn:member of the mitochondrial carrier family:mcf:putative mitochondrial carrier protein yhm1/shm1] [gn:yhm1:shm1:d1214] [gctc:2.2:2.8:5.3:5.9:6:5.9:3.9:6:12.2] [ec:2.1.2.1] [keggc:2.2:5.3:5.9:6:5.9:3.9:8] [sgdfe:7.3.0]
CONTIG5380	35167181_c1_13	3359	17462	627	209	YDR256C	541	2.7(10)-52	Saccharomyces cerevisiae	[ui:ydr256c] [pn:catalase a, peroxisomal: catalase a] [gn:cta1:ydr9320a] [gctc:2.2:5.14:12.12:12.6] [ec:1.11.1.6] [keggc:2.2:5.14] [sgdfe:9.8.0:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5380	4063813_c3_16	3360	17463	963	321	YDR256C	1180	5.4(10)-120	Saccharomyces cerevisiae	[ui:ydr256c] [pn:catalase a, peroxisomal: catalase a] [gn:cta1:ydr9320a] [gctc:2.2:5.14:12.12:12.6] [ec:1.11.1.6] [keggc:2.2:5.14] [sgdfe:9.8.0:11.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3794	11875936_f2_1	3361	17464	1431	477	YLR058C	2016	1.3(10)-208	Saccharomyces cerevisiae	[ui:ylr058c] [pn:serine hydroxymethyltransferase, cytoplasmic:serine hydroxymethyltransferase, cytosolic:serine methylase:glycine hydroxymethyltransferase:shm1] [gn:shm2:shm2:12156] [gtcf:2.2:3.4:4.1:5.3:5.9:6.5:8.1:8.2:9.3:9.6] [ec
CONTIG817	600125_f3_2	3362	17465	594	198	YHL008C	521	3.7(10)-50	Saccharomyces cerevisiae	[ui:ylh008c] [pn:similarity to m.formicum formate dehydrogenase:hypothetical 70.0 kd protein in prps4-ste20 intergenic region] [gtcf:2.2] [keggfc:14.2] [sgdfe:2.6:0] [db:gtc-saccharomyces cerevisiae]
CONTIG4187	35196900_f2_3	3363	17466	1260	420	YHR039C	1394	1.1(10)-142	Saccharomyces cerevisiae	[ui:ylh039c] [pn:similarity to aldehyde dehydrogenases:hypothetical aldehyde-dehydrogenase like protein in put2-strb2 intergenic region] [gtcf:2.2] [keggfc:14.2] [sgdfe:2.6:0] [db:gtc-saccharomyces cerevisiae]
CONTIG4700	12692528_f3_6	3364	17467	1248	416	YMR285C	840	5.7(10)-84	Saccharomyces cerevisiae	[ui:ylmr285c] [pn:similarity to ccr4p] [gtcf:2.2] [keggfc:14.2] [sgdfe:2.6:0] [db:gtc-saccharomyces cerevisiae]
CONTIG2216	26176250_c2_3	3365	17468	564	188	YOR388C	556	7.2(10)-54	Saccharomyces cerevisiae	[ui:yor388c] [pn:strong similarity to h.polymorpha formate dehydrogenase] [gtcf:2.2] [keggfc:14.2] [sgdfe:2.6:0] [db:gtc-saccharomyces cerevisiae]

CONTIG2216	12692127_c3_5	3366	17469	432	144	YOR388C	439	1.8(10)-41	Saccharomyces cerevisiae	[ui:yor388c] [pn:strong similarity to h.polyomorpha formate dehyd/rogenase] [gtcf:2.2] [keggfc:1.4.2] [sgdfc:2.6.0] [db:glc-saccharomyces cerevisiae]
CONTIG2613	12692127_f1_1	3367	17470	351	117	YOR388C	226	1.3(10)-18	Saccharomyces cerevisiae	[ui:yor388c] [pn:strong similarity to h.polyomorpha formate dehyd/rogenase] [gtcf:2.2] [keggfc:1.4.2] [sgdfc:2.6.0] [db:glc-saccharomyces cerevisiae]
CONTIG2613	3147050_f2_4	3368	17471	249	83	YOR388C	218	1.1(10)-17	Saccharomyces cerevisiae	[ui:yor388c] [pn:strong similarity to h.polyomorpha formate dehyd/rogenase] [gtcf:2.2] [keggfc:1.4.2] [sgdfc:2.6.0] [db:glc-saccharomyces cerevisiae]
CONTIG2613	26176250_f1_2	3369	17472	306	102	YOR388C	295	3.2(10)-26	Saccharomyces cerevisiae	[ui:yor388c] [pn:strong similarity to h.polyomorpha formate dehyd/rogenase] [gtcf:2.2] [keggfc:1.4.2] [sgdfc:2.6.0] [db:glc-saccharomyces cerevisiae]
CONTIG4206	24335941_f2_4	3370	17473	555	185	YOR388C	544	1.3(10)-52	Saccharomyces cerevisiae	[ui:yor388c] [pn:strong similarity to h.polyomorpha formate dehyd/rogenase] [gtcf:2.2] [keggfc:1.4.2] [sgdfc:2.6.0] [db:glc-saccharomyces cerevisiae]
CONTIG4790	36203812_c1_7	3371	17474	399	133	YOR388C	451	9.5(10)-43	Saccharomyces cerevisiae	[ui:yor388c] [pn:strong similarity to h.polyomorpha formate dehyd/rogenase] [gtcf:2.2] [keggfc:1.4.2] [sgdfc:2.6.0] [db:glc-saccharomyces cerevisiae]
CONTIG5272	22437686_f3_8	3372	17475	1182	394	YOR388C	1375	1.2(10)-140	Saccharomyces cerevisiae	[ui:yor388c] [pn:strong similarity to h.polyomorpha formate dehyd/rogenase] [gtcf:2.2] [keggfc:1.4.2] [sgdfc:2.6.0] [db:glc-saccharomyces cerevisiae]

CONTIG1771	3175836_f3_1	3373	17476	348	116	YLR027C	369	4.7(10)-34	Saccharomyces cerevisiae	[ui:ylr027c] [pn:aspartate amino transferase, cytosolic:aspartate amino transferase, cytoplasmic:transaminase a] [gn:aa12] [gicfc:2.4:2.6:5.1:5.10:5.15:5.2:5.5: 6.6] [ec:2.6.1.1] [keggfc:2.3:5.1:5.2:5.5:10:5.15] [sgdfe:1.1:1.2.1:9.2.
CONTIG2010	188900_f1_1	3374	17477	912	304	YLR027C	546	8.3(10)-53	Saccharomyces cerevisiae	[ui:ylr027c] [pn:aspartate amino transferase, cytosolic:aspartate amino transferase, cytoplasmic:transaminase a] [gn:aa12] [gicfc:2.4:2.6:5.1:5.10:5.15:5.2:5.5: 6.6] [ec:2.6.1.1] [keggfc:2.3:5.1:5.2:5.5:10:5.15] [sgdfe:1.1:1.2.1:9.2.
CONTIG3958	24225880_f1_2	3375	17478	867	289	YLR027C	869	4.9(10)-87	Saccharomyces cerevisiae	[ui:ylr027c] [pn:aspartate amino transferase, cytosolic:aspartate amino transferase, cytoplasmic:transaminase a] [gn:aa12] [gicfc:2.4:2.6:5.1:5.10:5.15:5.2:5.5: 6.6] [ec:2.6.1.1] [keggfc:2.3:5.1:5.2:5.5:10:5.15] [sgdfe:1.1:1.2.1:9.2.

CONTIG5189	33312513_c1_15	3376	17479	567	189	YLR027C	334	2.3(10)-30	Saccharomyces cerevisiae	[ui:Ylr027c] [pn:aspartate amino transferase, cytosolic:aspartate amino transferase, cytoplasmic:transaminase a] [gn:aat2] [gicfc:2.4:2.6:5.1:5.10:5.15:5.2:5:5:6.6] [ec:2.6.1.1] [keggfc:2.3:5.1:5.2:5.5:5.10:5.15] [sgdfe:1.1:1.2.1:9.2.]
CONTIG5189	19729707_c3_25	3377	17480	726	242	YLR027C	385	9.5(10)-36	Saccharomyces cerevisiae	[ui:Ylr027c] [pn:aspartate amino transferase, cytosolic:aspartate amino transferase, cytoplasmic:transaminase a] [gn:aat2] [gicfc:2.4:2.6:5.1:5.10:5.15:5.2:5:5:6.6] [ec:2.6.1.1] [keggfc:2.3:5.1:5.2:5.5:5.10:5.15] [sgdfe:1.1:1.2.1:9.2.]
CONTIG4997	22531562_f2_2	3378	17481	1581	527	YLR089C	1449	1.7(10)-148	Saccharomyces cerevisiae	[ui:Ylr089c] [pn:strong similarity to alanine transaminases:putative alanine aminotransferase, mitochondrial precursor:glutamic-- pyruvic transaminase:gpt:glutamic-- alanine transaminase] [gn:19449] [gicfc:2.4:2.6:5.1:5.2:6.6] [ec:2.6.
CONTIG5070	1179712_c1_6	3379	17482	531	177	YAL062W	563	1.3(10)-54	Saccharomyces cerevisiae	[ui:Yal062w] [pn:nadp-glutamate dehydrogenase:nadp-specific glutamate dehydrogenase 2:nadp- gdh 2] [gn:gdh3:fun51] [gicfc:2.6:5.1:5.3] [ec:1.4.1.4] [keggfc:2.5:5.1] [sgdfe:1.1.4:1.2.1] [db:gic-saccharomyces cerevisiae]

CONTIG5070	20348302_c3_12	3380	17483	897	299	YAL062W	1109	1.8(10)-112	Saccharomyces cerevisiae	[ui:yal062w] [pn:nadp-glutamate dehydrogenase:nadp-specific glutamate dehydrogenase 2:nadp-gdh 2] [gn:gdh3:fun51] [gicf:2.6.5.1:5.3] [ec:1.4.1.4] [keggf:2.5.5.1] [sgdf:1.1.4.1.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG830	11992200_f1_1	3381	17484	369	123	YAL012W	275	4.2(10)-24	Saccharomyces cerevisiae	[ui:yal012w] [pn:cystathionine gamma-lyase:gamma-cystathionase] [gn:cys3:cyl:str1:fun35] [gicf:2.6.5.4:5.5.6.4:6.6] [ec:4.4.1.1] [keggf:2.5.5.4:5.5.6.4] [sgdf:1.1.1:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG5658	13678188_f3_12	3382	17485	2760	920	YDL215C	1953	8.3(10)-225	Saccharomyces cerevisiae	[ui:ydl215c] [pn:nad-specific glutamate dehydrogenase:nad-gdh] [gn:gdh2:d0892] [gicf:2.6.5.1:5.3] [ec:1.4.1.2] [keggf:2.5.5.1] [sgdf:1.1.4.1.2.1:9.2.0] [db:gic-saccharomyces cerevisiae]
blx15140.x	24015908_c3_1	3383	17486	294	98	YDL215C	222	4.2(10)-17	Saccharomyces cerevisiae	[ui:ydl215c] [pn:nad-specific glutamate dehydrogenase:nad-gdh] [gn:gdh2:d0892] [gicf:2.6.5.1:5.3] [ec:1.4.1.2] [keggf:2.5.5.1] [sgdf:1.1.4.1.2.1:9.2.0] [db:gic-saccharomyces cerevisiae]

CONTIG3341	78142_cl_4	3384	17487	762	254	YDR019C	523	2.2(10)-50	Saccharomyces cerevisiae	[ui:ydr019c] [pn:glycine decarboxylase t subunit:aminomethyltransferase precursor:glycine cleavage system t protein] [gn:gev1.yd9335] [gctc:2.6:2.8:5.3:9.6] [ec:2.1.2.10] [keggfc:2.5:5.3:9.8] [sgdfc:1.1.4:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG346	4687750_f3_1	3385	17488	300	100	YDR019C	252	2.0(10)-21	Saccharomyces cerevisiae	[ui:ydr019c] [pn:glycine decarboxylase t subunit:aminomethyltransferase precursor:glycine cleavage system t protein] [gn:gev1.yd9335] [gctc:2.6:2.8:5.3:9.6] [ec:2.1.2.10] [keggfc:2.5:5.3:9.8] [sgdfc:1.1.4:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4640	4019436_f2_5	3386	17489	540	180	YDR321W	207	2.1(10)-16	Saccharomyces cerevisiae	[ui:ydr321w] [pn:asparaginase:t-asparaginase t:-asparagine amidohydrolase i:asp ij] [gn:asp1.d9798] [gctc:2.6:5.2:5.3:6.5] [ec:3.5.1.1] [keggfc:2.5:5.2:6.5] [sgdfc:1.1.4:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4492	32612890_cl_4	3387	17490	543	181	YGR124W	772	9.3(10)-77	Saccharomyces cerevisiae	[ui:ygr124w] [pn:asparagine synthetase:glutamine-hydrolyzing 2:glutamine-dependent asparagine synthetase 2] [gn:asn2.g6358] [gctc:2.6:5.2:6.6] [ec:6.3.5.4] [keggfc:2.5:5.2] [sgdfc:1.1.1] [db:gtc-saccharomyces cerevisiae]

CONTIG4397	31447508_c2_3	3388	17491	684	228	YLR155C	329	6.0(10)-40	Saccharomyces cerevisiae	[ui:y/lr155c] [pn:l-asparaginase ii:l-asparaginase ii precursor:l-asparagine amidohydrolase ii:asp ii] [gn:asp3a:asp3b:asp3c:asp3d:asp3:i9632] [gltc:2.6:5.2:5.3:6.5:1.1] [ec:3.5.1.1] [keggfc:2.5:5.2:6.5] [sgdfc:1.1:4:9.1.0] [db:gltc-s
CONTIG4327	22443936_c1_4	3389	17492	1152	384	YPR035W	1614	5.5(10)-166	Saccharomyces cerevisiae	[ui:y/pr035w] [pn:glutamine synthetase:glutamate--ammonia ligase] [gn:glm1:yp30851] [gltc:2.6:5.1:6.6:1.1.4] [ec:6.3.1.2] [keggfc:2.5:5.1:7.3] [sgdfc:1.1:1.2.1:9.2.0] [db:gltc-saccharomyces cerevisiae]
CONTIG3616	4068777_f3_2	3390	17493	1215	405	YPR145W	1214	1.3(10)-123	Saccharomyces cerevisiae	[ui:y/pr145w] [pn:asparagine synthetase:glutamine-hydrolyzing l:glutamine-dependent asparagine synthetase 1] [gn:asn1:p9659] [gltc:2.6:5.2:6.6] [ec:6.3.5.4] [keggfc:2.5:5.2] [sgdfc:1.1.1] [db:gltc-saccharomyces cerevisiae]
CONTIG5302	23937950_f3_5	3391	17494	3255	1085	YBR208C	3906	0	Saccharomyces cerevisiae	[ui:y/br208c] [pn:urea amidolyase] [gn:dur1:2] [gltc:2.6:4.1:5.3] [keggfc:1.4.2] [sgdfc:1.1:4:1.2.1:1.3.1] [db:gltc-saccharomyces cerevisiae]
CONTIG5355	13672637_f2_2	3392	17495	2004	668	YBR208C	1998	1.1(10)-206	Saccharomyces cerevisiae	[ui:y/br208c] [pn:urea amidolyase] [gn:dur1:2] [gltc:2.6:4.1:5.3] [keggfc:1.4.2] [sgdfc:1.1:4:1.2.1:1.3.1] [db:gltc-saccharomyces cerevisiae]

blx16771.x	26845062_f3_1	3393	17496	378	126	YBR208C	366	3.8(10)-32	Saccharomyces cerevisiae	[ui:ydb208c] [pn:urca amidolyase] [gn:dur1:2] [gctfc:2.6:4.1:5.3] [keggfc:14.2]
										[sgdfe:1.1.4:1.2.1:1.3.1] [db:gic-saccharomyces cerevisiae]
CONTIG1182	7041075_c1_4	3394	17497	1362	454	YDL171C	1415	4.5(10)-144	Saccharomyces cerevisiae	[ui:ydl171c] [pn:glutamate synthase:nappdh:gogat] [gn:glu1] [gctfc:2.6:6:6] [keggfc:14.2] [sgdfe:1.1.1:1.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG1182	11761568_c3_8	3395	17498	306	102	YDL171C	150	4.4(10)-9	Saccharomyces cerevisiae	[ui:ydl171c] [pn:glutamate synthase:nappdh:gogat] [gn:glu1] [gctfc:2.6:6:6] [keggfc:14.2] [sgdfe:1.1.1:1.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG2377	4867692_f1_1	3396	17499	1011	337	YDL171C	1153	6.9(10)-116	Saccharomyces cerevisiae	[ui:ydl171c] [pn:glutamate synthase:nappdh:gogat] [gn:glu1] [gctfc:2.6:6:6] [keggfc:14.2] [sgdfe:1.1.1:1.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG5054	2236567_c3_12	3397	17500	414	138	YDL171C	412	6.2(10)-37	Saccharomyces cerevisiae	[ui:ydl171c] [pn:glutamate synthase:nappdh:gogat] [gn:glu1] [gctfc:2.6:6:6] [keggfc:14.2] [sgdfe:1.1.1:1.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG5716	6250_c1_20	3398	17501	1590	530	YDL171C	1525	3.3(10)-156	Saccharomyces cerevisiae	[ui:ydl171c] [pn:glutamate synthase:nappdh:gogat] [gn:glu1] [gctfc:2.6:6:6] [keggfc:14.2] [sgdfe:1.1.1:1.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG813	32610800_f3_2	3399	17502	456	152	YDL171C	454	2.1(10)-41	Saccharomyces cerevisiae	[ui:ydl171c] [pn:glutamate synthase:nappdh:gogat] [gn:glu1] [gctfc:2.6:6:6] [keggfc:14.2] [sgdfe:1.1.1:1.2.1] [db:gic-saccharomyces cerevisiae]

b9x13v34.x	4149010_ft_1	3400	17503	483	161	YDL171C	660	2.6(10)-63	Saccharomyces cerevisiae	[ui:ydl171c] [pn:glutamate synthase:nappdh:goga] [gn:glut] [gicf:2.6:6.6] [keggf:14.2] [sgdfc:1.1:1.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG3324	4689200_c3_6	3401	17504	1089	363	YDR242W	347	2.3(10)-31	Saccharomyces cerevisiae	[ui:ydr242w] [pn:amidase:probable amidase] [gn:amd2:andy1:andy:d8419] [gicf:2.6:5.10:5.13:5.14:6.5] [ec:3.5.1.4] [keggf:5.10:5.13:5.14:6.5] [sgdfc:1.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG4963	19703576_c3_9	3402	17505	1311	437	YDR242W	381	2.5(10)-35	Saccharomyces cerevisiae	[ui:ydr242w] [pn:amidase:probable amidase] [gn:amd2:andy1:andy:d8419] [gicf:2.6:5.10:5.13:5.14:6.5] [ec:3.5.1.4] [keggf:5.10:5.13:5.14:6.5] [sgdfc:1.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG5006	9787676_c1_7	3403	17506	471	157	YDR242W	177	9.6(10)-13	Saccharomyces cerevisiae	[ui:ydr242w] [pn:amidase:probable amidase] [gn:amd2:andy1:andy:d8419] [gicf:2.6:5.10:5.13:5.14:6.5] [ec:3.5.1.4] [keggf:5.10:5.13:5.14:6.5] [sgdfc:1.2.1] [db:gic-saccharomyces cerevisiae]

CONTIG5529	10975912_cl_12	3404	17507	1728	576	YDR242W	577	4.2(10)-56	Saccharomyces cerevisiae	[ui:ydr242w] [pn:amidase:probable amidase] [gn:amd2:amy1:amyd:ydr419] [gicf:2.6:5.10:5.13:5.14:6:5] [ec:3.5.1.4] [keggfc:5.10:5.13:5.14:6:5] [sgdfc:1.2:1.1] [db:gic-saccharomyces cerevisiae]
CONTIG4622	22322182_fl_1	3405	17508	966	322	YDR353W	1330	6.9(10)-136	Saccharomyces cerevisiae	[ui:ydr353w] [pn:nadph:thioredoxin reductase] [gn:d9476] [gicf:2.6:4.2] [ec:1.6.4.5] [keggfc:4.2] [sgdfc:1.2:1.1:3.3] [db:gic-saccharomyces cerevisiae]
CONTIG4293	11797312_cl_4	3406	17509	651	217	YFL030W	493	3.3(10)-47	Saccharomyces cerevisiae	[ui:yfl030w] [pn:similarity to several transaminases:hypothetical 41.9 kd protein in hael-cak1 intergenic region] [gicf:2.6:5.3:6.6] [keggfc:14.2] [sgdfc:1.1:1.1:4:1.2:1.1] [db:gic-saccharomyces cerevisiae]
CONTIG4293	12273376_c2_6	3407	17510	477	159	YFL030W	322	4.5(10)-29	Saccharomyces cerevisiae	[ui:yfl030w] [pn:similarity to several transaminases:hypothetical 41.9 kd protein in hael-cak1 intergenic region] [gicf:2.6:5.3:6.6] [keggfc:14.2] [sgdfc:1.1:1.1:4:1.2:1.1] [db:gic-saccharomyces cerevisiae]

CONTIG319	15662687_c3_6	3408	17511	1758	586	YFR030W	1405	7.7(10)-144	Saccharomyces cerevisiae	[ui:yfr030w] [pn:assimilatory sulfite reductase flavin-binding subunit:sulfite reductase:nadph flavoprotein component] [gn:met10] [gicf:2.6:2.7:6.4:6.6] [ec:1.8.1.2] [keggf:2.6:6.4] [sgdfc:1.1:1.2.1] [db:gic-saccharomyces cerevisi
b9x10v94.y	24612758_f1_1	3409	17512	579	193	YFR030W	208	1.2(10)-15	Saccharomyces cerevisiae	[ui:yfr030w] [pn:assimilatory sulfite reductase flavin-binding subunit:sulfite reductase:nadph flavoprotein component] [gn:met10] [gicf:2.6:2.7:6.4:6.6] [ec:1.8.1.2] [keggf:2.6:6.4] [sgdfc:1.1:1.2.1] [db:gic-saccharomyces cerevisi
CONTIG3769	24417200_c1_4	3410	17513	807	269	YHR176W	166	2.8(10)-10	Saccharomyces cerevisiae	[ui:yhr176w] [pn:flavin-containing monooxygenase:hypothetical 42.4 kd protein in eno2-stb5 intergenic region] [gn:imo] [gicf:2.6] [keggf:14.2] [sgdfc:1.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG4300	24337807_f2_4	3411	17514	846	282	YHR176W	299	2.7(10)-36	Saccharomyces cerevisiae	[ui:yhr176w] [pn:flavin-containing monooxygenase:hypothetical 42.4 kd protein in eno2-stb5 intergenic region] [gn:imo] [gicf:2.6] [keggf:14.2] [sgdfc:1.2.1] [db:gic-saccharomyces cerevisiae]

CONTIG4916	2742805_f2_3	3412	17515	360	120	YIL051C	341	4.4(10)-31	Saccharomyces cerevisiae	[ui:yir051c] [pn:strong similarity to azotobacter nitrogen fixation nifA protein;hypothetical 15.9 kd protein in gpp1-sygl intergenic region] [gicf:2.6] [keggf:4.2] [sgdfc:1.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG2229	10156875_f3_3	3413	17516	555	185	YIR027C	553	1.5(10)-53	Saccharomyces cerevisiae	[ui:yir027c] [pn:allantoinase] [gn:dal1] [gicf:2.6:4.1] [ec:3.5.2.5] [keggf:4.1] [sgdfc:1.2.1:1.3.1] [db:gic-saccharomyces cerevisiae]
CONTIG2058	13004559_c1_6	3414	17517	1224	408	YIR027C	696	1.1(10)-68	Saccharomyces cerevisiae	[ui:yir027c] [pn:allantoinase] [gn:dal1] [gicf:2.6:4.1] [ec:3.5.2.5] [keggf:4.1] [sgdfc:1.2.1:1.3.1] [db:gic-saccharomyces cerevisiae]
CONTIG5524	23443807_f1_2	3415	17518	561	187	YIR029W	519	6.0(10)-50	Saccharomyces cerevisiae	[ui:yir029w] [pn:allantoinase:allantoinase] [gn:dal2:alc1] [gicf:2.6:4.1] [ec:3.5.3.4] [keggf:4.1] [sgdfc:1.2.1:1.3.1] [db:gic-saccharomyces cerevisiae]
CONTIG5774	32319550_c1_19	3416	17519	372	124	YIR029W	391	2.2(10)-36	Saccharomyces cerevisiae	[ui:yir029w] [pn:allantoinase:allantoinase] [gn:dal2:alc1] [gicf:2.6:4.1] [ec:3.5.3.4] [keggf:4.1] [sgdfc:1.2.1:1.3.1] [db:gic-saccharomyces cerevisiae]
CONTIG1724	837807_f3_2	3417	17520	645	215	YIR032C	391	2.2(10)-36	Saccharomyces cerevisiae	[ui:yir032c] [pn:ureidoglycolate hydrolase] [gn:dal3] [gicf:2.6:4.1] [ec:3.5.3.19] [keggf:4.1] [sgdfc:1.2.1:1.3.1] [db:gic-saccharomyces cerevisiae]

CONTIG5473	21517150_c2_1	3418	17521	1851	617	YJL172W	1041	2.8(10)-105	Saccharomyces cerevisiae	[ui:yjl172w] [pn:gly-x carboxypeptidase yscs precursor:carboxypeptidase s precursor:yscs:gly-x carboxypeptidase] [gn:cpst:cpst:0510] [glcfc:2.6:10.11:12.16] [ec:3.4.17.4] [kegglc:14.1] [sgdfe:1.2:1.6:5.2:9.10.0] [db:glc-saccharomyces
CONTIG963	906308_c1_2	3419	17522	687	229	YJL172W	565	8.0(10)-55	Saccharomyces cerevisiae	[ui:yjl172w] [pn:gly-x carboxypeptidase yscs precursor:carboxypeptidase s precursor:yscs:gly-x carboxypeptidase] [gn:cpst:cpst:0510] [glcfc:2.6:10.11:12.16] [ec:3.4.17.4] [kegglc:14.1] [sgdfe:1.2:1.6:5.2:9.10.0] [db:glc-saccharomyces
b3x19275.y	21673502_c2_2	3420	17523	399	133	YJL172W	224	8.9(10)-18	Saccharomyces cerevisiae	[ui:yjl172w] [pn:gly-x carboxypeptidase yscs precursor:carboxypeptidase s precursor:yscs:gly-x carboxypeptidase] [gn:cpst:cpst:0510] [glcfc:2.6:10.11:12.16] [ec:3.4.17.4] [kegglc:14.1] [sgdfe:1.2:1.6:5.2:9.10.0] [db:glc-saccharomyces

CONTIG5819	22396887_c3_58	3421	17524	1476	492	YJL060W	1178	8.8(10)-120	Saccharomyces cerevisiae	[ui:yj 060w] [pn:similarity to kynurenine aminotransferase and glutamine-phenylpyruvate transaminase:hyposuccinyl amino transferase yj 060w] [gn:j 138] [gctc:2.6:5.1:5.8] [ec:2.6.1.-] [keggfc:5.8:5.11] [sgdfe:1.2.1] [db:gtc-saccharo
CONTIG5718	14869017_f1_4	3422	17525	849	283	YJL035C	420	1.8(10)-39	Saccharomyces cerevisiae	[ui:yj 035c] [pn:weak similarity to p.gingivalis pgaa and b.japonicum nitrogen fixation protein:hyposuccinyl 28.3 kd protein in nsp1-kar2 intergenic region] [gn:j 246] [gctc:2.6] [keggfc:14.2] [sgdfe:1.2.1] [db:gtc-saccharomyces cere
CONTIG4318	12191427_f3_3	3423	17526	1602	534	YJR010W	1500	6.7(10)-154	Saccharomyces cerevisiae	[ui:yj 010w] [pn:sulfate adenyllyltransferase:atp-sulfurylase] [gn:met3.j 436] [gctc:2.6:2.7:4.1:6.4:6.6] [ec:2.7.7.4] [keggfc:2.6:4.1:6.4] [sgdfe:1.1.1:1.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5375	24308175_f1_1	3424	17527	888	296	YJR137C	284	1.5(10)-23	Saccharomyces cerevisiae	[ui:yj 137c] [pn:similarity to sulfite reductases:hyposuccinyl 161.2 kd protein in nmd5-hom6 intergenic region] [gn:j 26] [gctc:2.6] [keggfc:14.2] [sgdfe:1.2.1] [db:gtc-saccharomyces cerevisiae]

CONTIG5375	1407812_f1_2	3425	17528	183	61	YJR137C	153	1.3(10)-9	Saccharomyces cerevisiae	[ui:yjr137c] [pn:similarity to sulfite reductases:hypothetical 161.2 kd protein in nmd5-hom6 intergenic region] [gn:j2126] [gctc:2.6] [keggfc:14.2] [sgdfc:1.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5375	33600282_f3_4	3426	17529	2760	920	YJR137C	3116	0	Saccharomyces cerevisiae	[ui:yjr137c] [pn:similarity to sulfite reductases:hypothetical 161.2 kd protein in nmd5-hom6 intergenic region] [gn:j2126] [gctc:2.6] [keggfc:14.2] [sgdfc:1.2.1] [db:gtc-saccharomyces cerevisiae]
b3x16012.y	5208317_f2_2	3427	17530	741	247	YJR137C	223	4.7(10)-17	Saccharomyces cerevisiae	[ui:yjr137c] [pn:similarity to sulfite reductases:hypothetical 161.2 kd protein in nmd5-hom6 intergenic region] [gn:j2126] [gctc:2.6] [keggfc:14.2] [sgdfc:1.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5741	22297502_f1_2	3428	17531	1428	476	YJR149W	276	2.2(10)-42	Saccharomyces cerevisiae	[ui:yjr149w] [pn:similarity to 2-nitropropane dioxygenase:hypothetical 45.1 kd protein in rps7b-dal5 intergenic region] [gn:j2213] [gctc:2.6] [keggfc:14.2] [sgdfc:1.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5301	11751562_c2_16	3429	17532	774	258	YKL040C	374	1.3(10)-34	Saccharomyces cerevisiae	[ui:ykl040c] [pn:weak similarity to nitrogen fixation protein nifU:hypothetical 29.2 kd protein in phd1-pim1 intergenic region] [gn:ykl253] [gctc:2.6] [keggfc:14.2] [sgdfc:1.2.1] [db:gtc-saccharomyces cerevisiae]

CONTIG5774	25968927_c3_31	3430	17533	801	267	YKL040C	426	4.2(10)-40	Saccharomyces cerevisiae	[ui:yk1040c] [pn:weak similarity to nitrogen fixation protein nifU:hypothetical 29.2 kd protein in phd1-pim1 intergenic region] [gn:yk1253] [gicfc:2.6] [keggfc:14.2] [sgdfe:1.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG3426	30276880_fl_1	3431	17534	1425	475	YLR438W	1349	6.7(10)-138	Saccharomyces cerevisiae	[ui:yhr438w] [pn:ornithine aminotransferase:ornithine--oxo-acid aminotransferase] [gn:cat2:carb:19753] [gicfc:2.6:5.10:5.16:6.6] [ec:2.6.1.13] [keggfc:5.10:5.16] [sgdfe:1.1:1.2.1:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG5637	117132_fl_6	3432	17535	1368	456	YMR293C	888	4.7(10)-89	Saccharomyces cerevisiae	[ui:ymr293c] [pn:similarity to amidases] [gicfc:2.6] [keggfc:14.2] [sgdfe:1.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG4315	34179052_c3_13	3433	17536	1404	468	YOL058W	1478	1.3(10)-151	Saccharomyces cerevisiae	[ui:yol058w] [pn:argininosuccinate synthetase:argininosuccinate synthase:citrulline--aspartate ligase] [gn:arg1:o1228] [gicfc:2.6:5.10:5.16:5.2:6.6] [ec:6.3.4.5] [keggfc:5.2:5.10:5.16] [sgdfe:1.1:1.2.1:9.2.0] [db:gic-saccharomyces c
CONTIG2025	22454387_c3_5	3434	17537	621	207	YOR251C	217	6.0(10)-18	Saccharomyces cerevisiae	[ui:yor251c] [pn:similarity to thiosulfate sulfurtransferases] [gicfc:2.6:12.12] [keggfc:14.2] [sgdfe:1.2.1:11.3.0] [db:gic-saccharomyces cerevisiae]

CONTIG2025	23863407_c2_4	3435	17538	444	148	YOR251C	295	3.2(10)-26	Saccharomyces cerevisiae	[ui:yor251c] [pn:similarity to thiosulfate sulfurtransferases] [gtcf:2.6:12.12] [keggfc:14.2] [sgdfe:1.2.1:1.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5155	4723257_c3_18	3436	17539	573	191	YPL135W	519	6.0(10)-50	Saccharomyces cerevisiae	[ui:yp1135w] [pn:strong similarity to nitrogen fixation protein:nifH] [gtcf:2.6] [keggfc:14.2] [sgdfe:1.2.1] [db:gtc-saccharomyces cerevisiae]
b2x16881.y	24509683_f1_1	3437	17540	486	162	YPR167C	413	1.0(10)-38	Saccharomyces cerevisiae	[ui:yp167c] [pn:3"-phosphoadenylylsulfate reductase:phosphadenosine phosphosulfate reductase:paps reductase, thioredoxin dependent:padops reductase:3"-phosphoadenylylsulfate reductase] [gn:met16:p9325] [gtcf:2.6:6.6] [keggfc:14.1]
CONTIG3727	24707213_f1_2	3438	17541	930	310	YBR213W	301	7.5(10)-27	Saccharomyces cerevisiae	[ui:ybr213w] [pn:involved in the expression of paps reductase and sulfite reductase:met8 protein] [gn:met8:ybr1461] [gtcf:2.6:2.7:10.2] [keggfc:14.2] [sgdfe:1.2.2] [db:gtc-saccharomyces cerevisiae]
CONTIG4963	34251587_c1_7	3439	17542	708	236	YCR028C	538	5.7(10)-52	Saccharomyces cerevisiae	[ui:ycr028c] [pn:similarity to allantoate permease transporter:hypothetical 58.3 kd protein in pmp1-rim1 intergenic region] [gn:fen2.ycr28c] [gtcf:2.6:2.7:10.2:12.13:12.6] [keggfc:14.2] [sgdfe:1.1.2:1.2.2:1.5.2:1.6.4:7.7.0:1.7.0.0] [d

CONTIG1158	30578905_f2_1	3440	17543	870	290	YDL170W	103	1.3(10)-8	Saccharomyces cerevisiae	[ui:yd1170w] [pn:transcriptional activator for gaba catabolic genes:transcriptional activator protein] [gn:uga3] [gctc:2.6.2.7:10.1:10.2] [kegfc:14.2] [sgdfc:1.2.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3236	10370833_f2_2	3441	17544	1344	448	YDL170W	162	4.0(10)-12	Saccharomyces cerevisiae	[ui:yd1170w] [pn:transcriptional activator for gaba catabolic genes:transcriptional activator protein] [gn:uga3] [gctc:2.6.2.7:10.1:10.2] [kegfc:14.2] [sgdfc:1.2.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5500	2148252_f3_7	3442	17545	1482	494	YDL170W	125	0.00011	Saccharomyces cerevisiae	[ui:yd1170w] [pn:transcriptional activator for gaba catabolic genes:transcriptional activator protein] [gn:uga3] [gctc:2.6.2.7:10.1:10.2] [kegfc:14.2] [sgdfc:1.2.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1227	7083433_c3_4	3443	17546	237	79	YDR207C	114	1.0(10)-5	Saccharomyces cerevisiae	[ui:yd207c] [pn:negative transcriptional regulator:transcriptional regulator umc6:negative transcriptional regulator of ime2] [gn:umc6:car80:cargr1:nim2:yd8142] [gctc:2.6.2.7:10.1:10.2:12.8] [kegfc:14.2] [sgdfc:1.1.2:1.2.2:1.6.4.3.

CONTIG4708	1348311_f1_1	3444	17547	2907	969	YDR207C	115	0.005	Saccharomyces cerevisiae	[ui:ydr207c] [pn:negative transcriptional regulator:transcriptional regulator ume6:negative transcriptional regulator of ime2] [gn:ume6:car80:cargr1:nim2:ydr814 2] [gctc:2.6.2.7:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:1.1.2:1.2.2:1.6.4.3.
CONTIG5000	3907502_c1_8	3445	17548	1638	546	YDR207C	118	0.00119	Saccharomyces cerevisiae	[ui:ydr207c] [pn:negative transcriptional regulator:transcriptional regulator ume6:negative transcriptional regulator of ime2] [gn:ume6:car80:cargr1:nim2:ydr814 2] [gctc:2.6.2.7:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:1.1.2:1.2.2:1.6.4.3.
CONTIG5436	29337802_f2_8	3446	17549	1722	574	YDR207C	162	1.3(10)-8	Saccharomyces cerevisiae	[ui:ydr207c] [pn:negative transcriptional regulator:transcriptional regulator ume6:negative transcriptional regulator of ime2] [gn:ume6:car80:cargr1:nim2:ydr814 2] [gctc:2.6.2.7:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:1.1.2:1.2.2:1.6.4.3.

CONTIG4255	23444436_f1_2	3452	17555	1572	524	YER040W	191	5.2(10)-12	Saccharomyces cerevisiae	[ui:yer040w] [pn:transcription factor for positive nitrogen regulation:nitrogen regulatory protein] [gn:glu3] [gctc:2.6:2.7:10.1:10.2] [keggfc:14.2] [sgdfc:1.2.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4624	16287762_c2_6	3453	17556	888	296	YER040W	172	5.2(10)-12	Saccharomyces cerevisiae	[ui:yer040w] [pn:transcription factor for positive nitrogen regulation:nitrogen regulatory protein] [gn:glu3] [gctc:2.6:2.7:10.1:10.2] [keggfc:14.2] [sgdfc:1.2.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG544	22734512_f1_1	3454	17557	831	277	YER040W	96	0.04599	Saccharomyces cerevisiae	[ui:yer040w] [pn:transcription factor for positive nitrogen regulation:nitrogen regulatory protein] [gn:glu3] [gctc:2.6:2.7:10.1:10.2] [keggfc:14.2] [sgdfc:1.2.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5817	1182650_c2_52	3455	17558	1404	468	YER040W	124	0.00013	Saccharomyces cerevisiae	[ui:yer040w] [pn:transcription factor for positive nitrogen regulation:nitrogen regulatory protein] [gn:glu3] [gctc:2.6:2.7:10.1:10.2] [keggfc:14.2] [sgdfc:1.2.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4651	881451_c3_4	3456	17559	2160	720	YFL021W	245	1.3(10)-20	Saccharomyces cerevisiae	[ui:yf021w] [pn:transcription factor for nitrogen regulation:protein] [gn:gat1] [gicfc:2.6:2.7:10.1:10.2] [keggfc:14.2] [sgdfe:1.2:2.4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2922	5266002_f3_3	3457	17560	1440	480	YIR023W	179	9.4(10)-23	Saccharomyces cerevisiae	[ui:yir023w] [pn:transcriptional activator for allantoin and gaba catabolic genes:transcriptional activator protein da81:regulatory protein uga35] [gn:da81:uga35:durl] [gicfc:2.6:2.7:10.1:10.2] [keggfc:14.2] [sgdfe:1.1.2:1.2.2:1.3.5]
CONTIG2922	4298437_f2_2	3458	17561	990	330	YIR023W	270	2.6(10)-22	Saccharomyces cerevisiae	[ui:yir023w] [pn:transcriptional activator for allantoin and gaba catabolic genes:transcriptional activator protein da81:regulatory protein uga35] [gn:da81:uga35:durl] [gicfc:2.6:2.7:10.1:10.2] [keggfc:14.2] [sgdfe:1.1.2:1.2.2:1.3.5]
CONTIG3788	29401875_f2_1	3459	17562	591	197	YIR023W	165	4.4(10)-11	Saccharomyces cerevisiae	[ui:yir023w] [pn:transcriptional activator for allantoin and gaba catabolic genes:transcriptional activator protein da81:regulatory protein uga35] [gn:da81:uga35:durl] [gicfc:2.6:2.7:10.1:10.2] [keggfc:14.2] [sgdfe:1.1.2:1.2.2:1.3.5]

CONTIG5350	25390625_c2_14	3460	17363	756	252	YIR030C	276	3.3(10)-24	Saccharomyces cerevisiae	[ui:yir030c] [pn:involved in nitrogen-catabolite metabolism:protein] [gn:deg1] [gtcf:2.6:2.7:10.2] [keggfc:14.2] [sgdfe:1.2.2] [db:gtc-saccharomyces cerevisiae]
CONTIG4423	33395002_f3_5	3461	17364	618	206	YKR034W	253	9.1(10)-22	Saccharomyces cerevisiae	[ui:ykr034w] [pn:transcriptional repressor for allantoin and gaba catabolic genes:nitrogen regulatory protein dal80:regulatory protein uga43] [gn:dal80:uga43] [gtcf:2.6:2.7:10.1:10.2] [keggfc:14.2] [sgdfe:1.2.2:4.8:2:9.5.0] [db:gtc-s
CONTIG3432	13784427_f2_5	3462	17365	1158	386	YLR013W	126	6.5(10)-8	Saccharomyces cerevisiae	[ui:ylr013w] [pn:weak similarity to nitrogen regulatory proteins] [gtcf:2.6:2.7:10.2] [keggfc:14.2] [sgdfe:1.2.2:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG2823	16412508_f3_3	3463	17366	1530	510	YML099C	386	5.5(10)-70	Saccharomyces cerevisiae	[ui:yml099c] [pn:transcription factor involved in arginine metabolism:arginine metabolism regulation protein ii] [gn:arg2:arg81] [gtcf:2.6:2.7:10.1:10.2] [keggfc:14.2] [sgdfe:1.1.2:1.2.2:4.8:2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3422	35678951_13_1	3464	17567	1920	640	YML099C	219	1.2(10)-14	Saccharomyces cerevisiae	[ui:ym1099c] [pn:transcription factor involved in arginine metabolism:arginine metabolism regulation protein ii] [gn:arg2:arg81] [gctc:2.6.2.7:10.1:10.2] [keggtc:14.2] [sgdgc:1.1.2:1.2.2.4.8.2.9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG3860	2056555_c2_7	3465	17568	2283	761	YML099C	135	3.1(10)-5	Saccharomyces cerevisiae	[ui:ym1099c] [pn:transcription factor involved in arginine metabolism:arginine metabolism regulation protein ii] [gn:arg2:arg81] [gctc:2.6.2.7:10.1:10.2] [keggtc:14.2] [sgdgc:1.1.2:1.2.2.4.8.2.9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5347	19728392_11_2	3466	17569	1275	425	YNL216W	222	2.0(10)-18	Saccharomyces cerevisiae	[ui:yn1216w] [pn:dna-binding protein with repressor and activator activity:dna-binding protein rap1:sbf-c:repressor/activator site binding protein:tu1] [gn:rap1:grf1:n1310] [gctc:2.6.2.7:10.1:10.2:10.3:10.7:12.13:12.8] [keggtc:14.2]
CONTIG1882	823957_c3_8	3467	17570	426	142	YNL183C	266	5.0(10)-22	Saccharomyces cerevisiae	[ui:yn1183c] [pn:ser/thr protein kinase:nitrogen permease reactivator protein] [gn:rap1:n1631] [gctc:2.6.2.7:8.5.9.4:10.2:12.13:12.16] [ec:2.7.1.-] [keggtc:8.5.9.4] [sgdgc:1.2.2.8.8.0:1.5.0.0] [db:gic-saccharomyces cerevisiae]

CONTIG3963	23914686_f3_4	3468	17571	1692	564	YNL183C	986	1.8(10)-125	Saccharomyces cerevisiae	[ui:ynl183c] [pn:ser/hr protein kinase:nitrogen permease reactivator protein] [gn:npr1:nl631] [gctc:2.6:2.7:8.5:9.4:10.2:12.13:12.16] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:1.2:2.8.8.0:15.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG5149	10562550_c1_6	3469	17572	954	318	YNL103W	113	5.2(10)-11	Saccharomyces cerevisiae	[ui:ynl103w] [pn:transcriptional activator of sulfur metabolism:transcriptional activator of sulfur metabolism met4] [gn:met4:n2177] [gctc:2.6:2.7:10.1:10.2] [keggfc:14.2] [sgdfc:1.1.2:1.2.2.4.8.2:9.5.0] [db:gic-saccharomyces cerevis]
CONTIG4800	10276552_f2_1	3470	17573	960	320	YPL111W	822	4.7(10)-82	Saccharomyces cerevisiae	[ui:yp111w] [pn:arginase] [gn:car1:lp15w] [gctc:2.6:2.7:5.10:5.16:5.3:10.2] [ec:3.5.3.1] [keggfc:5.10:5.16] [sgdfc:1.1.4:1.2.2:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG1775	4094050_c3_2	3471	17574	378	126	YGR012W	203	6.4(10)-16	Saccharomyces cerevisiae	[ui:ygr012w] [pn:similarity to e.mitidians cysteine synthase:putative cysteine synthase:o-acetylserine sulfinydrylase:o- acetylserine:thiol-lyase:csase] [gctc:2.7:5.5:6.4:6.6] [ec:4.2.99.8] [keggfc:2.6:5.5:6.4] [sgdfc:1.1.1] [db:gic-sa

CONTIG5459	2361458_ft_1	3472	17575	840	280	YJRI30C	809	1.1(10)-80	Saccharomyces cerevisiae	[ui:yjrl30c] [pn:similarity to e nidulans cysteine synthase:putative cysteine synthase:o-acetylserine sulfhydrylase:o- acetylserine:thiol-lyase:csase] [gfc:2.7.5.6.4.6.6] [ec:4.2.99.8] [keggfc:2.6.5.5.6.4] [sgdfe:1.1.1] [db:gtc-sa]
CONTIG374	16502278_ft_1	3473	17576	798	266	YJRI30C	656	1.8(10)-64	Saccharomyces cerevisiae	[ui:yjrl30c] [pn:similarity to o- succinylhomoserine:putative cystathionine gamma-synthase:o- succinylhomoserine:thiol-lyase] [gn:j2063] [gfc:2.7.5.3.5.4.5.5.6.4.6.6] [ec:4.2.99.9] [keggfc:2.6.5.3.5.4.5.5.6.4] [sgdfe:1.1.1] [db:gtc-sa]
CONTIG3902	20113130_c1_9	3474	17577	213	71	YJRI30C	134	5.2(10)-8	Saccharomyces cerevisiae	[ui:yjrl30c] [pn:similarity to o- succinylhomoserine:putative cystathionine gamma-synthase:o- succinylhomoserine:thiol-lyase] [gn:j2063] [gfc:2.7.5.3.5.4.5.5.6.4.6.6] [ec:4.2.99.9] [keggfc:2.6.5.3.5.4.5.5.6.4] [sgdfe:1.1.1] [db:gtc-sa]
b9x11275.x	4195393_c3_4	3475	17578	510	170	YJRI30C	94	3.3(10)-5	Saccharomyces cerevisiae	[ui:yjrl30c] [pn:similarity to o- succinylhomoserine:putative cystathionine gamma-synthase:o- succinylhomoserine:thiol-lyase] [gn:j2063] [gfc:2.7.5.3.5.4.5.5.6.4.6.6] [ec:4.2.99.9] [keggfc:2.6.5.3.5.4.5.5.6.4] [sgdfe:1.1.1] [db:gtc-sa]

CONTIG5804	12929007_c1_48	3476	17579	1329	443	YLR303W	1533	2.1(10)-157	Saccharomyces cerevisiae	[ui:y/lr303w] [pn:o-acetylhomoserine sulphydrylase:oah sulphydrylase / o-acetylserine sulphydrylase:oas sulphydrylase] [gn:met17:met25:18003] [gicf:2.7.5.4:5.5:6.4:6.6] [keggfc:2.6:5.4:5.5:6.4] [sgdfc:1.1:9.2:0] [db:glc-saccharomyce
CONTIG5122	4035893_f3_3	3477	17580	804	268	YNL277W	357	2.1(10)-63	Saccharomyces cerevisiae	[ui:y/yl277w] [pn:homoserine o-acetyltransferase:homoserine o-trans- acetylase] [gn:met2:n0615] [gicf:2.7.5.4:6.6] [ec:2.3.1.31] [keggfc:2.6:5.4] [sgdfc:1.1:9.2:0] [db:glc-saccharomyces cerevisiae]
CONTIG5162	23445306_f2_2	3478	17581	1458	486	YDR402C	1109	1.8(10)-112	Saccharomyces cerevisiae	[ui:y/dr402c] [pn:cytochrome p450 56:cytochrome p450-dit2] [gn:dlt2:cyp56:d9509] [gicf:2.8.3.2:5.14:11.1:12.12:12.15] [ec:1.14.14.1] [keggfc:3.2:5.14] [sgdfc:3.4:0:9.1:0:11.3:0:11.4:0] [db:glc-saccharomyces cerevisiae]
CONTIG3996	10589592_f2_2	3479	17582	426	142	YDR402C	117	2.3(10)-6	Saccharomyces cerevisiae	[ui:y/dr402c] [pn:cytochrome p450 56:cytochrome p450-dit2] [gn:dlt2:cyp56:d9509] [gicf:2.8.3.2:5.14:11.1:12.12:12.15] [ec:1.14.14.1] [keggfc:3.2:5.14] [sgdfc:3.4:0:9.1:0:11.3:0:11.4:0] [db:glc-saccharomyces cerevisiae]

CONTIG5647	34020179_c1_11	3480	17583	234	78	YDR402C	163	2,6(10)-11	Saccharomyces cerevisiae	[ui:y/d402c] [pn:cytochrome p450 56:c:cytochrome p450-dit2] [gn:dl2:cyp56:d9509] [gicf:2.8:3.2:5.14:11.1:12.12:12.15] [ec:1.14.14.1] [keggfc:3.2:5.14] [sgdfc:3.4:0:9.1:0:1.3:0:1.4:0] [db:gic-saccharomyces cerevisiae]
CONTIG4384	861287_f3_5	3481	17584	1575	525	YHR007C	1782	8,6(10)-184	Saccharomyces cerevisiae	[ui:y/hr007c] [pn:cytochrome p450 lanosterol 14a-demethylase:cytochrome p450 11:14dm:lanosterol 14-alpha demethylase] [gn:erg11:cyp51:14dm] [gicf:2.8:3.2:3.4:5.14:8.1:8.2:12.12:12.16] [ec:1.14.14.1] [keggfc:3.2:5.14] [sgdfc:1.6.1:9.4.
CONTIG1870	24222802_f1_1	3482	17585	939	313	YLL057C	224	3,2(10)-17	Saccharomyces cerevisiae	[ui:y/ll057c] [pn:similarity to e.coli dioxygenase] [gicf:2.8:12.12] [keggfc:14.2] [sgdfc:11.3:0:11.4:0] [db:gic-saccharomyces cerevisiae]
CONTIG2070	24390875_f3_3	3483	17586	1293	431	YLL057C	348	7,9(10)-32	Saccharomyces cerevisiae	[ui:y/ll057c] [pn:similarity to e.coli dioxygenase] [gicf:2.8:12.12] [keggfc:14.2] [sgdfc:11.3:0:11.4:0] [db:gic-saccharomyces cerevisiae]
CONTIG5677	33390750_c3_26	3484	17587	1227	409	YLL057C	1020	4,9(10)-103	Saccharomyces cerevisiae	[ui:y/ll057c] [pn:similarity to e.coli dioxygenase] [gicf:2.8:12.12] [keggfc:14.2] [sgdfc:11.3:0:11.4:0] [db:gic-saccharomyces cerevisiae]
CONTIG5811	12923431_c1_25	3485	17588	1173	391	YLL057C	810	8,6(10)-81	Saccharomyces cerevisiae	[ui:y/ll057c] [pn:similarity to e.coli dioxygenase] [gicf:2.8:12.12] [keggfc:14.2] [sgdfc:11.3:0:11.4:0] [db:gic-saccharomyces cerevisiae]

CONTIG714	34252802_c1_3	3486	17589	393	131	YLL057C	337	1.2(10)-30	Saccharomyces cerevisiae	[ui:yll057c] [pn:similarity to e.coli dioxigenase] [gltc:2.8:12.12] [kegglc:14.2] [sgdgc:11.3:0:11.4:0] [db:gltc-saccharomyces cerevisiae]
CONTIG663	1047775_f1_1	3487	17590	696	232	YLL057C	445	4.2(10)-42	Saccharomyces cerevisiae	[ui:yll057c] [pn:similarity to e.coli dioxigenase] [gltc:2.8:12.12] [kegglc:14.2] [sgdgc:11.3:0:11.4:0] [db:gltc-saccharomyces cerevisiae]
CONTIG3969	4338280_f2_1	3488	17591	861	287	YMR015C	1058	4.5(10)-107	Saccharomyces cerevisiae	[ui:ymr015c] [pn:cytochrome p450:c-22 sterol desaturase] [gn:erg5:cyp61:ym9711] [gltc:2.8:3.4:8.1:8.2:12.12:16] [ec:1.14.14.-] [keggglc:14.1] [sgdgc:1.6:1:9.4:0:11.3:0:11.4:0] [db:gltc-saccharomyces cerevisiae]
CONTIG4915	4897175_f1_3	3489	17592	783	261	YMR015C	703	1.8(10)-69	Saccharomyces cerevisiae	[ui:ymr015c] [pn:cytochrome p450:c-22 sterol desaturase] [gn:erg5:cyp61:ym9711] [gltc:2.8:3.4:8.1:8.2:12.12:16] [ec:1.14.14.-] [keggglc:14.1] [sgdgc:1.6:1:9.4:0:11.3:0:11.4:0] [db:gltc-saccharomyces cerevisiae]
b3x16057.y	33751662_c3_4	3490	17593	765	255	YMR015C	672	3.7(10)-66	Saccharomyces cerevisiae	[ui:ymr015c] [pn:cytochrome p450:c-22 sterol desaturase] [gn:erg5:cyp61:ym9711] [gltc:2.8:3.4:8.1:8.2:12.12:16] [ec:1.14.14.-] [keggglc:14.1] [sgdgc:1.6:1:9.4:0:11.3:0:11.4:0] [db:gltc-saccharomyces cerevisiae]

CONTIG2335	9954125_c3_2	3491	17594	834	278	YAR035W	454	9.9(10)-43	Saccharomyces cerevisiae	[lui:yar035w] [pn:carnitine acetyltransferase, mitochondrial:putative mitochondrial carnitine o-acetyltransferase] [gn:yal1] [gicfc:2.8:5.2:12.2:12.6] [ec:2.3.1.7] [keggfc:5.2] [sgdfc:1.6:5.7:11.0:8.2:0.9:7.0] [db:gic-saccharomyces cer
CONTIG3931	12680325_f2_1	3492	17595	2013	671	YAR035W	841	3.1(10)-91	Saccharomyces cerevisiae	[lui:yar035w] [pn:carnitine acetyltransferase, mitochondrial:putative mitochondrial carnitine o-acetyltransferase] [gn:yal1] [gicfc:2.8:5.2:12.2:12.6] [ec:2.3.1.7] [keggfc:5.2] [sgdfc:1.6:5.7:11.0:8.2:0.9:7.0] [db:gic-saccharomyces cer
CONTIG457	480041_f3_1	3493	17596	789	263	YAR035W	482	5.0(10)-46	Saccharomyces cerevisiae	[lui:yar035w] [pn:carnitine acetyltransferase, mitochondrial:putative mitochondrial carnitine o-acetyltransferase] [gn:yal1] [gicfc:2.8:5.2:12.2:12.6] [ec:2.3.1.7] [keggfc:5.2] [sgdfc:1.6:5.7:11.0:8.2:0.9:7.0] [db:gic-saccharomyces cer
CONTIG2303	24226432_f1_1	3494	17597	924	308	YBL030C	957	2.2(10)-96	Saccharomyces cerevisiae	[lui:ybl030c] [pn:adp/atp carrier protein:mcf:adp/atp carrier protein 2:adp/atp translocase 2:adenine nucleotide translocator 2:ant 2] [gn:aac2:pet9:ybl0421] [gicfc:2.8:12.3] [keggfc:14.2] [sgdfc:1.3:7.7:6.0:8.2:0.9:7.0] [db:gic-saccha

CONTIG3611	7119027_f2_3	3495	17598	333	111	YBR091C	190	4.4(10)-15	Saccharomyces cerevisiae	[ui:ybr091c] [pn:mitochondrial biogenesis protein:mitochondrial regulator of splicing 5]
CONTIG3509	5274087_f3_5	3496	17599	678	226	YBR192W	312	5.2(10)-28	Saccharomyces cerevisiae	[ui:mms5:ybr0812] [gtcf:2.8] [kegfc:14.2] [sgdfc:8.2.0.9.7.0] [db:gtc-saccharomyces cerevisiae]
b9x12176.y	10819692_f2_2	3497	17600	279	93	YBR192W	361	3.2(10)-33	Saccharomyces cerevisiae	[ui:ybr192w] [pn:mitochondrial carrier protein:mc:mitochondrial carrier protein rim2] [gn:rim2:ybr1402] [gtcf:2.8:12.3] [kegfc:14.2] [sgdfc:2.5.0.7.6.0.8.2.0.9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5597	23437500_f1_1	3498	17601	882	294	YBR291C	1033	2.0(10)-104	Saccharomyces cerevisiae	[ui:ybr291c] [pn:citrate transport protein, mitochondrial:mc:putative mitochondrial carrier ybr291c] [gn:ctp1:ybr2039] [gtcf:2.8:12.2] [kegfc:14.2] [sgdfc:1.5.3.7.3.0.8.2.0.9.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5519	19960962_c2_8	3499	17602	2232	744	YER024W	657	1.3(10)-64	Saccharomyces cerevisiae	[ui:yer024w] [pn:similarity to carnitine o-acetyltransferase yat1p:hypothetical 103.3 kd protein in pro3-gcd1 intergenic region] [gtcf:2.8:12.2:12.6] [keggfc:14.2] [sgdfc:1.6:5.7:11.0:8.2:0] [db-gtc-saccharomyces cerevisiae]
CONTIG3626	36072182_c2_4	3500	17603	1020	340	YER053C	913	1.1(10)-91	Saccharomyces cerevisiae	[ui:yer053c] [pn:strong similarity to mitochondrial phosphate carrier protein:putative mitochondrial carrier yer053c] [gtcf:2.8:12.4:12.6:13.10] [keggfc:14.2] [sgdfc:1.4.3:1.8.2:7.2:3.8.2:0] [db-gtc-saccharomyces cerevisiae]
CONTIG5803	4722802_c1_25	3501	17604	1137	379	YGR028W	1022	3.0(10)-103	Saccharomyces cerevisiae	[ui:ygr028w] [pn:intra-mitochondrial sorting protein:msp1 protein:tat-binding homolog 4] [gn:msp1.yta4] [gtcf:2.8:10.7:11.1] [keggfc:14.2] [sgdfc:6.2:0:8.2:0:9:7.0] [db-gtc-saccharomyces cerevisiae]
CONTIG3874	31409627_c2_9	3502	17605	534	178	YGR082W	291	8.6(10)-26	Saccharomyces cerevisiae	[ui:ygr082w] [pn:mitochondrial outer membrane import receptor subunit, 20 kd:mitochondrial import receptor subunit tom20:mitochondrial 20 kd outer membrane protein:mas20 protein:translocase of outer membrane 20 kd subunit] [gn:tom20:ma

CONTIG4567	20422807_f3_4	3503	17606	783	261	YHR050W	629	1,3(10)-61	Saccharomyces cerevisiae	[ui:yn050w] [pn:suppressor of mitochondrial matrix mutant:transporter protein] [gn:sm2] [gic:2.8:1.1:12.6] [kegfc:14.2] [sgdfe:6.2:0.8:2.0:9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG1532	25554688_c2_4	3504	17607	1233	411	YHR117W	822	4,7(10)-82	Saccharomyces cerevisiae	[ui:yn117w] [pn:strong similarity to tom70p/mas70p:hypothetical 71.9 kd protein in cdc12-orc6 intergenic region] [gn:tom71] [gic:2.8] [kegfc:14.2] [sgdfe:8.2:0.9:7.0] [db:gic-saccharomyces cerevisiae]
CONTIG5759	20343942_c3_23	3505	17608	963	321	YIL134W	446	3,2(10)-42	Saccharomyces cerevisiae	[ui:yl134w] [pn:fad carrier protein:mc1, mitochondrial:mitochondrial fad carrier protein] [gn:fx1] [gic:2.8:12.6] [kegfc:14.2] [sgdfe:1.7:4.7.11:0.8:2.0:9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG2741	16805418_c2_9	3506	17609	348	116	YIL022W	345	1,6(10)-31	Saccharomyces cerevisiae	[ui:yl022w] [pn:mitochondrial inner membrane import receptor subunit:mitochondrial import inner membrane translocase subunit tim44 precursor:mitochondrial protein import protein 1:inner membrane import site protein 45:isp45:membrane i

CONTIG4344	1562_c1_7	3507	17610	447	149	YJL022W	265	1.1(10)-22	Saccharomyces cerevisiae	[ui:yjl022w] [pn:mitochondrial inner membrane import receptor subunit:mitochondrial import inner membrane translocase subunit tim44 precursor:mitochondrial protein import protein 1:inner membrane import site protein 45:isp45:membrane i
CONTIG2657	21595262_f1_2	3508	17611	513	171	YJL143W	575	7.0(10)-56	Saccharomyces cerevisiae	[ui:yjl143w] [pn:mitochondrial inner membrane import translocase subunit:mitochondrial import inner membrane translocase subunit tim17:mitochondrial protein import protein 2:mitochondrial inner membrane protein mim17] [gn:tim17:mp12:mi
CONTIG3799	23625277_c3_7	3509	17612	945	315	YJR077C	1082	1.3(10)-109	Saccharomyces cerevisiae	[ui:yjr077c] [pn:phosphate transport protein, mitochondrial:mc1:mitochondrial phosphate carrier protein:phosphate transport protein:mitochondrial import receptor:p32] [gn:mir1:j1837] [gcfc:2.8:12.4:13.10] [kegcfc:14.2] [sgdgc:1.4.3:1
CONTIG115	23525252_c2_1	3510	17613	780	260	YJL024C	1081	1.7(10)-109	Saccharomyces cerevisiae	[ui:yjl024c] [pn:heat shock protein of hsp70 family, cytosolic:heat shock protein ssa2] [gn:ssa2:10931] [gcfc:12.7:13.2] [kegcfc:14.2] [sgdgc:6.1:0.8:2.0:8.3:0.9:1.0:9.2:0.1 1.1.0] [db:gcfc-saccharomyces cerevisiae]

CONTIG3302	4767150_f2_1	3511	17614	696	232	YLL024C	974	3.7(10)-98	Saccharomyces cerevisiae	[ui:yll024c] [pn:heat shock protein of hsp70 family, cytosolic:heat shock protein ssa2] [gn:ssa2:10931] [gicfc:12.7:13.2] [keggfc:14.2] [sgdfe:6.1:0.8:2.0:8.3:0.9.1:0.9:2.0:1 1.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG4595	245275_c1_6	3512	17615	627	209	YLL024C	392	5.5(10)-36	Saccharomyces cerevisiae	[ui:yll024c] [pn:heat shock protein of hsp70 family, cytosolic:heat shock protein ssa2] [gn:ssa2:10931] [gicfc:12.7:13.2] [keggfc:14.2] [sgdfe:6.1:0.8:2.0:8.3:0.9.1:0.9:2.0:1 1.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG4595	35392500_g3_9	3513	17616	291	97	YLL024C	433	1.2(10)-40	Saccharomyces cerevisiae	[ui:yll024c] [pn:heat shock protein of hsp70 family, cytosolic:heat shock protein ssa2] [gn:ssa2:10931] [gicfc:12.7:13.2] [keggfc:14.2] [sgdfe:6.1:0.8:2.0:8.3:0.9.1:0.9:2.0:1 1.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG3436	35192193_g2_8	3514	17617	477	159	YLR034C	90	0.03599	Saccharomyces cerevisiae	[ui:ylr034c] [pn:strong similarity to smf2 protein] [gicfc:2.8] [keggfc:14.2] [sgdfe:8.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG5774	26424212_c1_21	3515	17618	741	247	YLR034C	602	9.5(10)-59	Saccharomyces cerevisiae	[ui:ylr034c] [pn:strong similarity to smf2 protein] [gicfc:2.8] [keggfc:14.2] [sgdfe:8.2.0] [db:gic-saccharomyces cerevisiae]

CONTIG5774	4944430_c3_35	3516	17619	921	307	YLR034C	659	8.8(10)-65	Saccharomyces cerevisiae	[ui:ylr034c] [pn:strong similarity to smf2 protein] [gicf:2.8] [keggf:14.2] [sgdfc:8.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG1263	9850016_f1_2	3517	17620	309	103	YLR295C	114	5.0(10)-7	Saccharomyces cerevisiae	[ui:ylr295c] [pn:fl10-ai-pase complex, subunit h] [gn:atp14] [gicf:2.8:12.6] [keggf:14.2] [sgdfc:1.8.2.5.0:7.8.0.8.2.0:9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG4198	269027_c2_7	3518	17621	942	314	YLR348C	762	1.1(10)-75	Saccharomyces cerevisiae	[ui:ylr348c] [pn:dicarboxylate carrier protein] [gicf:2.8:12.2:12.4:12.6:13.10] [keggf:14.2] [sgdfc:1.4.3:1.5.3:1.8.2.7.2.3:7.3.0.8.2.0:9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG4306	1367876_f3_2	3519	17622	267	89	YML042W	167	1.6(10)-11	Saccharomyces cerevisiae	[ui:yml042w] [pn:carnitine o-acetyltransferase:carnitine o-acetyltransferase precursor:carnitine acetylase] [gn:cat2:cat:yeat:ym8054] [gicf:2.8.3.4:5.2.8.1.8.2:12.2:12.6] [ec:2.3.1.7] [keggf:5.2] [sgdfc:1.6.1:8.2.0.8.4.0:9.7.0:9.8.0]
CONTIG2997	23828257_c2_3	3520	17623	1260	420	YMR203W	1211	2.7(10)-123	Saccharomyces cerevisiae	[ui:ymr203w] [pn:mitochondrial outer membrane import receptor subunit, 40 kd:mitochondrial import receptor subunit tom40:mitochondrial import-site-protein isp42:translocase of outer membrane 40 kd subunit] [gn:tom40:isp42:mom38:ym8325]

CONTIG1803	986632_ft_1	3521	17624	822	274	YMR301C	799	1.3(10)-79	Saccharomyces cerevisiae	[ui:ymr301c] [pn:atp-binding cassette transporter protein, mitochondrial:mitochondrial transporter atm1 precursor] [gn:atm1:mdy:ym9952] [gdcf:2.8:12.6] [kegfc:14.2] [sgdfe:7.9:0.8:2.0:9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG4293	33234452_c1_5	3522	17625	702	234	YMR301C	370	2.1(10)-33	Saccharomyces cerevisiae	[ui:ymr301c] [pn:atp-binding cassette transporter protein, mitochondrial:mitochondrial transporter atm1 precursor] [gn:atm1:mdy:ym9952] [gdcf:2.8:12.6] [kegfc:14.2] [sgdfe:7.9:0.8:2.0:9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG5759	16835932_c1_15	3523	17626	204	68	YNL070W	191	3.3(10)-15	Saccharomyces cerevisiae	[ui:ynl070w] [pn:mitochondrial outer membrane import receptor subunit, 7 kd:mitochondrial import receptor subunit tom7:translocase of outer membrane 7 kd subunit] [gn:tom7:mom7:n2378] [gdcf:2.8:10.7:11.1:12.6] [kegfc:14.2] [sgdfe:6.0]
CONTIG4156	6539567_c2_5	3524	17627	822	274	YNL064C	338	9.0(10)-31	Saccharomyces cerevisiae	[ui:ynl064c] [pn:mitochondrial and er import protein:mitochondrial protein import protein mas5:protein ydi1] [gn:mas5:ydi1:n2418:ynl2418c] [gdcf:2.8:12.10:12.16:12.8:13.2] [kegfc:14.2] [sgdfe:3.8:0.8:2.0:8.3:0.9:4.0:11.1.0] [db:gic-1] [db:gic-1]

CONTIG5691	6907502_g2_24	3525	17628	1194	398	YNL064C	1145	2.7(10)-116	Saccharomyces cerevisiae	[ui:ynl064c] [pn:mitochondrial and er import protein:mitochondrial protein import protein mas5:protein ydi1] [gn:mas5:ydi1:n2418:ynl2418c] [gtcf:2.8:12.10:12.16:12.8:13.2] [keggfc:14.2] [sgdfc:3.8:0.8:2.0:8.3:0.9:4.0:11.1.0] [db:gtc-]
CONTIG5753	21953556_f1_3	3526	17629	963	321	YNL064C	265	4.4(10)-45	Saccharomyces cerevisiae	[ui:ynl064c] [pn:mitochondrial and er import protein:mitochondrial protein import protein mas5:protein ydi1] [gn:mas5:ydi1:n2418:ynl2418c] [gtcf:2.8:12.10:12.16:12.8:13.2] [keggfc:14.2] [sgdfc:3.8:0.8:2.0:8.3:0.9:4.0:11.1.0] [db:gtc-]
bix19545.y	9774166_f3_2	3527	17630	582	194	YNL055C	428	2.6(10)-40	Saccharomyces cerevisiae	[ui:ynl055c] [pn:mitochondrial outer membrane porin:outer mitochondrial membrane protein porin:voltage-dependent anion-selective channel protein] [gn:omp2:vdac:por1:n2441:ynl2441c] [gtcf:2.8:12.6] [keggfc:14.2] [sgdfc:7.11:0.8:2.0:9.]
CONTIG5440	24035886_f3_11	3528	17631	675	225	YNR017W	614	5.0(10)-60	Saccharomyces cerevisiae	[ui:ynr017w] [pn:mitochondrial inner membrane import translocase subunit:mitochondrial import inner membrane translocase subunit tim23:mitochondrial protein import protein 3:mitochondrial protein import protein mas6:membrane import mac]

CONTIG3964	515700_c2_3	3529	17632	1614	538	YOR037W	288	6.5(10)-24	Saccharomyces cerevisiae	[ui:yor037w] [pn:cytochrome-c mitochondrial import factor:cytochrome c mitochondrial import factor cye2] [gn:cye2:or26] [gicf:2.8] [keggf:14.2] [sgdfe:8.2.0.9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG4142	14238135_c2_3	3530	17633	1080	360	YOR130C	98	0.019	Saccharomyces cerevisiae	[ui:yor130c] [pn:member of the mitochondrial carrier family:mc] [gn:arg11] [gicf:2.8:12.1] [keggf:14.2] [sgdfe:1.1.3:7.4.0.8.2.0.9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG4890	14629511_c2_7	3531	17634	939	313	YOR130C	469	1.2(10)-44	Saccharomyces cerevisiae	[ui:yor130c] [pn:member of the mitochondrial carrier family:mc] [gn:arg11] [gicf:2.8:12.1] [keggf:14.2] [sgdfe:1.1.3:7.4.0.8.2.0.9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG5518	33384662_f1_2	3532	17635	732	244	YOR232W	451	9.5(10)-43	Saccharomyces cerevisiae	[ui:yor232w] [pn:heat shock protein - chaperone:grpe protein homolog precursor] [gn:grpe1:grpe:ype1:mgel:o5099] [gicf:12.7] [keggf:14.2] [sgdfe:6.1.0.8.2.0.9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG5217	10735260_f3_7	3533	17636	900	300	YPL134C	866	1.0(10)-86	Saccharomyces cerevisiae	[ui:ypl134c] [pn:similarity to adp/aiap carrier proteins] [gicf:2.8:12.3] [keggf:14.2] [sgdfe:7.6.0.8.2.0] [db:gic-saccharomyces cerevisiae]

CONTIG546	892167_c3_5	3534	17637	1854	618	YPR021C	760	3.2(10)-83	Saccharomyces cerevisiae	[ui:yp021c] [pn:similarity to human citrate transporter protein] [gicf:2.8:12.2] [keggf:14.2] [sgdfc:1.5:3.7:3.0:8.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG5148	20742137_c1_6	3535	17638	1152	384	YPR058W	288	1.8(10)-25	Saccharomyces cerevisiae	[ui:yp058w] [pn:mitochondrial carrier protein:mcf:mitochondrial carrier protein precursor] [gn:ymc1] [gicf:2.8:12.6] [keggf:14.2] [sgdfc:7.1:0.8:2.0:9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG3294	1050437_c3_4	3536	17639	777	259	YPR058W	683	2.5(10)-67	Saccharomyces cerevisiae	[ui:yp058w] [pn:mitochondrial carrier protein:mcf:mitochondrial carrier protein precursor] [gn:ymc1] [gicf:2.8:12.6] [keggf:14.2] [sgdfc:7.1:0.8:2.0:9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG5768	4094812_f1_4	3537	17640	918	306	YPR058W	438	2.2(10)-41	Saccharomyces cerevisiae	[ui:yp058w] [pn:mitochondrial carrier protein:mcf:mitochondrial carrier protein precursor] [gn:ymc1] [gicf:2.8:12.6] [keggf:14.2] [sgdfc:7.1:0.8:2.0:9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG5371	21876430_f3_6	3538	17641	471	157	YAL039C	383	1.5(10)-35	Saccharomyces cerevisiae	[ui:yal039c] [pn:cytochrome c heme lyase:cch:holocytochrome-c synthase] [gn:cyc3] [gicf:2.8:9.10:9.12:10.7] [ec:4.4.1.17] [keggf:9.10] [sgdfc:1.7:2.6:3.0:9.7.0] [db:gic-saccharomyces cerevisiae]

CONTIG5332	4422036_f1_1	3539	17642	1845	615	YAL011W	147	9.0(10)-14	Saccharomyces cerevisiae	[ui:yal011w] [pn:protein of unknown function:hypothetical 74.1 kd protein in cys3-mdm10 intergenic region precursor] [gn:fun36] [gtcf:2.8] [keggfc:14.2] [sgdfc:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5332	26761063_f1_2	3540	17643	1728	576	YAL011W	163	7.5(10)-17	Saccharomyces cerevisiae	[ui:yal011w] [pn:protein of unknown function:hypothetical 74.1 kd protein in cys3-mdm10 intergenic region precursor] [gn:fun36] [gtcf:2.8] [keggfc:14.2] [sgdfc:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5503	25787775_f3_4	3541	17644	1563	521	YAL011W	108	0.01099	Saccharomyces cerevisiae	[ui:yal011w] [pn:protein of unknown function:hypothetical 74.1 kd protein in cys3-mdm10 intergenic region precursor] [gn:fun36] [gtcf:2.8] [keggfc:14.2] [sgdfc:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1672	14532750_c3_3	3542	17645	669	223	YAL010C	213	9.8(10)-17	Saccharomyces cerevisiae	[ui:yal010c] [pn:involved in mitochondrial morphology and inheritance:mitochondrial inheritance component mdm10] [gn:mdm10:fun37] [gtcf:2.8] [keggfc:14.2] [sgdfc:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG392	35173385_c2_3	3543	17646	843	281	YAL010C	274	4.5(10)-35	Saccharomyces cerevisiae	[ui:yal010c] [pn:involved in mitochondrial morphology and inheritance:mitochondrial inheritance component mdm10] [gn:mdm10:fun37] [gtcf:2.8] [keggfc:14.2] [sgdfc:9.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5043	6258567_c1_9	3544	17647	672	224	YBL038W	562	1.7(10)-54	Saccharomyces cerevisiae	[ui:ybl038w] [pn:ribosomal protein, mitochondrial;probable mitochondrial 60s ribosomal protein 116 precursor] [gn:mrp116:ml16:ybl0411] [gctc:2.8:10.4] [kegfc:14.2] [sgdfc:5.1.0:9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG5540	2239824_c1_13	3545	17648	2517	839	YBL022C	1039	2.3(10)-170	Saccharomyces cerevisiae	[ui:ybl022c] [pn:atp-dependent protease, mitochondrial;mitochondrial atp-dependent protease precursor] [gn:pim1:lon:ybl0440] [gctc:2.8:10.11:12.16] [ec:3.4.21.-] [kegfc:14.1] [sgdfc:6.4.0:6.5.3:9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG5197	25402150_f3_2	3546	17649	1074	358	YBL013W	291	7.2(10)-34	Saccharomyces cerevisiae	[ui:ybl013w] [pn:similarity to methionyl-trna formyltransferase;probable methionyl-trna formyltransferase precursor] [gn:ybl0313:ybl0311] [gctc:2.8:5.4:9.6:10.6] [ec:2.1.2.9] [kegfc:5.4:9.8:10.1] [sgdfc:4.6.0:9.7.0] [db:gic-saccharo
CONTIG1888	423567_c2_3	3547	17650	816	272	YBR003W	684	2.0(10)-67	Saccharomyces cerevisiae	[ui:ybr003w] [pn:hexaprenyl pyrophosphate synthetase precursor;hps] [gn:coq1:ybr0109] [gctc:2.8:3.1:7.1:9.10:9.11:9.12:11.3] [ec:2.5.1.-] [kegfc:7.2:9.13] [sgdfc:1.6:3.1:7.1:9.7.0] [db:gic-saccharomyces cerevisiae]

CONTIG2937	4350306_f2_2	3548	17651	552	184	YBR003W	324	2.7(10)-29	Saccharomyces cerevisiae	[ui:ybr003w] [pn:hexaprenyl pyrophosphate synthetase precursor:tps] [gn:cog1:ybr0109] [gctc:2.8:3.1:7.1:9.10:9.11:9.12:11.3] [ec:2.5.1.-] [keggfc:7.2:9.13] [sgdfe:1.6:3.1:7.1:9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG974	10634682_f2_1	3549	17652	342	114	YBR120C	200	3.7(10)-16	Saccharomyces cerevisiae	[ui:ybr120c] [pn:apo-cytochrome b pre-mrna processing protein:cytochrome b pre-mrna processing protein 6] [gn:cbp6:ybr0916] [gctc:2.8:10.7:10.9] [keggfc:14.2] [sgdfe:4.10.0:5.3:0:9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG4172	6850300_f2_1	3550	17653	648	216	YBR122C	144	3.2(10)-10	Saccharomyces cerevisiae	[ui:ybr122c] [pn:ribosomal protein yml36 precursor, mitochondrial:mitochondrial 60s ribosomal protein 136 precursor:yml36] [gn:mrp136:ybr0918] [gctc:2.8:10.4] [keggfc:14.2] [sgdfe:5.1.0:9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG1483	16847911_f3_1	3551	17654	450	150	YBR146W	429	2.1(10)-40	Saccharomyces cerevisiae	[ui:ybr146w] [pn:ribosomal protein s9 precursor, mitochondrial:probable mitochondrial 40s ribosomal protein s9 precursor] [gn:mrp9:ybr1123] [gctc:2.8:10.4] [keggfc:14.2] [sgdfe:5.1.0:9.7.0] [db:gic-saccharomyces cerevisiae]

CONTIG3627	11847287_f2_2	3552	17655	492	164	YBR185C	137	5.0(10)-9	Saccharomyces cerevisiae	[ui:ybr185c] [pn:respiratory chain assembly protein:mbal protein precursor] [gn:mbal:ybr1307] [gctc:2.8:12.16] [keggfc:14.2] [sgdfe:2.5:0.6:4.0:9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG3140	14977213_c1_3	3553	17656	807	269	YBR251W	203	1.8(10)-16	Saccharomyces cerevisiae	[ui:ybr251w] [pn:ribosomal protein s5, mitochondrial:probable mitochondrial 40s ribosomal protein s5] [gn:mpss:ybr1704] [gctc:2.8:10.4] [keggfc:14.2] [sgdfe:5.1:0.9:7.0] [db:gic-saccharomyces cerevisiae]
CONTIG5278	15678260_f1_3	3554	17657	534	178	YBR252W	492	4.4(10)-47	Saccharomyces cerevisiae	[ui:ybr252w] [pn:dutp pyrophosphatase precursor, mitochondrial:deoxyuridine 5"-triphosphate nucleotidohydrolase:dutpase:dutp pyrophosphatase] [gn:dut1:ybr1705] [gctc:2.8:4.2] [ec:3.6.1.23] [keggfc:4.2] [sgdfe:1.3:2.9:7.0] [db:gic-sac]
CONTIG2452	10582807_c1_4	3555	17658	381	127	YBR268W	180	5.0(10)-14	Saccharomyces cerevisiae	[ui:ybr268w] [pn:ribosomal protein yml37, mitochondrial:mitochondrial 60s ribosomal protein l37 precursor:yml37] [gn:mp137:ybr1736a] [gctc:2.8:10.4] [keggfc:14.2] [sgdfe:5.1:0.9:7.0] [db:gic-saccharomyces cerevisiae]

b3x13305.y	558192_c3_3	3556	17659	432	144	YBR282W	167	1.2(10)-12	Saccharomyces cerevisiae	[ui:ybr282w] [pn:ribosomal protein yml27 precursor, mitochondrial:mitochondrial 60s ribosomal protein 127 precursor:ym127] [gn:mrp127.ybr2019] [gdcf:2.8:10.4] [keggf:14.2] [sgdc:5.1:0.9:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4072	16850075_f2_1	3557	17660	279	93	YCL017C	387	5.7(10)-36	Saccharomyces cerevisiae	[ui:yel017c] [pn:involved in tna-processing and mitochondrial metabolism:nifs-like 54.5 kd protein] [gn:nfs1.spl1.yel17c] [gdcf:2.8:10.1:10.2:10.6] [keggf:14.2] [sgdc:4.5:0.9:5.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2311	593752_c3_6	3558	17661	1008	336	YCL017C	966	2.6(10)-97	Saccharomyces cerevisiae	[ui:yel017c] [pn:involved in tna-processing and mitochondrial metabolism:nifs-like 54.5 kd protein] [gn:nfs1.spl1.yel17c] [gdcf:2.8:10.1:10.2:10.6] [keggf:14.2] [sgdc:4.5:0.9:5.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3547	21640801_f3_2	3559	17662	645	215	YCR003W	186	1.2(10)-14	Saccharomyces cerevisiae	[ui:yel003w] [pn:ribosomal protein yml32, mitochondrial:mitochondrial 60s ribosomal protein 132 precursor:ym132] [gn:mrp132.yel3w.yel041] [gdcf:2.8:10.4] [keggf:14.2] [sgdc:5.1:0.9:7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4644	5907938_f3_5	3560	17663	528	176	YCR024C	399	3.1(10)-37	Saccharomyces cerevisiae	[ui:ycr024c] [pn:asn-trna synthetase, mitochondrial;probable asparaginyl-trna synthetase:asparagine-- trna ligase:asns] [gn:ycr24c:ycr242] [gtcf:2.8.5.2:10.6] [ec:6.1.1.22] [keggfc:5.2:10.1:10.2] [sgdfc:5.4.0:9.7.0] [db:gtc-saccharo
CONTIG5186	12772510_c3_20	3561	17664	987	329	YCR024C	612	8.4(10)-60	Saccharomyces cerevisiae	[ui:ycr024c] [pn:asn-trna synthetase, mitochondrial;probable asparaginyl-trna synthetase:asparagine-- trna ligase:asns] [gn:ycr24c:ycr242] [gtcf:2.8.5.2:10.6] [ec:6.1.1.22] [keggfc:5.2:10.1:10.2] [sgdfc:5.4.0:9.7.0] [db:gtc-saccharo
b3x15336.x	6664130_f2_1	3562	17665	297	99	YCR046C	91	0.00018	Saccharomyces cerevisiae	[ui:ycr046c] [pn:ribosomal protein, mitochondrial;hypothetical 19.4 kd protein in tsml-are1 intergenic region] [gn:pcr46:ycr46c] [gtcf:2.8:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.7.0] [db:gtc-saccharomyces cerevisiae]